



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:25 AM GMT

PDB ID : 3AL4
Title : Crystal structure of the swine-origin A (H1N1)-2009 influenza A virus hemagglutinin (HA) reveals similar antigenicity to that of the 1918 pandemic virus
Authors : Zhang, W.; Qi, J.X.; Shi, Y.; Li, Q.; Yan, J.H.; Gao, G.F.
Deposited on : 2010-07-22
Resolution : 2.87 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

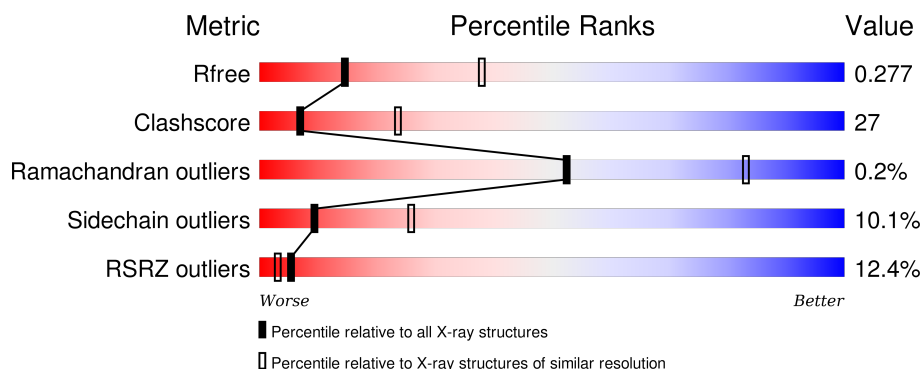
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.87 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1945 (2.90-2.86)
Clashscore	102246	2202 (2.90-2.86)
Ramachandran outliers	100387	2149 (2.90-2.86)
Sidechain outliers	100360	2152 (2.90-2.86)
RSRZ outliers	91569	1950 (2.90-2.86)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	333	<div> <div>9%</div> <div>54%</div> <div>36%</div> <div>6%</div> <div>.</div> </div>
1	C	333	<div> <div>8%</div> <div>52%</div> <div>41%</div> <div>.</div> <div>.</div> </div>
1	E	333	<div> <div>14%</div> <div>41%</div> <div>47%</div> <div>8%</div> <div>.</div> </div>
1	G	333	<div> <div>13%</div> <div>54%</div> <div>37%</div> <div>6%</div> <div>.</div> </div>
1	I	333	<div> <div>8%</div> <div>56%</div> <div>35%</div> <div>6%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
1	K	333	
2	B	181	
2	D	181	
2	F	181	
2	H	181	
2	J	181	
2	L	181	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NAG	C	607	-	-	-	X
3	NAG	L	601	-	-	X	X
4	NAG	A	602	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 23626 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	321	Total	C	N	O	S	0	0	0
			2505	1584	433	477	11			
1	C	321	Total	C	N	O	S	0	0	0
			2509	1586	433	479	11			
1	E	321	Total	C	N	O	S	0	0	0
			2509	1586	433	479	11			
1	G	321	Total	C	N	O	S	0	0	0
			2505	1584	433	477	11			
1	I	321	Total	C	N	O	S	0	0	0
			2509	1586	433	479	11			
1	K	321	Total	C	N	O	S	0	0	0
			2511	1588	433	479	11			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	ALA	-	EXPRESSION TAG	UNP C3W5S1
A	2	ASP	-	EXPRESSION TAG	UNP C3W5S1
A	3	LEU	-	EXPRESSION TAG	UNP C3W5S1
A	4	GLY	-	EXPRESSION TAG	UNP C3W5S1
A	5	SER	-	EXPRESSION TAG	UNP C3W5S1
A	6	ARG	-	EXPRESSION TAG	UNP C3W5S1
C	1	ALA	-	EXPRESSION TAG	UNP C3W5S1
C	2	ASP	-	EXPRESSION TAG	UNP C3W5S1
C	3	LEU	-	EXPRESSION TAG	UNP C3W5S1
C	4	GLY	-	EXPRESSION TAG	UNP C3W5S1
C	5	SER	-	EXPRESSION TAG	UNP C3W5S1
C	6	ARG	-	EXPRESSION TAG	UNP C3W5S1
E	1	ALA	-	EXPRESSION TAG	UNP C3W5S1
E	2	ASP	-	EXPRESSION TAG	UNP C3W5S1
E	3	LEU	-	EXPRESSION TAG	UNP C3W5S1
E	4	GLY	-	EXPRESSION TAG	UNP C3W5S1
E	5	SER	-	EXPRESSION TAG	UNP C3W5S1

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Chain	Residue	Modelled	Actual	Comment	Reference
E	6	ARG	-	EXPRESSION TAG	UNP C3W5S1
G	1	ALA	-	EXPRESSION TAG	UNP C3W5S1
G	2	ASP	-	EXPRESSION TAG	UNP C3W5S1
G	3	LEU	-	EXPRESSION TAG	UNP C3W5S1
G	4	GLY	-	EXPRESSION TAG	UNP C3W5S1
G	5	SER	-	EXPRESSION TAG	UNP C3W5S1
G	6	ARG	-	EXPRESSION TAG	UNP C3W5S1
I	1	ALA	-	EXPRESSION TAG	UNP C3W5S1
I	2	ASP	-	EXPRESSION TAG	UNP C3W5S1
I	3	LEU	-	EXPRESSION TAG	UNP C3W5S1
I	4	GLY	-	EXPRESSION TAG	UNP C3W5S1
I	5	SER	-	EXPRESSION TAG	UNP C3W5S1
I	6	ARG	-	EXPRESSION TAG	UNP C3W5S1
K	1	ALA	-	EXPRESSION TAG	UNP C3W5S1
K	2	ASP	-	EXPRESSION TAG	UNP C3W5S1
K	3	LEU	-	EXPRESSION TAG	UNP C3W5S1
K	4	GLY	-	EXPRESSION TAG	UNP C3W5S1
K	5	SER	-	EXPRESSION TAG	UNP C3W5S1
K	6	ARG	-	EXPRESSION TAG	UNP C3W5S1

- Molecule 2 is a protein called Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	162	Total	C	N	O	S	0	0	0
			1305	822	220	257	6			
2	D	162	Total	C	N	O	S	0	0	0
			1300	818	219	257	6			
2	F	161	Total	C	N	O	S	0	0	0
			1302	821	219	256	6			
2	H	162	Total	C	N	O	S	0	0	0
			1305	822	220	257	6			
2	J	162	Total	C	N	O	S	0	0	0
			1305	822	220	257	6			
2	L	161	Total	C	N	O	S	0	0	0
			1302	821	219	256	6			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	177	ARG	-	EXPRESSION TAG	UNP C3W5S1
B	178	LEU	-	EXPRESSION TAG	UNP C3W5S1
B	179	VAL	-	EXPRESSION TAG	UNP C3W5S1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	180	PRO	-	EXPRESSION TAG	UNP C3W5S1
B	181	ARG	-	EXPRESSION TAG	UNP C3W5S1
D	177	ARG	-	EXPRESSION TAG	UNP C3W5S1
D	178	LEU	-	EXPRESSION TAG	UNP C3W5S1
D	179	VAL	-	EXPRESSION TAG	UNP C3W5S1
D	180	PRO	-	EXPRESSION TAG	UNP C3W5S1
D	181	ARG	-	EXPRESSION TAG	UNP C3W5S1
F	177	ARG	-	EXPRESSION TAG	UNP C3W5S1
F	178	LEU	-	EXPRESSION TAG	UNP C3W5S1
F	179	VAL	-	EXPRESSION TAG	UNP C3W5S1
F	180	PRO	-	EXPRESSION TAG	UNP C3W5S1
F	181	ARG	-	EXPRESSION TAG	UNP C3W5S1
H	177	ARG	-	EXPRESSION TAG	UNP C3W5S1
H	178	LEU	-	EXPRESSION TAG	UNP C3W5S1
H	179	VAL	-	EXPRESSION TAG	UNP C3W5S1
H	180	PRO	-	EXPRESSION TAG	UNP C3W5S1
H	181	ARG	-	EXPRESSION TAG	UNP C3W5S1
J	177	ARG	-	EXPRESSION TAG	UNP C3W5S1
J	178	LEU	-	EXPRESSION TAG	UNP C3W5S1
J	179	VAL	-	EXPRESSION TAG	UNP C3W5S1
J	180	PRO	-	EXPRESSION TAG	UNP C3W5S1
J	181	ARG	-	EXPRESSION TAG	UNP C3W5S1
L	177	ARG	-	EXPRESSION TAG	UNP C3W5S1
L	178	LEU	-	EXPRESSION TAG	UNP C3W5S1
L	179	VAL	-	EXPRESSION TAG	UNP C3W5S1
L	180	PRO	-	EXPRESSION TAG	UNP C3W5S1
L	181	ARG	-	EXPRESSION TAG	UNP C3W5S1

- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	E	1	Total	C	N	O	0	0
			14	8	1	5		
3	E	1	Total	C	N	O	0	0
			14	8	1	5		
3	E	1	Total	C	N	O	0	0
			14	8	1	5		
3	F	1	Total	C	N	O	0	0
			14	8	1	5		
3	G	1	Total	C	N	O	0	0
			14	8	1	5		
3	G	1	Total	C	N	O	0	0
			14	8	1	5		
3	G	1	Total	C	N	O	0	0
			14	8	1	5		
3	K	1	Total	C	N	O	0	0
			14	8	1	5		
3	K	1	Total	C	N	O	0	0
			14	8	1	5		
3	K	1	Total	C	N	O	0	0
			14	8	1	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	K	1	Total	C	N	O	0	0
			14	8	1	5		
3	L	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	2	Total	C	N	O	0	0
			28	16	2	10		
4	A	2	Total	C	N	O	0	0
			28	16	2	10		
4	C	2	Total	C	N	O	0	0
			28	16	2	10		
4	E	2	Total	C	N	O	0	0
			28	16	2	10		
4	I	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 5 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	C	3	Total	C	N	O	0	0
			39	22	2	15		
5	I	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	36	Total	O	0	0
			36	36		
6	B	17	Total	O	0	0
			17	17		
6	C	38	Total	O	0	0
			38	38		
6	D	10	Total	O	0	0
			10	10		
6	E	31	Total	O	0	0
			31	31		
6	F	13	Total	O	0	0
			13	13		

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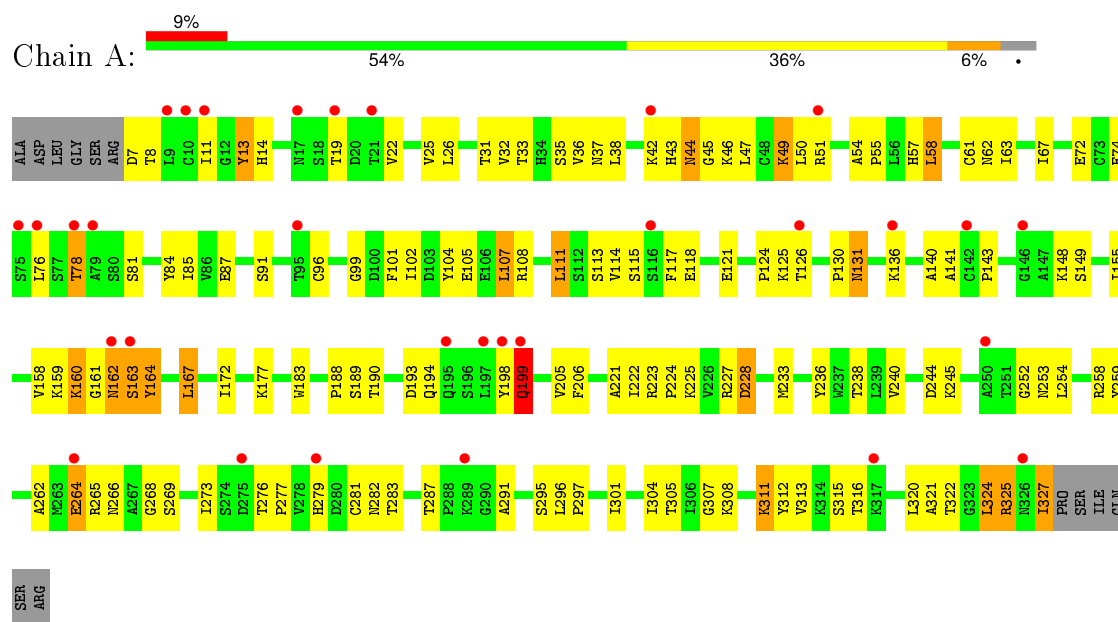
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	G	45	Total 45	O 45	0	0
6	H	23	Total 23	O 23	0	0
6	I	37	Total 37	O 37	0	0
6	J	21	Total 21	O 21	0	0
6	K	35	Total 35	O 35	0	0
6	L	11	Total 11	O 11	0	0

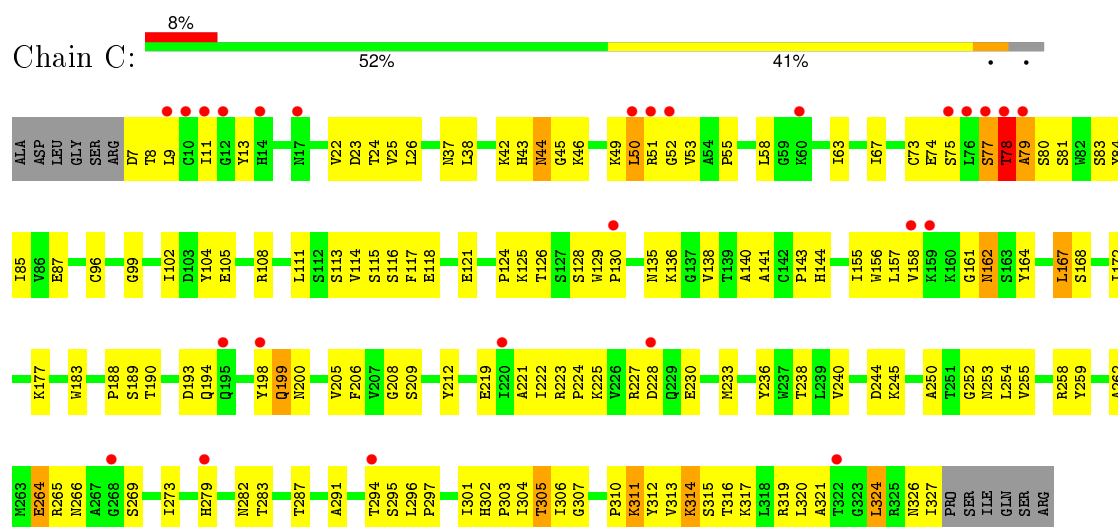
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

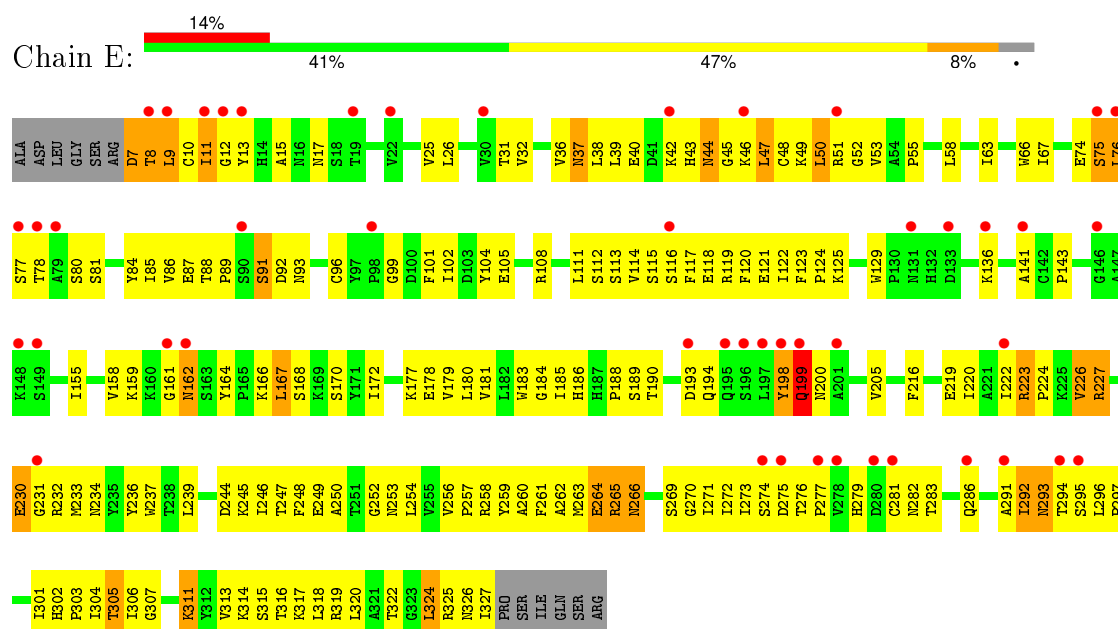
• Molecule 1: Hemagglutinin



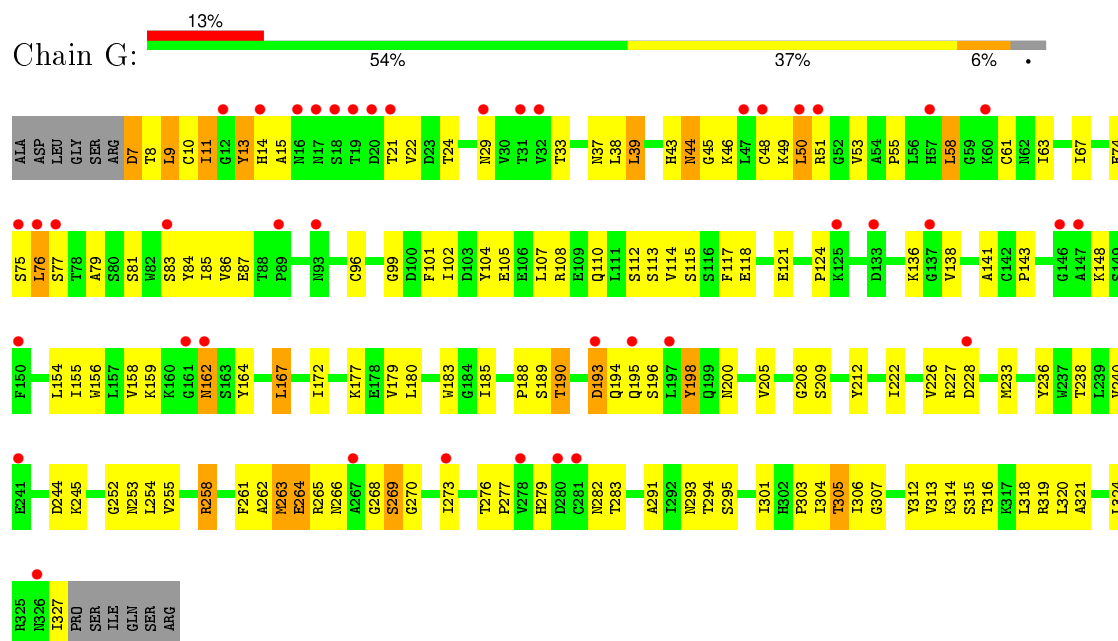
• Molecule 1: Hemagglutinin



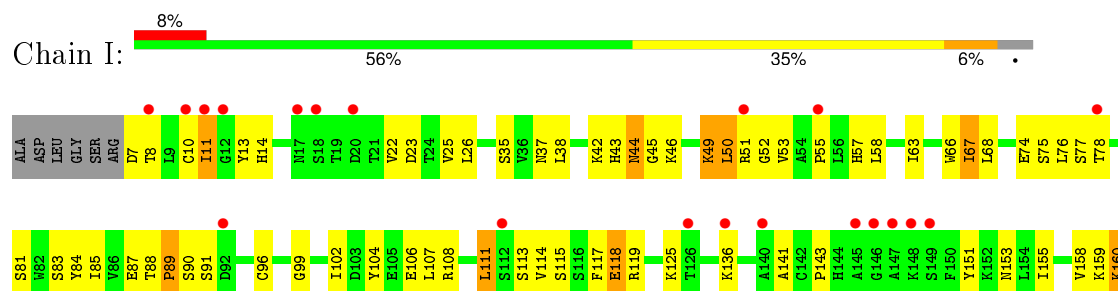
• Molecule 1: Hemagglutinin

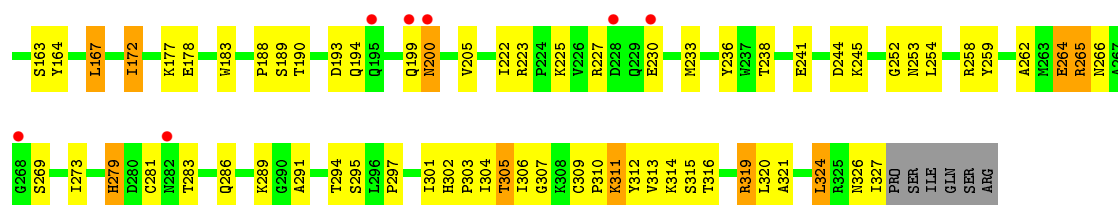


- Molecule 1: Hemagglutinin

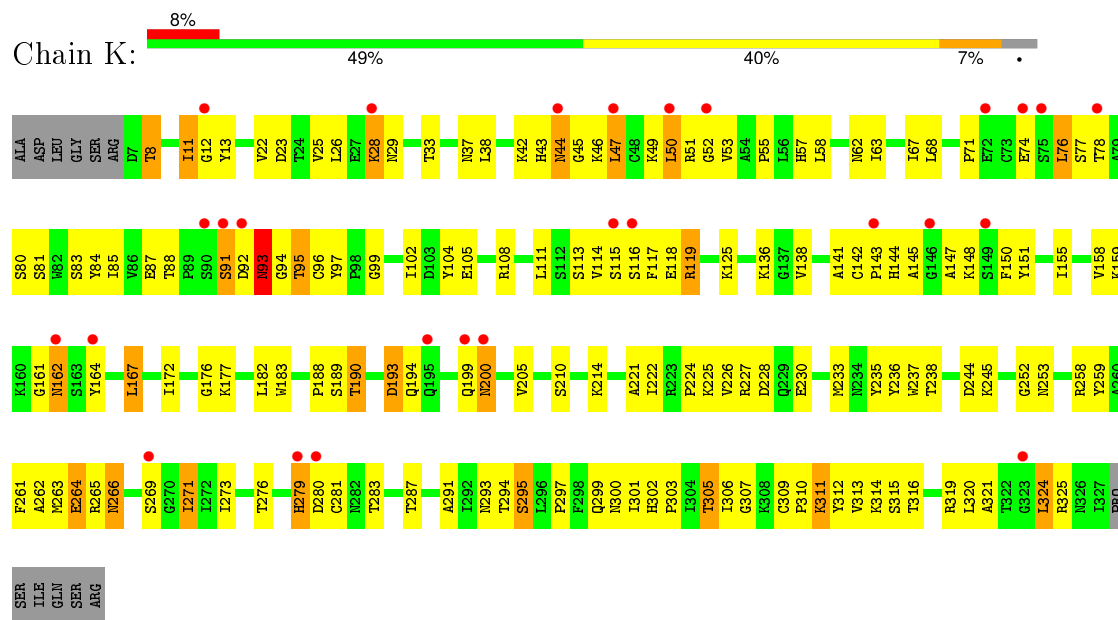


- Molecule 1: Hemagglutinin

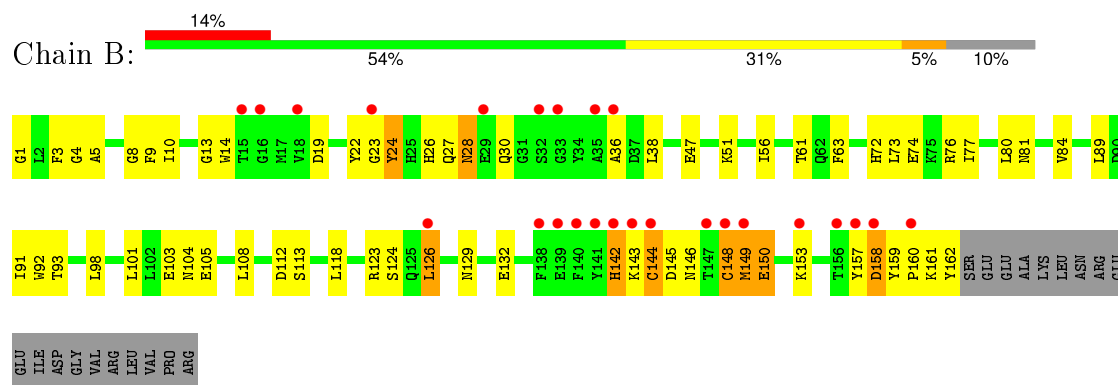




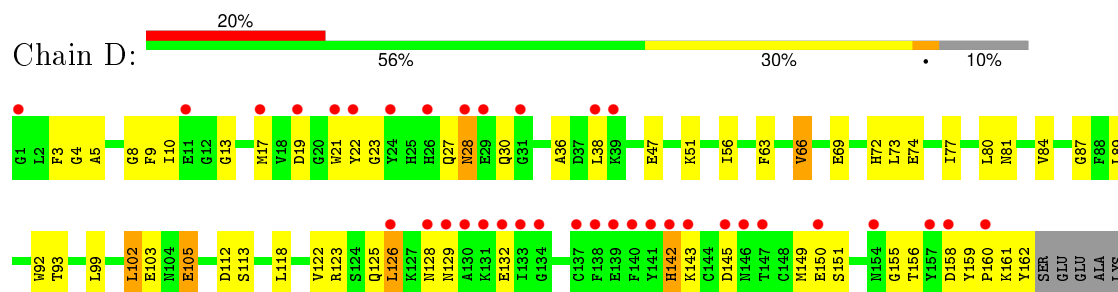
• Molecule 1: Hemagglutinin



• Molecule 2: Hemagglutinin



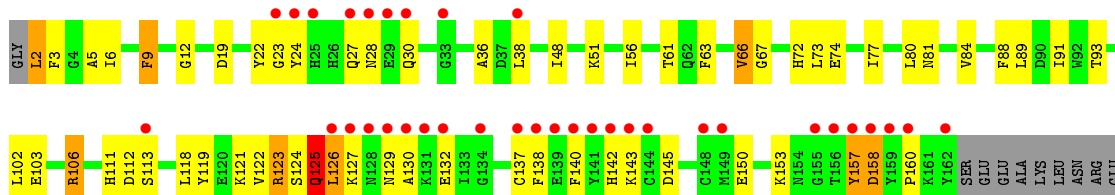
• Molecule 2: Hemagglutinin



LEU
ASN
ARG
GLU
GLU
ILE
ASP
GLY
VAL
LEU
LEU
VAL
PRO
ARG

• Molecule 2: Hemagglutinin

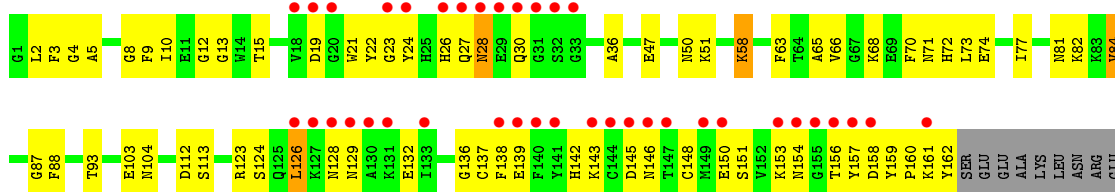
Chain F: 19% 55% 29% 11%



GLU
ILE
ASP
GLY
VAL
ARG
LEU
VAL
PRO
ARG

• Molecule 2: Hemagglutinin

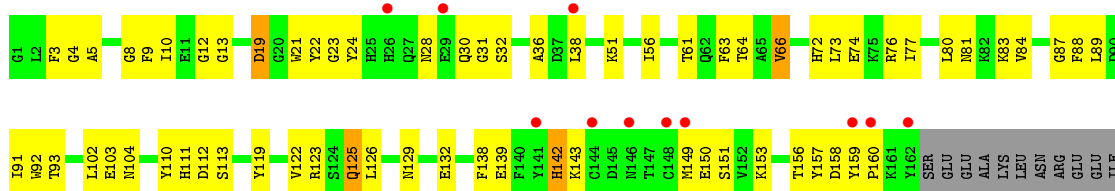
Chain H: 21% 51% 36% 10%



GLU
ILE
ASP
GLY
VAL
ARG
LEU
VAL
PRO
ARG

• Molecule 2: Hemagglutinin

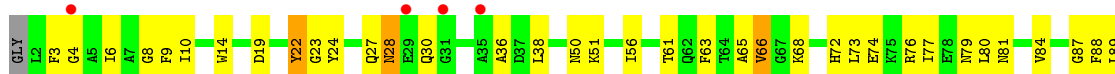
Chain J: 6% 52% 35% 10%

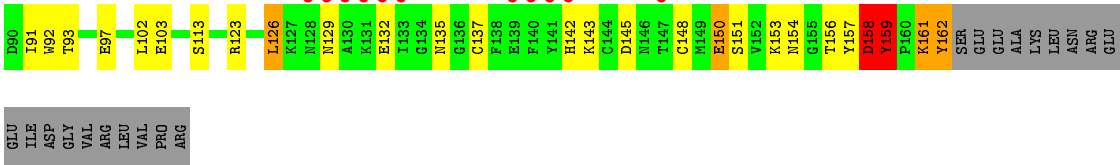


ASP
GLY
VAL
ARG
LEU
VAL
PRO
ARG

• Molecule 2: Hemagglutinin

Chain L: 8% 54% 30% 11%





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	66.02Å 115.19Å 114.98Å 62.31° 77.94° 81.05°	Depositor
Resolution (Å)	24.19 – 2.87 35.21 – 2.87	Depositor EDS
% Data completeness (in resolution range)	91.6 (24.19-2.87) 82.7 (35.21-2.87)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.53 (at 2.85Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.5_2)	Depositor
R, R_{free}	0.246 , 0.270 0.257 , 0.277	Depositor DCC
R_{free} test set	3293 reflections (5.36%)	DCC
Wilson B-factor (Å ²)	61.4	Xtriage
Anisotropy	0.127	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 70.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 64768 reflections	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	23626	wwPDB-VP
Average B, all atoms (Å ²)	81.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.06% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, NAG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.25	0/2568	0.56	5/3488 (0.1%)
1	C	0.26	0/2572	0.53	3/3493 (0.1%)
1	E	0.25	0/2572	0.62	7/3493 (0.2%)
1	G	0.26	0/2568	0.52	1/3488 (0.0%)
1	I	0.25	0/2572	0.51	3/3493 (0.1%)
1	K	0.28	0/2574	0.55	4/3497 (0.1%)
2	B	0.25	0/1333	0.43	0/1797
2	D	0.23	0/1328	0.38	0/1791
2	F	0.24	0/1330	0.45	1/1794 (0.1%)
2	H	0.25	0/1333	0.43	0/1797
2	J	0.25	0/1333	0.40	0/1797
2	L	0.28	0/1330	0.55	3/1794 (0.2%)
All	All	0.26	0/23413	0.52	27/31722 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	2
1	E	0	1
2	F	0	1
2	L	0	1
All	All	0	5

There are no bond length outliers.

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	226	VAL	O-C-N	-14.34	99.75	122.70
1	A	199	GLN	N-CA-CB	-11.55	89.81	110.60
2	L	159	TYR	N-CA-CB	-11.34	90.19	110.60
1	E	76	LEU	N-CA-CB	-10.33	89.75	110.40
1	E	226	VAL	CA-C-N	9.25	137.55	117.20
2	L	158	ASP	CB-CA-C	-9.12	92.16	110.40
1	A	198	TYR	N-CA-C	-8.63	87.71	111.00
1	E	226	VAL	C-N-CA	8.52	143.00	121.70
1	G	269	SER	CB-CA-C	-7.88	95.12	110.10
1	I	200	ASN	N-CA-CB	7.43	123.98	110.60
1	C	79	ALA	N-CA-CB	-7.41	99.72	110.10
1	A	51	ARG	N-CA-C	-7.37	91.11	111.00
1	K	92	ASP	N-CA-C	7.32	130.77	111.00
1	E	76	LEU	N-CA-C	7.26	130.60	111.00
1	A	51	ARG	N-CA-CB	-7.26	97.53	110.60
1	I	200	ASN	N-CA-C	-7.15	91.68	111.00
1	K	93	ASN	N-CA-CB	7.12	123.41	110.60
1	E	75	SER	N-CA-C	6.77	129.28	111.00
1	K	200	ASN	N-CA-C	-6.63	93.10	111.00
1	K	200	ASN	N-CA-CB	6.49	122.29	110.60
2	L	159	TYR	N-CA-C	5.84	126.77	111.00
1	C	199	GLN	CB-CA-C	-5.71	98.99	110.40
1	I	89	PRO	N-CA-C	-5.50	97.80	112.10
1	E	78	THR	N-CA-C	-5.49	96.19	111.00
1	C	79	ALA	N-CA-C	5.28	125.25	111.00
2	F	157	TYR	N-CA-C	-5.25	96.82	111.00
1	A	199	GLN	N-CA-C	5.08	124.70	111.00

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	73	CYS	Peptide
1	C	77	SER	Peptide
1	E	226	VAL	Mainchain
2	F	125	GLN	Peptide
2	L	159	TYR	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2505	0	2442	156	0
1	C	2509	0	2447	133	3
1	E	2509	0	2449	213	0
1	G	2505	0	2443	141	0
1	I	2509	0	2450	136	0
1	K	2511	0	2454	164	3
2	B	1305	0	1228	71	0
2	D	1300	0	1216	54	0
2	F	1302	0	1224	70	0
2	H	1305	0	1228	92	0
2	J	1305	0	1228	77	0
2	L	1302	0	1225	73	0
3	A	28	0	26	0	0
3	C	28	0	26	3	0
3	E	42	0	39	2	0
3	F	14	0	13	0	0
3	G	42	0	39	3	0
3	K	56	0	52	9	0
3	L	14	0	13	10	0
4	A	56	0	50	13	0
4	C	28	0	25	2	0
4	E	28	0	25	3	0
4	I	28	0	25	5	0
5	C	39	0	34	3	0
5	I	39	0	34	3	0
6	A	36	0	0	19	0
6	B	17	0	0	11	0
6	C	38	0	0	15	0
6	D	10	0	0	2	0
6	E	31	0	0	10	0
6	F	13	0	0	4	0
6	G	45	0	0	25	0
6	H	23	0	0	13	0
6	I	37	0	0	21	0
6	J	21	0	0	7	0
6	K	35	0	0	15	0
6	L	11	0	0	2	0
All	All	23626	0	22435	1215	3

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 27.

All (1215) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:17:ASN:HD21	3:E:601:NAG:C1	1.30	1.42
1:E:7:ASP:HA	2:F:27:GLN:O	1.37	1.21
1:E:66:TRP:HE1	1:E:77:SER:HB2	1.08	1.14
4:A:603:NAG:O7	1:K:280:ASP:OD1	1.65	1.14
1:C:282:ASN:OD1	3:C:607:NAG:O7	1.67	1.13
1:A:32:VAL:HA	6:A:338:HOH:O	1.44	1.13
1:K:52:GLY:HA3	3:K:603:NAG:H4	1.31	1.10
6:J:295:HOH:O	2:L:68:LYS:HD2	1.51	1.09
1:A:282:ASN:ND2	4:A:604:NAG:H61	1.68	1.08
1:I:66:TRP:HE3	6:I:353:HOH:O	1.37	1.07
1:G:320:LEU:HG	6:G:342:HOH:O	1.56	1.05
1:A:143:PRO:HA	6:A:341:HOH:O	1.57	1.03
1:G:327:ILE:HG12	6:G:338:HOH:O	1.56	1.02
1:G:155:ILE:HG13	1:G:258:ARG:HG3	1.41	1.02
1:A:19:THR:HB	3:L:601:NAG:H5	1.42	1.01
1:E:307:GLY:HA2	2:F:63:PHE:CE1	1.95	1.01
1:G:58:LEU:HA	1:G:76:LEU:HD11	1.41	1.00
1:E:177:LYS:HE3	1:E:264:GLU:OE2	1.62	1.00
1:E:49:LYS:O	1:E:283:THR:HG22	1.61	0.99
1:I:172:ILE:HD12	1:I:245:LYS:HB3	1.41	0.98
6:G:334:HOH:O	2:H:13:GLY:HA2	1.64	0.95
1:E:143:PRO:HD2	4:E:602:NAG:H83	1.43	0.95
1:E:164:TYR:CZ	1:E:252:GLY:HA2	2.02	0.94
1:E:113:SER:HB2	1:E:269:SER:CB	1.96	0.94
1:E:141:ALA:O	1:E:227:ARG:NH1	2.00	0.94
1:G:269:SER:OG	1:G:270:GLY:N	1.94	0.93
1:G:9:LEU:HD22	1:G:10:CYS:H	1.33	0.92
1:A:322:THR:HG23	6:A:349:HOH:O	1.68	0.92
1:I:83:SER:HB3	6:I:338:HOH:O	1.69	0.92
1:C:282:ASN:CG	3:C:607:NAG:O7	2.09	0.91
1:E:43:HIS:HB3	1:E:301:ILE:HD13	1.52	0.91
1:C:198:TYR:O	1:C:199:GLN:HB3	1.70	0.91
2:H:123:ARG:NH1	2:J:123:ARG:HH22	1.69	0.90
1:I:160:LYS:HG3	1:I:160:LYS:O	1.72	0.90
5:I:602:NAG:H61	5:I:603:BMA:O5	1.72	0.90
1:I:8:THR:HG22	2:J:139:GLU:HA	1.54	0.89
1:E:183:TRP:CE2	1:E:236:TYR:HB2	2.07	0.89
1:E:96:CYS:O	1:E:227:ARG:HD3	1.74	0.88
1:C:199:GLN:HG3	1:C:199:GLN:O	1.72	0.88
2:H:158:ASP:C	2:H:160:PRO:HD3	1.94	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:66:TRP:NE1	1:E:77:SER:HB2	1.89	0.87
1:I:153:ASN:HA	6:I:361:HOH:O	1.75	0.87
1:K:23:ASP:OD2	3:K:602:NAG:C8	2.23	0.86
1:K:312:TYR:HD1	6:K:362:HOH:O	1.57	0.86
1:C:240:VAL:HG23	6:C:359:HOH:O	1.74	0.86
1:I:66:TRP:CE3	6:I:353:HOH:O	2.18	0.86
2:D:161:LYS:HB3	6:D:187:HOH:O	1.74	0.86
1:I:259:TYR:HD1	6:I:361:HOH:O	1.59	0.86
1:I:114:VAL:HG11	1:I:117:PHE:HB2	1.57	0.86
2:H:124:SER:HB3	6:H:188:HOH:O	1.74	0.85
1:C:114:VAL:HG11	1:C:117:PHE:HB2	1.58	0.85
1:C:313:VAL:HG12	1:C:315:SER:H	1.42	0.85
1:K:114:VAL:HG11	1:K:117:PHE:HB2	1.59	0.85
2:B:105:GLU:HB2	6:B:190:HOH:O	1.75	0.85
1:G:179:VAL:HG13	6:G:373:HOH:O	1.75	0.84
1:A:62:ASN:HB3	6:A:339:HOH:O	1.76	0.84
1:A:19:THR:CG2	3:L:601:NAG:O6	2.25	0.83
1:A:159:LYS:HD3	1:A:199:GLN:H	1.41	0.83
1:A:25:VAL:HG23	6:B:190:HOH:O	1.77	0.83
1:K:313:VAL:HG12	1:K:315:SER:H	1.44	0.82
1:E:313:VAL:HG12	1:E:315:SER:H	1.44	0.82
1:A:325:ARG:HA	6:A:338:HOH:O	1.78	0.82
1:A:160:LYS:NZ	1:A:161:GLY:HA3	1.95	0.82
1:I:313:VAL:HG12	1:I:315:SER:H	1.44	0.82
1:E:48:CYS:CB	1:E:281:CYS:SG	2.67	0.81
1:G:327:ILE:HG21	6:H:184:HOH:O	1.78	0.81
1:E:7:ASP:CA	2:F:27:GLN:O	2.26	0.81
2:B:160:PRO:HD2	2:B:161:LYS:HG3	1.61	0.81
1:G:11:ILE:HD13	1:G:11:ILE:O	1.80	0.81
1:A:313:VAL:HG12	1:A:315:SER:H	1.44	0.81
1:E:11:ILE:HD12	2:F:119:TYR:HA	1.63	0.81
1:C:143:PRO:HD2	4:C:605:NAG:H83	1.63	0.81
1:E:223:ARG:HD3	1:E:232:ARG:HG2	1.63	0.80
1:G:313:VAL:HG12	1:G:315:SER:H	1.44	0.80
2:H:47:GLU:HB3	1:K:26:LEU:HB3	1.63	0.80
1:E:172:ILE:HD12	1:E:245:LYS:HB3	1.63	0.80
2:H:123:ARG:HH22	2:L:123:ARG:HH12	1.26	0.80
1:C:168:SER:HB3	1:K:176:GLY:HA2	1.62	0.79
1:K:312:TYR:CD1	6:K:362:HOH:O	2.32	0.79
1:A:114:VAL:HG11	1:A:117:PHE:HB2	1.63	0.78
6:I:365:HOH:O	1:K:214:LYS:HG3	1.82	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:319:ARG:HH11	1:I:319:ARG:CG	1.96	0.78
2:H:12:GLY:HA2	6:H:184:HOH:O	1.82	0.78
1:E:167:LEU:HD22	1:E:250:ALA:HB3	1.63	0.78
1:E:178:GLU:OE1	1:E:265:ARG:NH1	2.17	0.78
1:E:66:TRP:HE1	1:E:77:SER:CB	1.92	0.78
1:A:19:THR:HG21	3:L:601:NAG:O6	1.84	0.77
1:K:52:GLY:CA	3:K:603:NAG:H4	2.13	0.77
1:G:327:ILE:HG22	6:G:337:HOH:O	1.83	0.77
1:G:58:LEU:HA	1:G:76:LEU:CD1	2.12	0.77
1:K:293:ASN:ND2	3:K:604:NAG:O7	2.16	0.77
1:E:38:LEU:HD11	1:E:320:LEU:HD22	1.65	0.77
1:G:86:VAL:HG23	6:G:350:HOH:O	1.83	0.77
1:A:81:SER:HB3	1:A:115:SER:O	1.84	0.77
1:A:126:THR:HA	6:A:367:HOH:O	1.84	0.77
1:K:183:TRP:CE3	6:K:343:HOH:O	2.36	0.77
1:G:141:ALA:O	1:G:143:PRO:HD3	1.85	0.77
1:A:149:SER:N	6:A:341:HOH:O	2.18	0.77
1:C:254:LEU:HD22	6:C:354:HOH:O	1.85	0.76
1:A:36:VAL:HG22	6:A:349:HOH:O	1.84	0.76
1:K:324:LEU:HD23	1:K:324:LEU:N	2.00	0.76
1:G:255:VAL:HG12	6:G:346:HOH:O	1.85	0.76
1:G:38:LEU:HD11	1:G:320:LEU:HD22	1.67	0.76
1:I:68:LEU:O	1:I:151:TYR:HB3	1.87	0.75
1:G:11:ILE:HG12	2:H:10:ILE:HD13	1.67	0.75
1:K:144:HIS:O	1:K:147:ALA:HB3	1.87	0.75
1:G:185:ILE:HD11	6:G:356:HOH:O	1.86	0.75
1:G:305:THR:H	2:H:66:VAL:HB	1.52	0.75
1:E:125:LYS:HG3	1:E:258:ARG:HH11	1.49	0.75
2:H:123:ARG:HH22	2:L:123:ARG:NH1	1.83	0.75
2:H:158:ASP:O	2:H:160:PRO:HD3	1.87	0.75
1:K:305:THR:H	2:L:66:VAL:HG13	1.50	0.75
2:B:23:GLY:HA3	2:B:36:ALA:HA	1.69	0.74
1:E:113:SER:HB2	1:E:269:SER:HB3	1.69	0.74
1:G:177:LYS:HB2	1:G:263:MET:O	1.88	0.74
2:J:153:LYS:HB2	6:J:210:HOH:O	1.88	0.74
1:A:47:LEU:HD21	1:A:276:THR:HB	1.69	0.73
1:K:102:ILE:HG13	1:K:236:TYR:CE2	2.23	0.73
1:E:88:THR:O	1:E:91:SER:OG	2.06	0.73
1:K:311:LYS:HG2	2:L:92:TRP:CE2	2.24	0.73
1:E:113:SER:HB2	1:E:269:SER:HB2	1.69	0.73
1:G:156:TRP:CE3	6:G:369:HOH:O	2.40	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:313:VAL:HG13	2:L:93:THR:HA	1.70	0.73
1:E:164:TYR:CE2	1:E:252:GLY:HA2	2.23	0.72
1:E:311:LYS:HE2	2:F:61:THR:HG22	1.69	0.72
1:K:266:ASN:H	1:K:266:ASN:ND2	1.87	0.72
1:E:168:SER:HA	1:E:248:PHE:O	1.89	0.72
1:K:23:ASP:OD2	3:K:602:NAG:H81	1.88	0.72
1:I:141:ALA:O	1:I:143:PRO:HD3	1.90	0.72
1:E:125:LYS:CG	1:E:258:ARG:HH11	2.03	0.72
2:H:123:ARG:HH11	2:J:123:ARG:HH22	1.35	0.72
1:E:7:ASP:O	2:F:140:PHE:HD1	1.71	0.71
1:G:141:ALA:O	1:G:227:ARG:NH1	2.22	0.71
2:H:157:TYR:CE1	6:H:186:HOH:O	2.43	0.71
1:C:199:GLN:O	1:C:199:GLN:CG	2.38	0.71
1:K:23:ASP:OD2	3:K:602:NAG:H82	1.89	0.71
1:K:182:LEU:HA	6:K:343:HOH:O	1.89	0.71
1:G:11:ILE:HD11	2:H:136:GLY:HA3	1.72	0.71
1:C:317:LYS:NZ	5:C:602:NAG:H83	2.06	0.71
1:I:258:ARG:HB3	6:I:361:HOH:O	1.91	0.70
1:I:311:LYS:HG2	2:J:92:TRP:CE2	2.26	0.70
1:G:63:ILE:HD11	1:G:85:ILE:HG21	1.72	0.70
1:E:125:LYS:HB2	1:E:258:ARG:NH1	2.05	0.70
1:C:102:ILE:HG13	1:C:236:TYR:CE2	2.26	0.70
1:G:55:PRO:HB2	6:G:350:HOH:O	1.92	0.70
1:E:125:LYS:HB2	1:E:258:ARG:HH12	1.56	0.70
1:E:87:GLU:O	1:E:273:ILE:HA	1.92	0.70
1:E:189:SER:CB	1:E:230:GLU:HB2	2.22	0.70
1:E:317:LYS:HA	6:E:356:HOH:O	1.92	0.69
1:G:188:PRO:HG2	1:G:194:GLN:NE2	2.07	0.69
1:C:8:THR:OG1	2:D:27:GLN:HB3	1.92	0.69
1:E:50:LEU:O	1:E:283:THR:O	2.11	0.69
1:E:292:ILE:HD11	1:E:301:ILE:HD12	1.74	0.69
1:C:188:PRO:HG2	1:C:194:GLN:NE2	2.08	0.69
2:B:108:LEU:N	6:B:193:HOH:O	2.20	0.69
1:G:138:VAL:HB	1:G:148:LYS:O	1.93	0.69
6:G:370:HOH:O	2:H:15:THR:HG22	1.93	0.69
1:A:258:ARG:HE	1:A:259:TYR:HE1	1.41	0.69
1:K:258:ARG:HE	1:K:259:TYR:HE1	1.41	0.69
1:K:237:TRP:HA	6:K:343:HOH:O	1.91	0.68
1:G:29:ASN:OD1	3:G:602:NAG:N2	2.26	0.68
1:G:305:THR:HG22	2:H:66:VAL:HG23	1.75	0.68
2:F:118:LEU:O	2:F:122:VAL:HG13	1.94	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:324:LEU:HB3	2:J:111:HIS:CG	2.28	0.68
1:G:7:ASP:O	2:H:139:GLU:HA	1.92	0.68
1:C:317:LYS:HZ1	5:C:602:NAG:H83	1.59	0.68
1:G:55:PRO:HB3	1:G:84:TYR:CZ	2.27	0.68
1:K:141:ALA:O	1:K:143:PRO:HD3	1.93	0.68
1:C:63:ILE:HD11	1:C:85:ILE:HG21	1.76	0.67
1:E:188:PRO:HG2	1:E:194:GLN:NE2	2.09	0.67
1:A:107:LEU:HD22	1:A:111:LEU:HD22	1.76	0.67
1:A:31:THR:O	6:A:338:HOH:O	2.10	0.67
1:K:78:THR:HG22	1:K:78:THR:O	1.94	0.67
1:I:188:PRO:HG2	1:I:194:GLN:NE2	2.08	0.67
1:E:39:LEU:HB2	1:E:318:LEU:HB2	1.77	0.67
1:E:47:LEU:HD13	1:E:276:THR:HG21	1.76	0.67
1:K:8:THR:OG1	2:L:27:GLN:HB3	1.95	0.67
1:K:324:LEU:HD23	1:K:324:LEU:H	1.57	0.67
1:E:63:ILE:HD11	1:E:85:ILE:HG21	1.76	0.67
1:A:188:PRO:HG2	1:A:194:GLN:NE2	2.09	0.67
1:C:46:LYS:HE2	1:C:279:HIS:CE1	2.30	0.67
1:G:164:TYR:HB3	6:G:366:HOH:O	1.95	0.67
1:A:311:LYS:HG2	2:B:92:TRP:CE2	2.30	0.66
2:B:146:ASN:O	2:B:149:MET:HB2	1.95	0.66
1:I:319:ARG:HG2	1:I:319:ARG:HH11	1.61	0.66
1:G:49:LYS:O	1:G:283:THR:HG22	1.96	0.66
1:I:44:ASN:HD21	1:I:291:ALA:H	1.44	0.66
1:I:241:GLU:HG2	6:I:369:HOH:O	1.94	0.66
1:K:63:ILE:HD11	1:K:85:ILE:HG21	1.76	0.66
1:A:63:ILE:HD11	1:A:85:ILE:HG21	1.75	0.66
1:G:11:ILE:HG12	2:H:10:ILE:CD1	2.26	0.66
1:C:24:THR:HB	2:D:105:GLU:HB2	1.76	0.66
1:A:159:LYS:HE2	1:A:199:GLN:HG2	1.78	0.66
1:K:177:LYS:HE3	1:K:264:GLU:OE2	1.95	0.66
1:E:48:CYS:HB3	1:E:281:CYS:SG	2.36	0.66
1:A:164:TYR:CE1	1:A:252:GLY:HA2	2.31	0.66
1:C:188:PRO:HG2	1:C:194:GLN:HE21	1.61	0.66
1:E:183:TRP:CE2	1:E:236:TYR:CB	2.78	0.65
1:G:102:ILE:HG13	1:G:236:TYR:CE2	2.32	0.65
1:G:155:ILE:CG1	1:G:258:ARG:HG3	2.22	0.65
1:C:198:TYR:CZ	1:C:253:ASN:HA	2.31	0.65
1:I:199:GLN:O	1:I:200:ASN:OD1	2.13	0.65
1:A:125:LYS:HB2	1:A:258:ARG:NH1	2.10	0.65
1:I:289:LYS:HE2	1:I:301:ILE:HG23	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:325:ARG:CA	6:A:338:HOH:O	2.42	0.65
1:E:258:ARG:HE	1:E:259:TYR:HE1	1.43	0.65
6:K:353:HOH:O	2:L:22:TYR:HA	1.96	0.65
1:A:160:LYS:O	1:A:160:LYS:HD3	1.95	0.65
1:E:125:LYS:HG3	1:E:155:ILE:HD11	1.79	0.65
1:C:313:VAL:HG13	2:D:93:THR:HA	1.78	0.65
1:I:102:ILE:HG13	1:I:236:TYR:CE2	2.32	0.65
2:L:135:ASN:OD1	2:L:137:CYS:N	2.30	0.65
1:E:183:TRP:NE1	1:E:236:TYR:HB2	2.12	0.64
1:A:38:LEU:HD11	1:A:320:LEU:HD22	1.79	0.64
1:G:188:PRO:HG2	1:G:194:GLN:HE21	1.63	0.64
1:K:307:GLY:HA2	2:L:63:PHE:CE1	2.33	0.64
1:C:46:LYS:HE2	1:C:279:HIS:ND1	2.13	0.64
1:I:106:GLU:OE2	6:I:341:HOH:O	2.14	0.64
1:I:188:PRO:HG2	1:I:194:GLN:HE21	1.63	0.64
1:K:188:PRO:HG2	1:K:194:GLN:NE2	2.12	0.64
1:C:311:LYS:HG2	2:D:92:TRP:CE2	2.33	0.64
1:G:313:VAL:HG13	2:H:93:THR:HA	1.80	0.63
1:E:188:PRO:HG2	1:E:194:GLN:HE21	1.63	0.63
1:K:297:PRO:HG3	2:L:56:ILE:HA	1.80	0.63
1:K:172:ILE:HD12	1:K:245:LYS:HB3	1.80	0.63
1:C:125:LYS:HB2	1:C:258:ARG:NH1	2.13	0.63
2:D:158:ASP:OD2	2:D:160:PRO:HD2	1.97	0.63
1:I:313:VAL:HG13	2:J:93:THR:HA	1.79	0.63
1:I:106:GLU:CD	6:I:341:HOH:O	2.35	0.63
2:H:81:ASN:O	2:H:84:VAL:HG23	1.97	0.63
1:A:224:PRO:HG2	1:C:209:SER:HA	1.79	0.63
2:H:159:TYR:CD2	2:H:159:TYR:O	2.52	0.63
1:E:108:ARG:HB3	1:E:271:ILE:CD1	2.27	0.63
2:D:142:HIS:CG	6:D:187:HOH:O	2.51	0.63
1:A:141:ALA:O	1:A:143:PRO:HD3	1.97	0.63
1:A:102:ILE:HG13	1:A:236:TYR:CE2	2.33	0.63
1:I:297:PRO:HG3	2:J:56:ILE:HA	1.80	0.63
1:I:63:ILE:HD11	1:I:85:ILE:HG21	1.81	0.63
1:G:227:ARG:O	1:G:228:ASP:HB2	1.97	0.63
1:E:87:GLU:O	1:E:274:SER:N	2.32	0.63
1:E:58:LEU:HD11	1:E:63:ILE:HD13	1.81	0.63
2:L:30:GLN:HE22	2:L:145:ASP:CB	2.12	0.63
1:A:313:VAL:HG13	2:B:93:THR:HA	1.81	0.63
1:K:58:LEU:HD11	1:K:63:ILE:HD13	1.81	0.63
1:G:208:GLY:HA2	1:G:212:TYR:O	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:178:GLU:OE1	1:I:265:ARG:NH1	2.32	0.63
1:C:141:ALA:O	1:C:143:PRO:HD3	1.99	0.62
1:G:11:ILE:CD1	1:G:11:ILE:N	2.62	0.62
1:K:38:LEU:HD11	1:K:320:LEU:HD22	1.81	0.62
1:K:159:LYS:HZ2	1:K:199:GLN:HG3	1.64	0.62
1:A:143:PRO:HD2	4:A:602:NAG:H81	1.82	0.62
1:G:58:LEU:HB3	1:G:61:CYS:O	1.99	0.62
1:G:164:TYR:CZ	1:G:252:GLY:HA2	2.34	0.62
1:I:96:CYS:HB2	1:I:141:ALA:O	1.99	0.62
2:B:105:GLU:C	6:B:193:HOH:O	2.38	0.62
2:H:51:LYS:HB2	1:K:26:LEU:HD23	1.82	0.62
1:C:172:ILE:HD12	1:C:245:LYS:HB3	1.81	0.62
2:J:76:ARG:HA	6:J:295:HOH:O	1.98	0.62
6:H:196:HOH:O	2:J:64:THR:HG22	1.98	0.62
1:A:188:PRO:HG2	1:A:194:GLN:HE21	1.63	0.62
2:J:31:GLY:HA2	6:J:234:HOH:O	2.00	0.62
1:E:141:ALA:O	1:E:143:PRO:HD3	2.00	0.62
1:I:259:TYR:CD1	6:I:361:HOH:O	2.41	0.62
2:B:104:ASN:O	6:B:193:HOH:O	2.16	0.62
1:K:71:PRO:HB3	1:K:144:HIS:HB2	1.81	0.62
1:E:125:LYS:CG	1:E:258:ARG:NH1	2.63	0.62
2:H:154:ASN:O	2:H:154:ASN:OD1	2.17	0.62
1:G:172:ILE:HD12	1:G:245:LYS:HB3	1.81	0.62
1:G:13:TYR:HA	2:H:21:TRP:O	2.00	0.62
1:E:84:TYR:CZ	1:E:286:GLN:HG2	2.35	0.62
1:I:38:LEU:HD11	1:I:320:LEU:HD22	1.81	0.62
2:D:30:GLN:HE22	2:D:145:ASP:CB	2.13	0.61
1:E:99:GLY:HA2	6:E:340:HOH:O	1.99	0.61
1:K:145:ALA:C	1:K:147:ALA:H	2.03	0.61
1:G:183:TRP:NE1	6:G:356:HOH:O	2.31	0.61
2:H:143:LYS:HE2	2:H:143:LYS:HA	1.80	0.61
1:E:324:LEU:HB3	2:F:111:HIS:CG	2.35	0.61
1:A:307:GLY:HA2	2:B:63:PHE:CE1	2.36	0.61
1:K:312:TYR:CD2	2:L:89:LEU:HD13	2.35	0.61
2:B:30:GLN:HE22	2:B:145:ASP:CB	2.13	0.61
2:H:26:HIS:HB3	6:H:183:HOH:O	2.00	0.61
1:C:305:THR:H	2:D:66:VAL:HG13	1.65	0.61
1:K:138:VAL:HG23	1:K:148:LYS:HE3	1.83	0.61
1:C:164:TYR:CZ	1:C:252:GLY:HA2	2.36	0.60
2:B:30:GLN:HE22	2:B:145:ASP:HB2	1.66	0.60
1:I:77:SER:O	1:I:78:THR:OG1	2.17	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:30:GLN:HE22	2:F:145:ASP:CB	2.13	0.60
2:H:51:LYS:HA	1:K:25:VAL:HG12	1.83	0.60
1:E:36:VAL:HG13	1:E:322:THR:HG21	1.83	0.60
1:A:125:LYS:HB2	1:A:258:ARG:HH11	1.66	0.60
1:K:63:ILE:O	1:K:67:ILE:HG13	2.01	0.60
1:C:58:LEU:HD11	1:C:63:ILE:HD13	1.83	0.60
1:A:141:ALA:C	1:A:143:PRO:HD3	2.22	0.60
1:G:50:LEU:HD11	1:G:306:ILE:HG22	1.84	0.60
1:E:167:LEU:O	1:E:249:GLU:HA	2.01	0.60
1:C:11:ILE:HD11	2:D:122:VAL:HG21	1.82	0.60
2:H:2:LEU:HD11	2:J:110:TYR:HA	1.83	0.60
1:E:183:TRP:CZ2	1:E:236:TYR:HB3	2.36	0.60
1:I:141:ALA:C	1:I:143:PRO:HD3	2.22	0.60
1:I:67:ILE:HG12	6:I:353:HOH:O	2.00	0.60
1:I:125:LYS:HB2	1:I:258:ARG:NH1	2.16	0.60
1:C:38:LEU:HD11	1:C:320:LEU:HD22	1.82	0.60
1:G:8:THR:HA	2:H:138:PHE:O	2.02	0.60
1:I:258:ARG:HE	1:I:259:TYR:HE1	1.47	0.60
1:I:58:LEU:HD11	1:I:63:ILE:HD13	1.83	0.60
1:G:180:LEU:HD12	6:G:347:HOH:O	2.01	0.60
1:I:319:ARG:NH1	1:I:319:ARG:CG	2.61	0.60
1:E:102:ILE:HB	6:E:357:HOH:O	2.01	0.60
1:E:314:LYS:HE2	2:F:89:LEU:HD21	1.84	0.60
1:E:36:VAL:O	1:E:320:LEU:N	2.30	0.60
1:C:63:ILE:O	1:C:67:ILE:HG13	2.02	0.60
1:G:81:SER:HB3	1:G:115:SER:O	2.02	0.60
1:E:7:ASP:O	2:F:140:PHE:CD1	2.54	0.59
1:G:105:GLU:OE2	2:H:71:ASN:HB3	2.02	0.59
1:A:172:ILE:HD12	1:A:245:LYS:HB3	1.83	0.59
2:B:124:SER:HB3	6:B:212:HOH:O	2.01	0.59
1:K:49:LYS:HG3	1:K:281:CYS:O	2.03	0.59
2:B:26:HIS:HB2	2:B:149:MET:CE	2.32	0.59
2:L:129:ASN:ND2	2:L:161:LYS:HB2	2.17	0.59
1:A:49:LYS:O	1:A:283:THR:HG22	2.02	0.59
1:K:81:SER:HB3	1:K:115:SER:O	2.02	0.59
1:K:188:PRO:HG2	1:K:194:GLN:HE21	1.67	0.59
1:I:88:THR:C	1:I:89:PRO:O	2.39	0.59
2:B:51:LYS:HG3	1:E:25:VAL:HG12	1.83	0.59
1:A:63:ILE:O	1:A:67:ILE:HG13	2.02	0.59
1:I:164:TYR:CZ	1:I:252:GLY:HA2	2.37	0.59
1:G:63:ILE:O	1:G:67:ILE:HG13	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:58:LEU:HD12	1:G:76:LEU:HD11	1.85	0.59
2:F:122:VAL:HG23	2:F:138:PHE:HE1	1.67	0.59
1:E:47:LEU:HD13	1:E:276:THR:CG2	2.31	0.59
1:C:258:ARG:HE	1:C:259:TYR:HE1	1.50	0.59
1:C:50:LEU:HD11	1:C:306:ILE:HG22	1.84	0.59
1:E:170:SER:HB3	1:E:247:THR:HA	1.83	0.59
2:H:30:GLN:HE22	2:H:145:ASP:CB	2.16	0.59
1:C:326:ASN:C	1:C:327:ILE:HG13	2.23	0.59
1:I:81:SER:HB3	1:I:115:SER:O	2.03	0.58
1:A:223:ARG:HG3	1:C:206:PHE:HZ	1.67	0.58
1:C:13:TYR:HB2	1:C:324:LEU:HD11	1.85	0.58
2:L:143:LYS:HA	2:L:143:LYS:HE2	1.85	0.58
1:E:227:ARG:NH2	4:E:602:NAG:O3	2.36	0.58
1:E:63:ILE:O	1:E:67:ILE:HG13	2.02	0.58
1:I:159:LYS:HB2	1:I:163:SER:O	2.03	0.58
2:H:123:ARG:HD2	2:H:132:GLU:OE1	2.03	0.58
2:B:101:LEU:O	6:B:190:HOH:O	2.17	0.58
1:E:96:CYS:O	1:E:227:ARG:CD	2.50	0.58
1:A:160:LYS:HZ3	1:A:161:GLY:HA3	1.67	0.58
1:G:136:LYS:HB2	1:G:158:VAL:HG21	1.85	0.58
2:L:150:GLU:HG2	3:L:601:NAG:H61	1.85	0.58
1:E:292:ILE:CD1	1:E:301:ILE:HD12	2.32	0.58
2:J:123:ARG:HD2	2:J:132:GLU:OE1	2.02	0.58
2:J:123:ARG:HG3	2:J:138:PHE:HE2	1.68	0.58
2:F:122:VAL:CG2	2:F:138:PHE:HE1	2.16	0.58
1:C:80:SER:O	1:C:116:SER:HA	2.04	0.58
1:E:115:SER:HB2	1:E:266:ASN:OD1	2.04	0.58
1:A:57:HIS:O	1:A:76:LEU:HD13	2.03	0.58
2:D:123:ARG:HD2	2:D:132:GLU:OE1	2.03	0.58
1:K:83:SER:O	1:K:269:SER:OG	2.09	0.58
1:K:125:LYS:HB2	1:K:258:ARG:NH1	2.19	0.58
2:D:123:ARG:O	2:D:126:LEU:O	2.22	0.58
1:I:57:HIS:O	1:I:76:LEU:HD11	2.04	0.58
1:G:44:ASN:HD21	1:G:291:ALA:H	1.50	0.58
2:H:3:PHE:CE1	2:H:113:SER:HB2	2.38	0.58
1:G:154:LEU:HB3	6:G:346:HOH:O	2.03	0.58
1:K:150:PHE:HB3	6:K:348:HOH:O	2.02	0.58
1:C:135:ASN:HB3	4:I:605:NAG:H83	1.85	0.58
1:K:199:GLN:O	1:K:200:ASN:OD1	2.21	0.58
1:K:44:ASN:HD21	1:K:291:ALA:H	1.52	0.58
2:B:76:ARG:NH1	2:D:69:GLU:O	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:143:LYS:HA	2:F:143:LYS:HE2	1.85	0.58
1:A:72:GLU:HG3	4:A:602:NAG:HN2	1.68	0.57
1:C:121:GLU:OE2	1:C:124:PRO:HA	2.02	0.57
2:D:143:LYS:HA	2:D:143:LYS:HE2	1.85	0.57
2:B:123:ARG:HD2	2:B:132:GLU:OE1	2.03	0.57
2:F:123:ARG:CG	2:F:124:SER:N	2.66	0.57
1:C:44:ASN:HD21	1:C:291:ALA:H	1.51	0.57
1:C:245:LYS:HZ3	1:K:116:SER:HB3	1.70	0.57
2:L:135:ASN:OD1	2:L:137:CYS:SG	2.62	0.57
2:F:24:TYR:CD1	2:F:153:LYS:HE3	2.39	0.57
1:E:189:SER:HB3	1:E:230:GLU:HB2	1.86	0.57
2:D:27:GLN:HG3	2:D:27:GLN:O	2.05	0.57
1:E:189:SER:HB2	1:E:230:GLU:HB2	1.85	0.57
1:I:289:LYS:HE2	1:I:301:ILE:CG2	2.34	0.57
1:I:225:LYS:HG2	1:I:230:GLU:HG3	1.86	0.57
2:L:24:TYR:CD1	2:L:153:LYS:HE3	2.40	0.57
1:E:8:THR:HG22	2:F:138:PHE:O	2.04	0.57
1:K:164:TYR:CZ	1:K:252:GLY:HA2	2.38	0.57
1:G:9:LEU:HD22	1:G:10:CYS:N	2.11	0.57
1:K:50:LEU:HD12	1:K:50:LEU:O	2.04	0.57
2:H:123:ARG:O	2:H:126:LEU:O	2.22	0.57
2:J:24:TYR:CD1	2:J:153:LYS:HE3	2.40	0.57
1:E:180:LEU:HA	1:E:239:LEU:HD23	1.87	0.57
1:A:44:ASN:HD21	1:A:291:ALA:H	1.53	0.57
2:L:150:GLU:CG	3:L:601:NAG:H61	2.35	0.57
1:A:55:PRO:HB3	1:A:84:TYR:CZ	2.40	0.57
1:A:19:THR:HG22	3:L:601:NAG:O6	2.05	0.57
2:H:159:TYR:N	2:H:160:PRO:HD3	2.18	0.57
1:I:305:THR:H	2:J:66:VAL:HG13	1.69	0.57
2:J:125:GLN:NE2	2:J:157:TYR:HB3	2.19	0.57
1:I:55:PRO:HB3	1:I:84:TYR:CZ	2.39	0.57
1:K:49:LYS:HB3	1:K:53:VAL:O	2.04	0.57
1:C:198:TYR:OH	1:C:253:ASN:HA	2.05	0.56
1:I:259:TYR:N	6:I:361:HOH:O	2.38	0.56
1:C:81:SER:HB3	1:C:115:SER:O	2.05	0.56
3:K:604:NAG:O7	3:K:604:NAG:C1	2.51	0.56
1:E:125:LYS:CB	1:E:258:ARG:NH1	2.68	0.56
1:G:49:LYS:HB3	1:G:53:VAL:O	2.05	0.56
2:L:30:GLN:HE22	2:L:145:ASP:HB2	1.70	0.56
1:I:118:GLU:HG2	1:I:262:ALA:HB3	1.86	0.56
1:A:159:LYS:HB2	1:A:163:SER:O	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:129:ASN:OD1	2:L:159:TYR:CE2	2.58	0.56
1:G:190:THR:HA	6:G:341:HOH:O	2.04	0.56
1:C:118:GLU:HG2	1:C:262:ALA:HB3	1.86	0.56
1:G:55:PRO:HB3	1:G:84:TYR:CE1	2.41	0.56
1:E:99:GLY:CA	6:E:340:HOH:O	2.52	0.56
1:K:167:LEU:HD23	1:K:167:LEU:O	2.06	0.56
1:E:223:ARG:HD3	1:E:232:ARG:CG	2.33	0.56
1:E:81:SER:HB3	1:E:115:SER:O	2.06	0.56
2:D:125:GLN:HE22	2:D:155:GLY:HA2	1.70	0.56
1:C:55:PRO:HB3	1:C:84:TYR:CZ	2.41	0.56
2:H:58:LYS:HG3	2:L:97:GLU:HB3	1.86	0.56
2:F:30:GLN:HE22	2:F:145:ASP:HB2	1.71	0.56
1:E:44:ASN:HD21	1:E:291:ALA:H	1.54	0.56
2:D:128:ASN:HB3	2:D:162:TYR:HE1	1.71	0.56
1:I:307:GLY:HA2	2:J:63:PHE:CE1	2.41	0.56
1:I:50:LEU:HD12	1:I:50:LEU:O	2.06	0.56
1:G:96:CYS:O	1:G:227:ARG:HD3	2.04	0.56
1:K:145:ALA:C	1:K:147:ALA:N	2.59	0.56
1:G:121:GLU:OE2	1:G:124:PRO:HA	2.06	0.56
2:H:24:TYR:CD1	2:H:153:LYS:HE3	2.40	0.56
1:E:216:PHE:CE2	1:E:236:TYR:CZ	2.94	0.56
2:L:154:ASN:CG	3:L:601:NAG:O7	2.45	0.56
2:L:123:ARG:O	2:L:126:LEU:O	2.23	0.55
1:E:219:GLU:O	1:E:223:ARG:NH2	2.32	0.55
1:E:118:GLU:O	1:E:118:GLU:HG3	2.06	0.55
2:D:30:GLN:HE22	2:D:145:ASP:HB2	1.70	0.55
1:A:159:LYS:HD3	1:A:199:GLN:HB2	1.88	0.55
1:K:55:PRO:HB3	1:K:84:TYR:CZ	2.42	0.55
2:L:51:LYS:HE3	2:L:103:GLU:OE1	2.06	0.55
1:E:15:ALA:HB1	1:E:327:ILE:O	2.06	0.55
1:E:55:PRO:HB3	1:E:84:TYR:CZ	2.41	0.55
1:G:118:GLU:HG2	1:G:262:ALA:HB3	1.88	0.55
2:H:68:LYS:HE3	2:L:79:ASN:HB3	1.87	0.55
1:E:167:LEU:HD23	1:E:167:LEU:O	2.05	0.55
1:K:324:LEU:N	1:K:324:LEU:CD2	2.68	0.55
1:A:327:ILE:HG21	2:B:13:GLY:H	1.72	0.55
1:E:129:TRP:CE2	1:E:256:VAL:HG21	2.42	0.55
1:I:125:LYS:HB2	1:I:258:ARG:HH11	1.70	0.55
1:K:12:GLY:N	2:L:14:TRP:CH2	2.75	0.55
2:H:27:GLN:HG3	2:H:27:GLN:O	2.07	0.55
2:F:132:GLU:HA	2:F:138:PHE:HD2	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:44:ASN:ND2	1:I:291:ALA:H	2.04	0.55
2:H:82:LYS:HE3	6:H:196:HOH:O	2.06	0.55
1:A:160:LYS:HZ2	1:A:161:GLY:HA3	1.70	0.55
2:H:51:LYS:HA	1:K:25:VAL:O	2.07	0.55
1:K:49:LYS:NZ	1:K:280:ASP:HA	2.21	0.55
4:A:604:NAG:O3	4:A:605:NAG:O5	2.22	0.55
1:C:168:SER:CB	1:K:176:GLY:HA2	2.35	0.55
1:K:141:ALA:O	1:K:227:ARG:NH1	2.38	0.55
1:A:324:LEU:HD23	1:A:324:LEU:H	1.71	0.55
1:E:50:LEU:O	1:E:50:LEU:HD12	2.06	0.54
6:I:349:HOH:O	2:L:50:ASN:ND2	2.39	0.54
2:F:67:GLY:HA2	6:F:185:HOH:O	2.08	0.54
2:F:123:ARG:HG2	2:F:124:SER:N	2.22	0.54
2:L:81:ASN:O	2:L:84:VAL:HG12	2.07	0.54
1:A:58:LEU:HD21	1:A:63:ILE:HD13	1.90	0.54
1:A:49:LYS:HB3	1:A:54:ALA:HA	1.89	0.54
1:A:35:SER:HB2	1:A:320:LEU:O	2.07	0.54
1:E:125:LYS:HD3	1:E:258:ARG:NH1	2.22	0.54
1:I:326:ASN:O	1:I:327:ILE:HD13	2.08	0.54
1:A:33:THR:HG23	1:A:325:ARG:O	2.07	0.54
1:A:13:TYR:OH	2:B:10:ILE:O	2.23	0.54
2:F:81:ASN:O	2:F:84:VAL:HG12	2.07	0.54
1:G:58:LEU:HD21	1:G:63:ILE:HD13	1.89	0.54
1:E:164:TYR:CE2	1:E:252:GLY:CA	2.89	0.54
2:B:81:ASN:O	2:B:84:VAL:HG12	2.07	0.54
1:C:312:TYR:CD2	2:D:89:LEU:HD13	2.43	0.54
6:K:358:HOH:O	2:L:65:ALA:HB3	2.07	0.54
2:J:83:LYS:NZ	6:J:190:HOH:O	2.30	0.54
1:E:50:LEU:HD21	1:E:306:ILE:HG22	1.90	0.54
1:E:155:ILE:HD11	1:E:258:ARG:HD2	1.88	0.54
1:I:10:CYS:O	2:J:24:TYR:HA	2.08	0.54
2:J:81:ASN:O	2:J:84:VAL:HG12	2.08	0.54
2:H:30:GLN:HE22	2:H:145:ASP:HB2	1.73	0.54
1:C:136:LYS:HB2	1:C:158:VAL:HG21	1.89	0.54
1:A:11:ILE:HD12	2:B:24:TYR:CD2	2.43	0.54
1:A:148:LYS:HA	6:A:341:HOH:O	2.07	0.54
1:E:164:TYR:CE2	1:E:252:GLY:N	2.76	0.54
1:A:160:LYS:HB3	6:A:358:HOH:O	2.08	0.54
1:A:160:LYS:HD3	1:A:160:LYS:C	2.28	0.54
2:B:143:LYS:HA	2:B:143:LYS:HE2	1.90	0.54
2:H:128:ASN:HB2	2:H:159:TYR:OH	2.09	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:58:LEU:HA	1:A:76:LEU:HD13	1.89	0.54
2:J:143:LYS:HE2	2:J:143:LYS:HA	1.90	0.54
2:F:158:ASP:C	2:F:160:PRO:HD3	2.28	0.53
1:K:96:CYS:O	1:K:227:ARG:HD3	2.09	0.53
1:A:164:TYR:CZ	1:A:252:GLY:HA2	2.44	0.53
1:I:25:VAL:CG2	2:J:102:LEU:HD12	2.39	0.53
1:I:49:LYS:HE3	1:I:52:GLY:O	2.09	0.53
1:G:307:GLY:HA2	2:H:63:PHE:CE1	2.43	0.53
2:J:19:ASP:OD2	2:J:19:ASP:N	2.41	0.53
1:A:143:PRO:O	4:A:602:NAG:C8	2.56	0.53
2:L:129:ASN:HD22	2:L:129:ASN:N	2.05	0.53
1:I:118:GLU:CG	1:I:262:ALA:HB3	2.38	0.53
2:F:51:LYS:HE3	2:F:103:GLU:OE1	2.08	0.53
1:K:155:ILE:HG13	1:K:258:ARG:HB2	1.90	0.53
1:C:125:LYS:HB2	1:C:258:ARG:HH11	1.71	0.53
1:E:314:LYS:CE	2:F:89:LEU:HD21	2.38	0.53
2:H:51:LYS:HB2	1:K:26:LEU:CD2	2.39	0.53
2:B:26:HIS:HB2	2:B:149:MET:HE3	1.90	0.53
1:E:40:GLU:HB2	1:E:296:LEU:HD12	1.90	0.53
1:G:306:ILE:HA	2:H:65:ALA:HA	1.91	0.53
2:D:51:LYS:HE3	2:D:103:GLU:OE1	2.08	0.53
2:L:157:TYR:CE1	6:L:262:HOH:O	2.54	0.53
1:I:113:SER:HB2	1:I:269:SER:CB	2.38	0.53
1:A:113:SER:HB2	1:A:269:SER:CB	2.39	0.53
1:A:155:ILE:HG13	1:A:258:ARG:HB2	1.91	0.53
1:E:47:LEU:HD22	1:E:276:THR:HB	1.90	0.53
2:B:51:LYS:HE3	2:B:103:GLU:OE1	2.09	0.53
1:A:225:LYS:HD3	1:K:80:SER:HB3	1.89	0.53
1:E:305:THR:H	2:F:66:VAL:HG13	1.74	0.53
1:C:297:PRO:HG3	2:D:56:ILE:HA	1.90	0.53
1:G:155:ILE:N	6:G:346:HOH:O	2.41	0.53
1:C:205:VAL:HG13	6:C:354:HOH:O	2.07	0.53
1:C:136:LYS:HE3	6:C:367:HOH:O	2.07	0.53
2:J:23:GLY:HA3	2:J:36:ALA:HA	1.91	0.53
2:F:72:HIS:CD2	2:F:73:LEU:HG	2.44	0.53
1:E:13:TYR:CD2	2:F:6:ILE:HG12	2.44	0.53
6:C:357:HOH:O	2:D:13:GLY:CA	2.56	0.52
1:K:167:LEU:HD23	1:K:167:LEU:C	2.29	0.52
1:C:113:SER:HB2	1:C:269:SER:CB	2.39	0.52
1:A:282:ASN:ND2	4:A:604:NAG:C6	2.53	0.52
2:H:9:PHE:CD1	2:H:10:ILE:HG13	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:216:PHE:HE2	1:E:236:TYR:CE2	2.27	0.52
3:K:602:NAG:H82	6:K:344:HOH:O	2.10	0.52
1:C:78:THR:HG22	1:C:79:ALA:H	1.75	0.52
1:E:167:LEU:C	1:E:167:LEU:HD23	2.29	0.52
1:G:141:ALA:C	1:G:143:PRO:HD3	2.29	0.52
1:E:108:ARG:O	1:E:271:ILE:HD11	2.09	0.52
1:I:327:ILE:HG21	2:J:12:GLY:HA2	1.90	0.52
1:I:136:LYS:HB2	1:I:158:VAL:HG21	1.91	0.52
1:I:23:ASP:OD2	5:I:601:NAG:O7	2.27	0.52
1:E:136:LYS:HB2	1:E:158:VAL:HG21	1.91	0.52
1:G:255:VAL:CG1	6:G:346:HOH:O	2.48	0.52
2:H:123:ARG:HH12	2:J:123:ARG:HH12	1.58	0.52
1:I:11:ILE:HD12	2:J:119:TYR:HA	1.90	0.52
2:H:74:GLU:HA	6:I:341:HOH:O	2.09	0.52
1:A:312:TYR:CD2	2:B:89:LEU:HD13	2.45	0.52
2:H:123:ARG:NH1	2:J:123:ARG:NH2	2.50	0.52
2:D:81:ASN:O	2:D:84:VAL:HG12	2.09	0.52
1:C:99:GLY:HA3	1:C:233:MET:O	2.09	0.52
1:G:205:VAL:HG11	1:G:254:LEU:HD13	1.92	0.52
2:L:135:ASN:OD1	2:L:137:CYS:CB	2.57	0.52
2:B:159:TYR:N	2:B:160:PRO:HD3	2.25	0.52
1:E:172:ILE:HA	1:E:245:LYS:HA	1.92	0.52
1:K:125:LYS:HB2	1:K:258:ARG:HH11	1.73	0.52
1:A:11:ILE:CD1	2:B:24:TYR:CD2	2.93	0.52
2:B:24:TYR:CD1	2:B:153:LYS:HE3	2.45	0.52
1:A:205:VAL:HG22	6:A:366:HOH:O	2.10	0.52
1:G:9:LEU:O	1:G:10:CYS:SG	2.68	0.52
1:E:43:HIS:HB3	1:E:301:ILE:CD1	2.35	0.52
4:I:604:NAG:O3	4:I:605:NAG:O5	2.22	0.52
1:G:24:THR:HG22	2:H:104:ASN:HB3	1.92	0.52
2:F:122:VAL:HG23	2:F:138:PHE:CE1	2.45	0.51
1:G:183:TRP:HZ3	1:G:238:THR:HG22	1.75	0.51
1:I:50:LEU:HB3	6:I:338:HOH:O	2.11	0.51
2:F:123:ARG:O	2:F:126:LEU:O	2.28	0.51
2:B:27:GLN:HG3	2:B:27:GLN:O	2.10	0.51
2:D:23:GLY:HA3	2:D:36:ALA:HA	1.92	0.51
2:H:51:LYS:HE3	2:H:103:GLU:OE1	2.10	0.51
1:E:44:ASN:HD22	1:E:45:GLY:N	2.07	0.51
1:A:325:ARG:C	6:A:338:HOH:O	2.48	0.51
2:L:123:ARG:HD2	2:L:132:GLU:OE1	2.10	0.51
1:E:170:SER:HA	1:E:246:ILE:O	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:252:GLY:O	6:A:366:HOH:O	2.19	0.51
1:E:104:TYR:O	1:E:108:ARG:HG3	2.10	0.51
1:I:14:HIS:HB2	2:J:21:TRP:HA	1.93	0.51
1:E:177:LYS:CE	1:E:264:GLU:OE2	2.47	0.51
1:E:105:GLU:HA	1:E:108:ARG:HD3	1.91	0.51
1:A:118:GLU:HG2	1:A:262:ALA:HB3	1.92	0.51
2:B:3:PHE:HZ	2:F:2:LEU:HD13	1.75	0.51
2:J:159:TYR:N	2:J:160:PRO:CD	2.74	0.51
1:E:293:ASN:O	1:E:293:ASN:CG	2.48	0.51
2:B:142:HIS:CG	2:B:142:HIS:O	2.62	0.51
1:A:177:LYS:HD2	1:A:262:ALA:HB1	1.93	0.51
1:K:136:LYS:HB2	1:K:158:VAL:HG21	1.91	0.51
2:L:72:HIS:CD2	2:L:73:LEU:HG	2.46	0.51
2:B:1:GLY:N	6:B:192:HOH:O	2.42	0.51
1:K:300:ASN:HA	6:K:362:HOH:O	2.11	0.51
1:C:238:THR:HG23	6:C:359:HOH:O	2.11	0.51
1:C:141:ALA:C	1:C:143:PRO:HD3	2.31	0.51
1:G:305:THR:HG22	2:H:66:VAL:CG2	2.40	0.51
1:A:58:LEU:HB3	1:A:61:CYS:O	2.10	0.51
1:I:57:HIS:O	1:I:76:LEU:CD1	2.58	0.51
1:A:11:ILE:HD11	2:B:118:LEU:HD23	1.91	0.51
1:E:297:PRO:HG3	2:F:56:ILE:HA	1.93	0.51
1:G:77:SER:O	1:G:79:ALA:N	2.43	0.51
1:E:113:SER:CB	1:E:269:SER:HB2	2.40	0.51
1:K:311:LYS:HG2	2:L:92:TRP:CD2	2.45	0.51
1:C:44:ASN:ND2	1:C:291:ALA:H	2.09	0.51
1:C:77:SER:C	1:C:78:THR:OG1	2.48	0.51
1:C:144:HIS:HA	6:C:371:HOH:O	2.10	0.51
1:E:17:ASN:CG	3:E:601:NAG:C1	2.73	0.50
1:I:155:ILE:HG13	1:I:258:ARG:HB2	1.91	0.50
1:G:305:THR:O	2:H:66:VAL:N	2.44	0.50
1:E:261:PHE:HD2	6:E:352:HOH:O	1.93	0.50
2:J:51:LYS:HE3	2:J:103:GLU:OE1	2.09	0.50
2:J:91:ILE:HG13	6:J:185:HOH:O	2.11	0.50
2:J:129:ASN:HD22	2:J:129:ASN:N	2.09	0.50
2:J:72:HIS:CD2	2:J:73:LEU:HG	2.46	0.50
2:D:72:HIS:CD2	2:D:73:LEU:HG	2.47	0.50
1:I:205:VAL:HG11	1:I:254:LEU:HD13	1.94	0.50
1:I:87:GLU:O	1:I:273:ILE:HA	2.11	0.50
2:L:150:GLU:OE1	3:L:601:NAG:H61	2.12	0.50
1:C:250:ALA:HB2	6:C:354:HOH:O	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:105:GLU:CD	1:G:105:GLU:H	2.14	0.50
1:A:13:TYR:HB2	1:A:324:LEU:HD11	1.93	0.50
1:E:181:VAL:O	1:E:237:TRP:HA	2.10	0.50
1:G:76:LEU:HD22	1:G:76:LEU:O	2.11	0.50
2:F:124:SER:O	2:F:127:LYS:HE3	2.11	0.50
1:G:48:CYS:O	1:G:84:TYR:OH	2.23	0.50
2:H:145:ASP:CG	6:H:185:HOH:O	2.49	0.50
1:I:189:SER:HB2	1:I:222:ILE:HD13	1.94	0.50
1:E:220:ILE:N	6:E:342:HOH:O	2.44	0.50
1:G:44:ASN:ND2	1:G:291:ALA:H	2.09	0.50
2:F:23:GLY:HA3	2:F:36:ALA:HA	1.93	0.50
1:A:189:SER:HB2	1:A:222:ILE:HD13	1.94	0.50
1:K:51:ARG:O	3:K:603:NAG:H2	2.12	0.50
1:E:25:VAL:CG2	2:F:102:LEU:HD12	2.42	0.50
2:J:158:ASP:CG	2:J:160:PRO:HD2	2.32	0.50
1:K:87:GLU:O	1:K:273:ILE:HA	2.11	0.50
1:C:155:ILE:HG13	1:C:258:ARG:HB2	1.93	0.50
2:D:145:ASP:OD2	2:D:145:ASP:N	2.45	0.50
2:B:123:ARG:O	2:B:126:LEU:O	2.29	0.50
4:A:603:NAG:O7	1:K:280:ASP:CG	2.45	0.49
1:E:307:GLY:HA2	2:F:63:PHE:CZ	2.44	0.49
1:E:166:LYS:HA	1:E:250:ALA:O	2.12	0.49
1:K:113:SER:HB2	1:K:269:SER:OG	2.12	0.49
2:J:159:TYR:CG	2:J:160:PRO:HD3	2.46	0.49
2:L:23:GLY:HA3	2:L:36:ALA:HA	1.93	0.49
1:C:219:GLU:O	1:C:223:ARG:NH2	2.33	0.49
1:E:113:SER:CB	1:E:269:SER:CB	2.83	0.49
1:I:43:HIS:HB3	1:I:301:ILE:HD13	1.94	0.49
1:A:225:LYS:CD	1:K:80:SER:HB3	2.42	0.49
2:J:159:TYR:CD2	2:J:160:PRO:HD3	2.47	0.49
1:C:307:GLY:HA2	2:D:63:PHE:CE1	2.47	0.49
1:G:43:HIS:HB3	1:G:301:ILE:HD13	1.94	0.49
2:D:129:ASN:N	2:D:129:ASN:HD22	2.10	0.49
2:B:72:HIS:CD2	2:B:73:LEU:HG	2.47	0.49
1:I:51:ARG:HG3	6:I:338:HOH:O	2.11	0.49
2:L:145:ASP:OD2	2:L:145:ASP:N	2.45	0.49
1:A:158:VAL:HG22	6:A:343:HOH:O	2.10	0.49
1:A:50:LEU:O	1:A:283:THR:O	2.29	0.49
1:G:22:VAL:HG21	1:G:321:ALA:HB2	1.94	0.49
1:E:170:SER:CB	1:E:247:THR:HA	2.41	0.49
1:E:86:VAL:HA	1:E:272:ILE:O	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:357:HOH:O	2:D:13:GLY:HA2	2.13	0.49
2:J:125:GLN:HE21	2:J:157:TYR:HB3	1.78	0.49
1:A:324:LEU:N	1:A:324:LEU:HD23	2.27	0.49
2:F:158:ASP:O	2:F:160:PRO:HD3	2.13	0.49
1:G:22:VAL:HG12	1:G:319:ARG:HG2	1.95	0.49
2:B:9:PHE:CD1	2:B:10:ILE:HG13	2.48	0.49
2:L:158:ASP:N	2:L:158:ASP:OD1	2.46	0.49
1:K:271:ILE:O	1:K:271:ILE:HG13	2.12	0.49
1:I:8:THR:HG22	2:J:139:GLU:CA	2.35	0.49
1:K:44:ASN:ND2	1:K:46:LYS:H	2.10	0.49
1:K:252:GLY:C	1:K:253:ASN:HD22	2.16	0.49
1:C:189:SER:HB2	1:C:222:ILE:HD13	1.95	0.49
1:A:167:LEU:O	1:A:167:LEU:HD12	2.12	0.49
1:C:104:TYR:CE2	1:C:108:ARG:HD2	2.48	0.49
1:G:321:ALA:O	6:G:342:HOH:O	2.20	0.49
1:G:11:ILE:HD12	2:H:136:GLY:O	2.12	0.49
1:G:83:SER:HG	1:G:84:TYR:HD2	1.57	0.49
1:E:189:SER:HB3	1:E:230:GLU:C	2.33	0.49
2:F:9:PHE:C	2:F:9:PHE:CD1	2.86	0.49
1:A:159:LYS:CD	1:A:199:GLN:HG2	2.43	0.49
1:A:159:LYS:CE	1:A:199:GLN:HG2	2.42	0.49
1:I:25:VAL:HG21	2:J:102:LEU:HD12	1.95	0.49
1:C:189:SER:HA	1:C:221:ALA:O	2.12	0.49
1:A:49:LYS:HG3	1:A:281:CYS:O	2.13	0.49
1:G:11:ILE:HD12	1:G:11:ILE:N	2.28	0.49
2:L:135:ASN:OD1	2:L:135:ASN:C	2.52	0.49
1:K:159:LYS:HZ2	1:K:199:GLN:CG	2.26	0.49
1:C:78:THR:CG2	1:C:79:ALA:H	2.26	0.49
1:E:80:SER:O	1:E:116:SER:HA	2.13	0.49
2:H:72:HIS:CD2	2:H:73:LEU:HG	2.48	0.49
1:A:96:CYS:O	1:A:227:ARG:HD3	2.13	0.48
1:E:101:PHE:HB3	1:E:104:TYR:HB2	1.94	0.48
1:I:252:GLY:C	1:I:253:ASN:HD22	2.17	0.48
1:C:9:LEU:HB2	2:D:149:MET:SD	2.53	0.48
5:I:602:NAG:C6	5:I:603:BMA:O5	2.54	0.48
1:E:183:TRP:CZ2	1:E:236:TYR:CB	2.95	0.48
1:K:236:TYR:O	6:K:343:HOH:O	2.20	0.48
1:K:78:THR:O	1:K:78:THR:CG2	2.61	0.48
1:E:184:GLY:HA2	1:E:234:ASN:O	2.13	0.48
2:J:76:ARG:CA	6:J:295:HOH:O	2.58	0.48
1:A:161:GLY:O	1:A:162:ASN:HB2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:118:GLU:HG2	1:K:262:ALA:HB3	1.94	0.48
2:H:23:GLY:HA3	2:H:36:ALA:HA	1.94	0.48
1:E:141:ALA:C	1:E:143:PRO:HD3	2.34	0.48
1:G:9:LEU:N	2:H:138:PHE:O	2.46	0.48
2:J:119:TYR:CE1	2:J:138:PHE:CZ	3.01	0.48
1:I:96:CYS:O	1:I:227:ARG:HD3	2.12	0.48
1:C:177:LYS:HD2	1:C:262:ALA:HB1	1.95	0.48
1:K:189:SER:HB2	1:K:222:ILE:HD13	1.95	0.48
2:F:129:ASN:HD22	2:F:129:ASN:N	2.11	0.48
1:K:8:THR:OG1	2:L:27:GLN:CB	2.60	0.48
1:A:205:VAL:HG11	1:A:254:LEU:HD13	1.95	0.48
1:C:121:GLU:CD	1:C:124:PRO:HA	2.34	0.48
1:C:43:HIS:HB3	1:C:301:ILE:HD13	1.94	0.48
1:C:156:TRP:CD1	6:C:346:HOH:O	2.55	0.48
2:L:150:GLU:HG2	3:L:601:NAG:C6	2.42	0.48
1:E:38:LEU:HD11	1:E:320:LEU:HD13	1.94	0.48
2:B:28:ASN:OD1	2:B:146:ASN:ND2	2.46	0.48
1:I:177:LYS:HD2	1:I:262:ALA:HB1	1.95	0.48
2:B:150:GLU:O	2:B:153:LYS:N	2.47	0.48
1:E:51:ARG:O	1:E:282:ASN:OD1	2.32	0.48
1:E:224:PRO:HA	6:E:362:HOH:O	2.13	0.48
1:A:130:PRO:HG2	1:A:131:ASN:OD1	2.13	0.48
2:H:74:GLU:CA	6:I:341:HOH:O	2.62	0.48
2:F:145:ASP:OD2	2:F:145:ASP:N	2.45	0.48
1:E:44:ASN:ND2	1:E:46:LYS:H	2.11	0.48
2:H:161:LYS:O	2:H:162:TYR:C	2.52	0.48
2:J:142:HIS:O	2:J:142:HIS:CG	2.66	0.48
1:E:216:PHE:CE2	1:E:236:TYR:CE2	3.02	0.48
1:K:71:PRO:CB	1:K:144:HIS:HB2	2.43	0.48
1:G:252:GLY:C	1:G:253:ASN:HD22	2.17	0.48
1:A:252:GLY:C	1:A:253:ASN:HD22	2.16	0.48
1:E:185:ILE:N	1:E:234:ASN:O	2.33	0.48
1:K:95:THR:HA	6:K:355:HOH:O	2.13	0.48
1:K:95:THR:OG1	1:K:97:TYR:O	2.32	0.48
1:C:22:VAL:HG12	1:C:319:ARG:HG2	1.96	0.48
1:C:167:LEU:O	1:C:167:LEU:HD12	2.14	0.48
1:G:303:PRO:HG3	1:G:312:TYR:CE2	2.49	0.48
1:K:44:ASN:ND2	1:K:291:ALA:H	2.11	0.48
1:E:167:LEU:HD22	1:E:250:ALA:CB	2.40	0.47
1:I:143:PRO:HD2	4:I:604:NAG:H83	1.94	0.47
1:K:46:LYS:HE2	1:K:279:HIS:CE1	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:221:ALA:O	1:C:223:ARG:NH1	2.46	0.47
1:C:129:TRP:N	1:C:130:PRO:HD3	2.28	0.47
1:I:319:ARG:NH1	1:I:319:ARG:HG3	2.29	0.47
1:K:309:CYS:O	2:L:61:THR:HG21	2.14	0.47
1:I:311:LYS:HG2	2:J:92:TRP:CD2	2.48	0.47
1:E:89:PRO:HD2	1:E:275:ASP:OD2	2.14	0.47
2:D:9:PHE:CD1	2:D:10:ILE:HG13	2.49	0.47
1:I:83:SER:CB	6:I:338:HOH:O	2.44	0.47
1:E:121:GLU:HA	1:E:259:TYR:HA	1.96	0.47
1:I:311:LYS:HG2	2:J:92:TRP:NE1	2.29	0.47
1:E:189:SER:HB2	1:E:222:ILE:HD13	1.96	0.47
1:I:13:TYR:HB2	1:I:324:LEU:HD11	1.97	0.47
1:I:46:LYS:HE2	1:I:279:HIS:CE1	2.49	0.47
2:H:2:LEU:O	2:J:113:SER:OG	2.24	0.47
1:E:13:TYR:CE2	2:F:6:ILE:HA	2.49	0.47
1:K:43:HIS:HB3	1:K:301:ILE:HD13	1.95	0.47
2:D:74:GLU:HB3	2:D:77:ILE:HD11	1.95	0.47
1:K:57:HIS:O	1:K:76:LEU:HD23	2.13	0.47
1:A:311:LYS:HG2	2:B:92:TRP:CD2	2.49	0.47
2:H:84:VAL:HG13	2:J:84:VAL:HG21	1.96	0.47
2:B:157:TYR:CD2	2:B:158:ASP:O	2.67	0.47
1:I:104:TYR:CE2	1:I:108:ARG:HD2	2.49	0.47
2:J:132:GLU:HG2	2:J:138:PHE:CE2	2.50	0.47
1:K:303:PRO:HG3	1:K:312:TYR:CZ	2.50	0.47
2:J:158:ASP:OD1	2:J:160:PRO:HD2	2.13	0.47
1:I:294:THR:HG21	1:I:310:PRO:HG2	1.97	0.47
1:I:99:GLY:HA3	1:I:233:MET:O	2.14	0.47
1:A:320:LEU:O	6:A:349:HOH:O	2.21	0.47
1:K:114:VAL:CG1	1:K:117:PHE:HB2	2.40	0.47
1:C:205:VAL:HG11	1:C:254:LEU:HD13	1.97	0.47
2:D:128:ASN:HB3	2:D:162:TYR:CE1	2.48	0.47
1:G:110:GLN:NE2	2:L:72:HIS:O	2.46	0.47
1:A:26:LEU:HB3	2:D:47:GLU:HB3	1.96	0.47
1:A:141:ALA:O	1:A:227:ARG:NH1	2.48	0.47
1:G:327:ILE:C	6:G:337:HOH:O	2.53	0.47
1:G:112:SER:HB2	1:G:270:GLY:HA2	1.96	0.47
2:B:108:LEU:HB2	6:B:193:HOH:O	2.14	0.47
1:G:261:PHE:N	6:G:373:HOH:O	2.28	0.47
1:G:180:LEU:N	6:G:373:HOH:O	2.48	0.47
1:A:162:ASN:HA	1:A:162:ASN:HD22	1.55	0.47
2:H:47:GLU:CB	1:K:26:LEU:HB3	2.38	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:244:ASP:OD2	1:G:245:LYS:N	2.48	0.47
1:K:104:TYR:CE2	1:K:108:ARG:HD2	2.50	0.47
1:G:167:LEU:HD12	1:G:167:LEU:O	2.14	0.47
1:C:87:GLU:O	1:C:273:ILE:HA	2.14	0.47
1:C:294:THR:HG21	1:C:310:PRO:HG2	1.96	0.47
1:E:161:GLY:O	1:E:162:ASN:HB2	2.13	0.47
1:G:51:ARG:C	6:G:365:HOH:O	2.53	0.47
1:A:297:PRO:HG3	2:B:56:ILE:HA	1.96	0.47
1:G:209:SER:HA	1:K:224:PRO:HG2	1.96	0.47
1:C:224:PRO:HG2	1:E:245:LYS:O	2.15	0.47
1:K:102:ILE:HG13	1:K:236:TYR:CD2	2.49	0.47
1:I:143:PRO:HD2	4:I:604:NAG:C8	2.44	0.47
1:E:85:ILE:O	1:E:272:ILE:N	2.38	0.47
2:H:145:ASP:OD2	2:H:145:ASP:N	2.43	0.47
1:C:324:LEU:HD23	1:C:324:LEU:H	1.79	0.47
1:E:122:ILE:HB	1:E:260:ALA:CB	2.45	0.47
1:I:25:VAL:HG12	2:L:51:LYS:HG3	1.96	0.47
1:I:312:TYR:CD2	2:J:89:LEU:HD13	2.50	0.47
1:E:123:PHE:HB2	1:E:257:PRO:O	2.15	0.47
1:G:114:VAL:HG21	1:G:117:PHE:HB2	1.97	0.47
1:K:22:VAL:HG12	1:K:319:ARG:HG2	1.96	0.47
1:K:8:THR:CB	2:L:27:GLN:HB3	2.45	0.47
1:E:44:ASN:C	1:E:44:ASN:HD22	2.19	0.47
2:H:19:ASP:HB2	2:H:36:ALA:HB3	1.97	0.47
1:I:107:LEU:HG	1:I:111:LEU:HD22	1.97	0.47
2:B:129:ASN:N	2:B:129:ASN:HD22	2.11	0.47
1:A:87:GLU:O	1:A:273:ILE:HA	2.14	0.47
2:F:106:ARG:HE	2:F:106:ARG:HB3	1.60	0.46
1:A:131:ASN:OD1	1:A:131:ASN:N	2.47	0.46
1:C:49:LYS:O	1:C:283:THR:HG22	2.16	0.46
1:G:33:THR:HG23	1:G:324:LEU:O	2.15	0.46
1:A:99:GLY:HA3	1:A:233:MET:O	2.14	0.46
1:E:50:LEU:CD2	1:E:306:ILE:HG22	2.45	0.46
1:C:135:ASN:HB3	4:I:605:NAG:C8	2.44	0.46
1:C:44:ASN:ND2	1:C:46:LYS:H	2.13	0.46
1:A:44:ASN:ND2	1:A:291:ALA:H	2.12	0.46
1:A:44:ASN:O	1:A:46:LYS:HE3	2.15	0.46
2:F:19:ASP:HB2	2:F:36:ALA:HB3	1.97	0.46
1:K:294:THR:HG21	1:K:310:PRO:HG2	1.97	0.46
1:G:104:TYR:CE2	1:G:108:ARG:HD2	2.50	0.46
1:G:226:VAL:O	1:G:227:ARG:HB2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:25:VAL:HG21	2:F:102:LEU:HD12	1.97	0.46
2:J:142:HIS:O	2:J:142:HIS:CD2	2.69	0.46
1:K:99:GLY:HA3	1:K:233:MET:O	2.16	0.46
1:A:227:ARG:O	1:A:228:ASP:HB2	2.15	0.46
1:A:36:VAL:N	6:A:349:HOH:O	2.47	0.46
2:B:142:HIS:CE1	2:B:161:LYS:NZ	2.83	0.46
1:E:38:LEU:CD1	1:E:320:LEU:HB2	2.45	0.46
2:B:19:ASP:HB2	2:B:36:ALA:HB3	1.96	0.46
1:I:309:CYS:O	2:J:61:THR:HG21	2.16	0.46
1:A:72:GLU:HG3	4:A:602:NAG:N2	2.30	0.46
1:K:23:ASP:OD1	1:K:28:LYS:HB3	2.16	0.46
1:C:227:ARG:NH2	4:C:605:NAG:O3	2.49	0.46
1:A:42:LYS:HE3	1:A:42:LYS:HB2	1.81	0.46
1:I:81:SER:HA	1:I:114:VAL:HG12	1.96	0.46
1:G:194:GLN:O	1:G:198:TYR:O	2.33	0.46
1:I:183:TRP:HZ3	1:I:238:THR:HG22	1.81	0.46
1:K:42:LYS:HB2	1:K:42:LYS:HE3	1.78	0.46
1:E:172:ILE:HG13	1:E:244:ASP:O	2.16	0.46
1:K:183:TRP:HZ3	1:K:238:THR:HG22	1.80	0.46
1:G:44:ASN:HD22	1:G:45:GLY:N	2.14	0.46
1:I:302:HIS:HA	1:I:303:PRO:HD3	1.83	0.46
2:H:13:GLY:N	6:H:184:HOH:O	2.28	0.46
1:C:96:CYS:O	1:C:227:ARG:HD3	2.16	0.46
1:E:125:LYS:HG3	1:E:155:ILE:CD1	2.44	0.46
1:E:155:ILE:HG13	1:E:258:ARG:HB2	1.98	0.46
1:C:311:LYS:HA	1:C:311:LYS:HD3	1.76	0.46
1:K:50:LEU:HD21	1:K:306:ILE:HG22	1.98	0.46
2:H:88:PHE:CZ	2:L:87:GLY:HA3	2.51	0.46
1:I:316:THR:HG22	6:I:344:HOH:O	2.15	0.46
2:L:9:PHE:CD1	2:L:10:ILE:HG13	2.50	0.46
1:I:167:LEU:HD12	1:I:167:LEU:O	2.15	0.46
1:E:49:LYS:HB3	1:E:53:VAL:O	2.16	0.46
1:E:11:ILE:CG2	1:E:12:GLY:N	2.79	0.46
1:K:244:ASP:OD2	1:K:245:LYS:N	2.49	0.46
1:E:108:ARG:HB3	1:E:271:ILE:HD13	1.97	0.46
2:L:19:ASP:HB2	2:L:36:ALA:HB3	1.98	0.46
1:C:83:SER:HB3	6:C:334:HOH:O	2.16	0.46
2:L:28:ASN:C	2:L:28:ASN:HD22	2.19	0.46
1:E:93:ASN:ND2	4:E:602:NAG:O7	2.50	0.46
1:K:81:SER:HA	1:K:114:VAL:HG12	1.96	0.46
2:H:87:GLY:HA3	2:J:88:PHE:CZ	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:87:GLU:O	1:G:273:ILE:HA	2.15	0.46
1:E:7:ASP:OD1	1:E:7:ASP:N	2.49	0.45
4:A:603:NAG:O7	1:K:49:LYS:HE3	2.15	0.45
1:E:177:LYS:HB2	1:E:263:MET:O	2.16	0.45
1:A:81:SER:HA	1:A:114:VAL:HG12	1.98	0.45
1:E:39:LEU:HB3	6:E:356:HOH:O	2.16	0.45
1:I:44:ASN:HD22	1:I:45:GLY:N	2.14	0.45
1:G:44:ASN:ND2	1:G:46:LYS:H	2.14	0.45
1:E:114:VAL:HG21	1:E:117:PHE:HB2	1.98	0.45
1:E:178:GLU:CD	1:E:265:ARG:NH1	2.70	0.45
1:G:105:GLU:CD	2:H:71:ASN:HD22	2.19	0.45
2:D:151:SER:HB2	2:D:156:THR:O	2.15	0.45
1:E:252:GLY:C	1:E:253:ASN:HD22	2.20	0.45
2:F:119:TYR:CZ	2:F:138:PHE:CZ	3.04	0.45
2:F:119:TYR:O	2:F:122:VAL:HG22	2.16	0.45
1:I:319:ARG:HG3	1:I:319:ARG:HH11	1.80	0.45
1:E:322:THR:O	2:F:48:ILE:HG21	2.16	0.45
1:A:268:GLY:O	2:B:63:PHE:HE2	2.00	0.45
2:L:161:LYS:O	2:L:162:TYR:C	2.54	0.45
2:B:123:ARG:NH2	6:B:191:HOH:O	2.49	0.45
1:A:8:THR:OG1	2:B:27:GLN:HB3	2.17	0.45
1:A:22:VAL:HG21	1:A:321:ALA:HB2	1.99	0.45
1:K:47:LEU:HD13	1:K:276:THR:CG2	2.46	0.45
1:C:302:HIS:HA	1:C:303:PRO:HD3	1.84	0.45
1:A:43:HIS:HB3	1:A:301:ILE:HD13	1.97	0.45
1:K:105:GLU:H	1:K:105:GLU:CD	2.20	0.45
2:D:19:ASP:HB2	2:D:36:ALA:HB3	1.97	0.45
1:E:9:LEU:HA	1:E:9:LEU:HD23	1.49	0.45
2:B:74:GLU:HB3	2:B:77:ILE:HD11	1.97	0.45
1:G:99:GLY:HA3	1:G:233:MET:O	2.15	0.45
1:C:81:SER:HA	1:C:114:VAL:HG12	1.99	0.45
1:K:8:THR:OG1	2:L:27:GLN:O	2.34	0.45
1:K:13:TYR:HA	6:K:353:HOH:O	2.16	0.45
1:I:225:LYS:CG	1:I:230:GLU:HG3	2.46	0.45
2:B:4:GLY:O	2:B:8:GLY:HA3	2.17	0.45
2:H:74:GLU:HB3	2:H:77:ILE:HD11	1.99	0.45
1:E:179:VAL:HA	1:E:261:PHE:O	2.17	0.45
2:J:159:TYR:N	2:J:160:PRO:HD3	2.31	0.45
1:G:14:HIS:CD2	1:G:15:ALA:N	2.84	0.45
1:E:31:THR:HG22	1:E:326:ASN:HB3	1.99	0.45
1:I:314:LYS:HE3	1:I:314:LYS:HB2	1.68	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:162:TYR:C	2:B:162:TYR:CD1	2.89	0.45
1:A:47:LEU:CD2	1:A:276:THR:HB	2.44	0.45
1:G:29:ASN:CG	3:G:602:NAG:N2	2.68	0.45
1:K:47:LEU:HD22	1:K:276:THR:O	2.17	0.45
1:K:33:THR:HG23	1:K:325:ARG:O	2.16	0.45
1:C:252:GLY:C	1:C:253:ASN:HD22	2.20	0.45
2:F:125:GLN:NE2	2:F:157:TYR:CG	2.85	0.45
2:H:51:LYS:HG3	1:K:25:VAL:HG12	1.99	0.45
1:E:104:TYR:CE2	1:E:108:ARG:HD2	2.52	0.45
2:J:125:GLN:HG3	2:J:125:GLN:O	2.16	0.45
1:I:14:HIS:N	2:J:21:TRP:O	2.49	0.45
1:A:177:LYS:HE3	1:A:264:GLU:OE2	2.16	0.45
1:K:314:LYS:HE3	1:K:314:LYS:HB2	1.65	0.45
1:C:282:ASN:ND2	3:C:607:NAG:O7	2.50	0.45
1:A:143:PRO:HD2	4:A:602:NAG:C8	2.46	0.45
1:G:9:LEU:HA	1:G:9:LEU:HD23	1.78	0.45
2:J:19:ASP:HB2	2:J:36:ALA:HB3	1.98	0.45
2:L:3:PHE:CE1	2:L:113:SER:HB2	2.52	0.45
2:F:5:ALA:HB3	2:F:112:ASP:OD2	2.16	0.45
1:A:104:TYR:CE2	1:A:108:ARG:HD2	2.51	0.45
2:B:47:GLU:HB3	1:E:26:LEU:HB3	1.98	0.45
1:I:44:ASN:ND2	1:I:46:LYS:H	2.14	0.45
1:E:324:LEU:N	1:E:324:LEU:HD23	2.32	0.45
2:F:74:GLU:HB3	2:F:77:ILE:HD11	1.99	0.45
2:F:130:ALA:N	6:F:184:HOH:O	2.50	0.45
2:J:9:PHE:CD1	2:J:10:ILE:HG13	2.52	0.44
1:C:177:LYS:HE3	1:C:264:GLU:OE2	2.17	0.44
2:D:99:LEU:HA	2:D:102:LEU:HD23	1.99	0.44
1:E:13:TYR:CE1	2:F:6:ILE:HG23	2.52	0.44
1:C:221:ALA:H	1:C:223:ARG:NH1	2.15	0.44
1:C:105:GLU:CD	1:C:105:GLU:H	2.21	0.44
1:K:95:THR:HG21	1:K:235:TYR:CE1	2.52	0.44
1:E:276:THR:HA	1:E:277:PRO:HD3	1.88	0.44
1:E:325:ARG:HD3	6:E:355:HOH:O	2.17	0.44
1:A:72:GLU:CG	4:A:602:NAG:HN2	2.29	0.44
1:K:302:HIS:HA	1:K:303:PRO:HD3	1.82	0.44
2:H:51:LYS:HG3	1:K:25:VAL:CG1	2.48	0.44
2:H:68:LYS:HE3	2:L:79:ASN:CB	2.46	0.44
1:E:198:TYR:O	1:E:200:ASN:N	2.50	0.44
1:C:42:LYS:HB2	1:C:42:LYS:HE3	1.75	0.44
1:E:96:CYS:HB2	1:E:141:ALA:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:273:ILE:N	1:E:273:ILE:HD12	2.33	0.44
1:C:273:ILE:N	1:C:273:ILE:HD12	2.32	0.44
2:D:5:ALA:HB3	2:D:112:ASP:OD2	2.18	0.44
2:D:4:GLY:O	2:D:8:GLY:HA3	2.17	0.44
1:A:19:THR:HB	3:L:601:NAG:C5	2.31	0.44
1:C:44:ASN:HD22	1:C:45:GLY:N	2.16	0.44
2:B:145:ASP:OD2	2:B:145:ASP:N	2.50	0.44
1:C:324:LEU:HD23	1:C:324:LEU:N	2.33	0.44
1:I:177:LYS:HE3	1:I:264:GLU:OE2	2.17	0.44
1:A:78:THR:OG1	1:A:78:THR:O	2.35	0.44
1:I:63:ILE:HG23	6:I:353:HOH:O	2.17	0.44
2:F:119:TYR:CE1	2:F:138:PHE:CZ	3.06	0.44
1:A:47:LEU:N	1:A:47:LEU:HD23	2.33	0.44
1:C:245:LYS:HD2	1:K:264:GLU:OE1	2.18	0.44
1:A:11:ILE:HD13	2:B:24:TYR:CE2	2.53	0.44
1:K:11:ILE:O	2:L:10:ILE:HD13	2.18	0.44
1:K:102:ILE:HG12	1:K:235:TYR:O	2.16	0.44
2:D:159:TYR:N	2:D:160:PRO:CD	2.80	0.44
1:E:327:ILE:HG21	2:F:12:GLY:HA2	1.99	0.44
1:A:136:LYS:HB2	1:A:158:VAL:HG21	1.99	0.44
1:G:276:THR:HA	1:G:277:PRO:HD3	1.90	0.44
2:L:74:GLU:HB3	2:L:77:ILE:HD11	1.99	0.44
2:H:129:ASN:ND2	2:H:159:TYR:CE1	2.86	0.44
1:K:28:LYS:O	1:K:29:ASN:C	2.56	0.44
1:G:14:HIS:CG	1:G:15:ALA:N	2.85	0.44
2:J:87:GLY:HA3	2:L:88:PHE:CZ	2.52	0.44
1:C:51:ARG:HB2	1:C:52:GLY:H	1.64	0.44
2:H:50:ASN:HD22	1:K:25:VAL:C	2.20	0.43
2:B:9:PHE:CE1	2:B:10:ILE:HG13	2.53	0.43
1:K:225:LYS:NZ	1:K:230:GLU:HG3	2.33	0.43
2:D:87:GLY:HA3	2:F:88:PHE:CZ	2.53	0.43
1:G:74:GLU:O	1:G:75:SER:HB3	2.18	0.43
2:B:5:ALA:HB3	2:B:112:ASP:OD2	2.18	0.43
2:D:118:LEU:HA	2:D:118:LEU:HD12	1.89	0.43
1:I:283:THR:HG21	1:I:286:GLN:OE1	2.18	0.43
1:C:227:ARG:O	1:C:228:ASP:HB2	2.16	0.43
1:E:167:LEU:HD21	1:E:254:LEU:HD23	2.00	0.43
1:A:296:LEU:HA	1:A:297:PRO:HD3	1.83	0.43
1:K:22:VAL:HG21	1:K:321:ALA:HB2	2.00	0.43
1:E:37:ASN:HA	1:E:319:ARG:HA	2.00	0.43
1:K:119:ARG:HB2	1:K:261:PHE:CE2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:216:PHE:HE2	1:E:236:TYR:CZ	2.36	0.43
2:F:123:ARG:NH2	2:F:132:GLU:OE1	2.51	0.43
1:C:23:ASP:OD2	5:C:602:NAG:O7	2.35	0.43
1:K:227:ARG:O	1:K:228:ASP:HB2	2.17	0.43
1:C:121:GLU:CD	6:C:341:HOH:O	2.57	0.43
1:I:273:ILE:HD12	1:I:273:ILE:N	2.33	0.43
1:C:167:LEU:C	1:C:167:LEU:HD12	2.38	0.43
2:J:4:GLY:O	2:J:8:GLY:HA3	2.18	0.43
2:F:122:VAL:CG2	2:F:138:PHE:CE1	3.01	0.43
1:E:266:ASN:HA	6:E:364:HOH:O	2.17	0.43
2:B:3:PHE:CE1	2:B:113:SER:HB2	2.54	0.43
1:A:167:LEU:HD12	1:A:167:LEU:C	2.39	0.43
1:C:22:VAL:HG21	1:C:321:ALA:HB2	2.00	0.43
1:K:62:ASN:ND2	1:K:93:ASN:O	2.51	0.43
1:G:162:ASN:HD22	1:G:162:ASN:HA	1.51	0.43
1:A:281:CYS:HA	4:A:604:NAG:H82	2.00	0.43
2:H:123:ARG:NH2	2:L:123:ARG:NH1	2.60	0.43
1:K:226:VAL:O	1:K:227:ARG:HB2	2.19	0.43
1:E:104:TYR:OH	1:E:108:ARG:NH1	2.52	0.43
1:K:93:ASN:HB3	1:K:94:GLY:H	1.55	0.43
2:H:28:ASN:C	2:H:28:ASN:HD22	2.22	0.43
2:F:123:ARG:C	2:F:125:GLN:H	2.21	0.43
1:C:96:CYS:HB2	1:C:141:ALA:O	2.18	0.43
1:E:125:LYS:CD	1:E:258:ARG:NH1	2.81	0.43
1:E:87:GLU:N	1:E:272:ILE:O	2.37	0.43
1:A:164:TYR:HD2	1:A:164:TYR:C	2.22	0.43
1:K:44:ASN:HD22	1:K:45:GLY:N	2.16	0.43
1:C:25:VAL:HG12	2:F:51:LYS:HG3	2.00	0.43
1:E:302:HIS:HA	1:E:303:PRO:HD3	1.83	0.43
2:H:4:GLY:O	2:H:8:GLY:HA3	2.18	0.43
2:B:105:GLU:CB	6:B:190:HOH:O	2.52	0.43
1:E:105:GLU:H	1:E:105:GLU:CD	2.21	0.43
2:J:159:TYR:CE1	2:J:160:PRO:HG3	2.54	0.43
1:I:302:HIS:CE1	1:I:304:ILE:HB	2.53	0.43
2:H:151:SER:HB2	2:H:156:THR:O	2.19	0.43
1:C:161:GLY:O	1:C:162:ASN:HB2	2.19	0.43
2:F:121:LYS:HG2	6:F:186:HOH:O	2.18	0.43
1:K:49:LYS:O	1:K:283:THR:HG22	2.19	0.43
1:G:9:LEU:O	2:H:137:CYS:CB	2.67	0.43
1:G:177:LYS:HE3	1:G:264:GLU:OE2	2.18	0.43
2:L:4:GLY:O	2:L:8:GLY:HA3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:189:SER:HB2	1:G:222:ILE:HD13	2.01	0.43
1:A:96:CYS:HB2	1:A:141:ALA:O	2.18	0.43
1:I:13:TYR:OH	2:J:10:ILE:O	2.31	0.43
1:E:314:LYS:HE3	1:E:314:LYS:HB2	1.69	0.43
1:I:88:THR:HB	1:I:89:PRO:O	2.18	0.43
1:A:13:TYR:HB2	1:A:14:HIS:H	1.53	0.43
2:J:91:ILE:HD13	2:L:91:ILE:HG21	1.99	0.43
1:K:162:ASN:HA	1:K:162:ASN:HD22	1.55	0.43
2:J:119:TYR:CZ	2:J:138:PHE:CZ	3.06	0.43
2:F:122:VAL:O	2:F:126:LEU:HG	2.18	0.43
1:A:276:THR:HA	1:A:277:PRO:HD3	1.84	0.43
1:K:266:ASN:ND2	1:K:266:ASN:N	2.60	0.43
2:H:58:LYS:HA	2:H:58:LYS:HD2	1.51	0.43
1:E:179:VAL:HG22	1:E:262:ALA:HA	2.00	0.43
1:E:118:GLU:HG2	1:E:262:ALA:HB3	2.00	0.43
1:A:11:ILE:HD11	2:B:118:LEU:CD2	2.49	0.43
1:A:113:SER:HB2	1:A:269:SER:HB3	2.01	0.43
1:G:195:GLN:HA	1:G:198:TYR:O	2.19	0.42
2:D:123:ARG:C	2:D:125:GLN:H	2.22	0.42
1:G:44:ASN:C	1:G:44:ASN:HD22	2.22	0.42
2:F:2:LEU:HD23	2:F:2:LEU:HA	1.85	0.42
2:H:146:ASN:HB2	6:H:197:HOH:O	2.18	0.42
1:I:42:LYS:HE3	1:I:42:LYS:HB2	1.77	0.42
1:A:91:SER:HB3	6:A:364:HOH:O	2.20	0.42
2:B:14:TRP:HZ3	2:B:23:GLY:O	2.02	0.42
1:E:39:LEU:HD23	1:E:317:LYS:HA	2.00	0.42
1:C:162:ASN:HA	1:C:162:ASN:HD22	1.56	0.42
2:J:151:SER:HB2	2:J:156:THR:O	2.18	0.42
2:H:5:ALA:HB3	2:H:112:ASP:OD2	2.19	0.42
1:I:50:LEU:HD21	1:I:306:ILE:HG22	2.01	0.42
1:I:68:LEU:HD23	1:I:68:LEU:HA	1.79	0.42
2:H:66:VAL:HG22	6:H:246:HOH:O	2.18	0.42
2:H:70:PHE:HB3	2:H:74:GLU:HB2	2.01	0.42
1:K:295:SER:O	2:L:56:ILE:HG23	2.19	0.42
1:K:44:ASN:C	1:K:44:ASN:HD22	2.23	0.42
1:I:113:SER:HB2	1:I:269:SER:HB3	2.01	0.42
1:C:233:MET:SD	1:C:255:VAL:HG21	2.59	0.42
1:I:114:VAL:CG1	1:I:117:PHE:HB2	2.38	0.42
1:C:141:ALA:O	1:C:227:ARG:NH1	2.53	0.42
2:B:19:ASP:HB2	2:B:36:ALA:CB	2.50	0.42
1:I:311:LYS:HG2	2:J:92:TRP:CD1	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:308:LYS:HG2	2:B:61:THR:OG1	2.18	0.42
1:K:210:SER:HB2	1:K:244:ASP:OD1	2.19	0.42
1:I:88:THR:CB	1:I:89:PRO:O	2.67	0.42
1:C:13:TYR:HA	2:D:21:TRP:O	2.19	0.42
1:E:112:SER:HB2	1:E:270:GLY:CA	2.50	0.42
1:I:22:VAL:HG21	1:I:321:ALA:HB2	2.00	0.42
1:A:105:GLU:CD	1:A:105:GLU:H	2.23	0.42
1:A:140:ALA:O	1:A:143:PRO:HG3	2.20	0.42
1:G:113:SER:HB2	1:G:269:SER:HB3	2.01	0.42
1:K:299:GLN:CD	6:K:362:HOH:O	2.57	0.42
1:C:183:TRP:HZ3	1:C:238:THR:HG22	1.84	0.42
1:I:311:LYS:CG	2:J:92:TRP:CD1	3.02	0.42
1:A:164:TYR:C	1:A:164:TYR:CD2	2.91	0.42
2:H:145:ASP:O	2:H:148:CYS:HB3	2.18	0.42
1:C:314:LYS:HE3	1:C:314:LYS:HB2	1.71	0.42
1:A:160:LYS:NZ	1:A:161:GLY:CA	2.76	0.42
2:F:123:ARG:C	2:F:125:GLN:N	2.70	0.42
1:A:58:LEU:C	1:A:76:LEU:CD1	2.88	0.42
1:K:177:LYS:HD2	1:K:262:ALA:HB1	1.99	0.42
1:I:167:LEU:HD12	1:I:167:LEU:C	2.40	0.42
1:C:138:VAL:HG22	6:C:352:HOH:O	2.18	0.42
2:D:28:ASN:HD22	2:D:28:ASN:C	2.21	0.42
1:A:304:ILE:HD12	1:A:304:ILE:N	2.35	0.42
1:G:314:LYS:HE3	1:G:314:LYS:HB2	1.66	0.42
1:I:244:ASP:OD2	1:I:245:LYS:N	2.52	0.42
1:E:155:ILE:CD1	1:E:258:ARG:HB2	2.50	0.42
2:J:3:PHE:CE1	2:J:113:SER:HB2	2.54	0.42
1:E:51:ARG:HB2	1:E:52:GLY:H	1.70	0.42
1:G:273:ILE:N	1:G:273:ILE:HD12	2.35	0.42
1:E:159:LYS:HZ2	1:E:199:GLN:HG2	1.85	0.42
1:I:11:ILE:HD11	2:J:122:VAL:HG21	2.00	0.42
2:D:105:GLU:OE2	2:F:106:ARG:NH2	2.53	0.42
1:I:223:ARG:O	1:I:230:GLU:HG2	2.19	0.42
1:G:121:GLU:CD	1:G:124:PRO:HA	2.40	0.42
1:C:221:ALA:H	1:C:223:ARG:HH12	1.66	0.42
1:G:304:ILE:N	1:G:304:ILE:HD12	2.35	0.42
1:G:155:ILE:HG13	1:G:258:ARG:CG	2.29	0.42
1:I:35:SER:OG	1:I:319:ARG:NH1	2.51	0.42
1:G:55:PRO:CB	6:G:350:HOH:O	2.58	0.42
1:A:7:ASP:OD2	2:B:28:ASN:HB2	2.20	0.42
1:I:44:ASN:C	1:I:44:ASN:HD22	2.23	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:118:LEU:HA	2:B:118:LEU:HD12	1.88	0.42
2:D:17:MET:SD	2:D:23:GLY:HA3	2.60	0.42
1:I:22:VAL:HB	2:J:104:ASN:ND2	2.34	0.42
1:G:282:ASN:HB2	3:G:603:NAG:O7	2.19	0.42
2:D:3:PHE:CE1	2:D:113:SER:HB2	2.55	0.42
1:K:311:LYS:NZ	2:L:61:THR:HG22	2.34	0.42
1:I:311:LYS:HA	1:I:311:LYS:HD3	1.79	0.42
1:A:273:ILE:N	1:A:273:ILE:HD12	2.34	0.42
1:K:161:GLY:O	1:K:162:ASN:HB2	2.20	0.42
1:E:164:TYR:CE1	1:E:252:GLY:HA2	2.54	0.41
1:I:8:THR:O	2:J:149:MET:CE	2.68	0.41
1:C:311:LYS:HG2	2:D:92:TRP:CD2	2.54	0.41
2:D:158:ASP:CG	2:D:160:PRO:HD2	2.40	0.41
1:C:225:LYS:NZ	1:C:230:GLU:HG3	2.36	0.41
1:A:183:TRP:HZ3	1:A:238:THR:HG22	1.85	0.41
1:G:39:LEU:HB2	1:G:318:LEU:HB2	2.00	0.41
2:B:26:HIS:HB2	2:B:149:MET:HE2	2.00	0.41
1:C:296:LEU:HA	1:C:297:PRO:HD3	1.81	0.41
1:A:101:PHE:HB3	1:A:104:TYR:HB2	2.02	0.41
1:A:121:GLU:CD	1:A:124:PRO:HA	2.40	0.41
2:L:151:SER:HB2	2:L:156:THR:O	2.20	0.41
1:E:231:GLY:O	1:E:232:ARG:NH1	2.52	0.41
1:G:305:THR:CG2	6:H:194:HOH:O	2.68	0.41
2:F:19:ASP:HB2	2:F:36:ALA:CB	2.50	0.41
1:G:159:LYS:HE2	1:G:196:SER:O	2.21	0.41
1:I:63:ILE:O	1:I:67:ILE:HG13	2.20	0.41
2:B:142:HIS:NE2	2:B:144:CYS:SG	2.94	0.41
1:E:36:VAL:HG13	1:E:322:THR:CG2	2.48	0.41
1:C:244:ASP:OD2	1:C:245:LYS:N	2.53	0.41
1:K:307:GLY:HA2	2:L:63:PHE:CD1	2.55	0.41
1:E:185:ILE:O	1:E:234:ASN:N	2.51	0.41
1:C:208:GLY:HA2	1:C:212:TYR:O	2.21	0.41
1:G:293:ASN:C	1:G:293:ASN:OD1	2.59	0.41
1:K:25:VAL:HG21	2:L:102:LEU:HD12	2.01	0.41
1:A:311:LYS:NZ	2:B:61:THR:HG22	2.36	0.41
1:E:296:LEU:HA	1:E:297:PRO:HD3	1.82	0.41
2:L:19:ASP:HB2	2:L:36:ALA:CB	2.51	0.41
1:K:8:THR:HG1	2:L:27:GLN:HB3	1.84	0.41
1:G:190:THR:HG23	1:G:193:ASP:HB2	2.02	0.41
2:D:102:LEU:HG	2:D:103:GLU:N	2.32	0.41
1:C:113:SER:HB2	1:C:269:SER:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:19:ASP:HB2	2:H:36:ALA:CB	2.50	0.41
2:D:9:PHE:CE1	2:D:10:ILE:HG13	2.55	0.41
2:J:74:GLU:HB3	2:J:77:ILE:HD11	2.01	0.41
1:E:42:LYS:HE3	1:E:42:LYS:HB2	1.77	0.41
2:H:12:GLY:CA	6:H:184:HOH:O	2.54	0.41
1:E:313:VAL:HG13	2:F:93:THR:HA	2.02	0.41
1:K:25:VAL:CG2	2:L:102:LEU:HD12	2.51	0.41
1:E:244:ASP:OD2	1:E:245:LYS:N	2.52	0.41
1:G:118:GLU:CG	1:G:262:ALA:HB3	2.48	0.41
2:L:28:ASN:C	2:L:28:ASN:ND2	2.74	0.41
2:D:28:ASN:ND2	2:D:28:ASN:C	2.74	0.41
1:A:121:GLU:OE2	1:A:124:PRO:HA	2.20	0.41
1:G:180:LEU:HB2	1:G:263:MET:HE1	2.03	0.41
1:C:258:ARG:NH2	6:C:341:HOH:O	2.53	0.41
2:D:19:ASP:HB2	2:D:36:ALA:CB	2.51	0.41
1:G:167:LEU:C	1:G:167:LEU:HD12	2.40	0.41
2:B:91:ILE:HG21	2:F:91:ILE:HD13	2.03	0.41
1:G:10:CYS:C	1:G:11:ILE:HG23	2.41	0.41
1:E:11:ILE:HG23	1:E:12:GLY:N	2.36	0.41
1:C:140:ALA:O	1:C:143:PRO:HG3	2.21	0.41
1:E:38:LEU:HG	1:E:320:LEU:HB2	2.03	0.41
1:K:144:HIS:O	1:K:145:ALA:HB3	2.21	0.41
1:K:311:LYS:HA	1:K:311:LYS:HD3	1.79	0.41
1:K:159:LYS:HD3	1:K:199:GLN:HB2	2.02	0.41
1:A:244:ASP:OD2	1:A:245:LYS:N	2.53	0.41
1:E:119:ARG:HB2	1:E:261:PHE:CE2	2.56	0.41
1:I:25:VAL:HG22	2:J:102:LEU:HD12	2.03	0.41
1:I:49:LYS:HE2	1:I:49:LYS:HB2	1.53	0.41
1:K:189:SER:HA	1:K:221:ALA:O	2.21	0.41
1:K:47:LEU:HD13	1:K:276:THR:HB	2.03	0.41
1:E:304:ILE:N	1:E:304:ILE:HD12	2.36	0.41
1:K:190:THR:HG23	1:K:193:ASP:HB2	2.03	0.41
2:F:3:PHE:CE1	2:F:113:SER:HB2	2.55	0.41
1:K:51:ARG:HB2	1:K:52:GLY:H	1.69	0.41
1:A:49:LYS:HG3	1:A:49:LYS:H	1.56	0.41
1:C:304:ILE:HD12	1:C:304:ILE:N	2.35	0.41
1:I:67:ILE:HG13	1:I:67:ILE:H	1.55	0.40
1:A:206:PHE:HZ	1:E:223:ARG:HE	1.69	0.40
1:E:121:GLU:OE2	1:E:124:PRO:HA	2.22	0.40
1:G:138:VAL:N	6:G:369:HOH:O	2.54	0.40
1:C:44:ASN:C	1:C:44:ASN:HD22	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:145:ASP:OD2	2:B:148:CYS:HB3	2.21	0.40
1:A:44:ASN:C	1:A:44:ASN:HD22	2.23	0.40
1:A:44:ASN:HD22	1:A:45:GLY:N	2.18	0.40
1:K:299:GLN:OE1	6:K:362:HOH:O	2.21	0.40
1:C:168:SER:OG	1:K:176:GLY:HA3	2.22	0.40
2:H:74:GLU:OE2	2:L:76:ARG:NH2	2.39	0.40
1:E:120:PHE:HE2	1:E:262:ALA:N	2.18	0.40
1:E:293:ASN:O	1:E:293:ASN:ND2	2.54	0.40
1:K:68:LEU:O	1:K:151:TYR:HB3	2.21	0.40
1:K:88:THR:O	1:K:91:SER:OG	2.32	0.40
2:L:148:CYS:SG	6:L:262:HOH:O	2.63	0.40
1:A:189:SER:HA	1:A:221:ALA:O	2.22	0.40
2:F:121:LYS:HA	6:F:187:HOH:O	2.20	0.40
2:J:5:ALA:HB3	2:J:112:ASP:OD2	2.21	0.40
1:G:11:ILE:CD1	2:H:136:GLY:O	2.69	0.40
1:E:121:GLU:CD	1:E:124:PRO:HA	2.41	0.40
1:K:13:TYR:CE2	2:L:6:ILE:HA	2.56	0.40
1:E:314:LYS:HB2	2:F:89:LEU:HD11	2.04	0.40
1:A:44:ASN:ND2	1:A:46:LYS:H	2.19	0.40
1:I:304:ILE:HD12	1:I:304:ILE:N	2.36	0.40
1:E:186:HIS:HA	1:E:233:MET:HA	2.02	0.40
2:J:123:ARG:HG3	2:J:138:PHE:CE2	2.52	0.40
1:C:13:TYR:C	6:C:357:HOH:O	2.60	0.40
1:I:327:ILE:HB	2:J:13:GLY:H	1.86	0.40
2:B:24:TYR:CD1	2:B:24:TYR:N	2.89	0.40
1:G:101:PHE:HB3	1:G:104:TYR:HB2	2.04	0.40
2:H:28:ASN:C	2:H:28:ASN:ND2	2.75	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:74:GLU:OE1	1:K:144:HIS:NE2[1_455]	1.89	0.31
1:C:74:GLU:OE1	1:K:144:HIS:CD2[1_455]	2.04	0.16
1:C:74:GLU:OE2	1:K:144:HIS:ND1[1_455]	2.13	0.07

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	319/333 (96%)	286 (90%)	32 (10%)	1 (0%)	46	78
1	C	319/333 (96%)	296 (93%)	22 (7%)	1 (0%)	46	78
1	E	319/333 (96%)	291 (91%)	24 (8%)	4 (1%)	15	44
1	G	319/333 (96%)	299 (94%)	19 (6%)	1 (0%)	46	78
1	I	319/333 (96%)	294 (92%)	25 (8%)	0	100	100
1	K	319/333 (96%)	288 (90%)	31 (10%)	0	100	100
2	B	160/181 (88%)	143 (89%)	17 (11%)	0	100	100
2	D	160/181 (88%)	146 (91%)	14 (9%)	0	100	100
2	F	159/181 (88%)	147 (92%)	12 (8%)	0	100	100
2	H	160/181 (88%)	145 (91%)	15 (9%)	0	100	100
2	J	160/181 (88%)	148 (92%)	12 (8%)	0	100	100
2	L	159/181 (88%)	145 (91%)	14 (9%)	0	100	100
All	All	2872/3084 (93%)	2628 (92%)	237 (8%)	7 (0%)	52	83

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	92	ASP
1	E	199	GLN
1	A	199	GLN
1	E	75	SER
1	G	268	GLY
1	C	78	THR
1	E	227	ARG

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	281/292 (96%)	249 (89%)	32 (11%)	7	19
1	C	282/292 (97%)	255 (90%)	27 (10%)	10	28
1	E	282/292 (97%)	247 (88%)	35 (12%)	6	15
1	G	281/292 (96%)	252 (90%)	29 (10%)	9	24
1	I	282/292 (97%)	251 (89%)	31 (11%)	8	21
1	K	282/292 (97%)	249 (88%)	33 (12%)	7	18
2	B	139/156 (89%)	126 (91%)	13 (9%)	11	30
2	D	138/156 (88%)	128 (93%)	10 (7%)	18	44
2	F	139/156 (89%)	124 (89%)	15 (11%)	8	22
2	H	139/156 (89%)	132 (95%)	7 (5%)	30	64
2	J	139/156 (89%)	127 (91%)	12 (9%)	13	35
2	L	139/156 (89%)	127 (91%)	12 (9%)	13	35
All	All	2523/2688 (94%)	2267 (90%)	256 (10%)	9	26

All (256) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	TYR
1	A	37	ASN
1	A	44	ASN
1	A	49	LYS
1	A	58	LEU
1	A	74	GLU
1	A	78	THR
1	A	107	LEU
1	A	111	LEU
1	A	131	ASN
1	A	160	LYS
1	A	162	ASN
1	A	163	SER
1	A	164	TYR

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Mol	Chain	Res	Type
1	A	167	LEU
1	A	190	THR
1	A	193	ASP
1	A	199	GLN
1	A	228	ASP
1	A	240	VAL
1	A	264	GLU
1	A	265	ARG
1	A	266	ASN
1	A	279	HIS
1	A	287	THR
1	A	295	SER
1	A	305	THR
1	A	311	LYS
1	A	316	THR
1	A	324	LEU
1	A	325	ARG
1	A	327	ILE
2	B	22	TYR
2	B	24	TYR
2	B	28	ASN
2	B	38	LEU
2	B	80	LEU
2	B	98	LEU
2	B	126	LEU
2	B	142	HIS
2	B	144	CYS
2	B	148	CYS
2	B	149	MET
2	B	150	GLU
2	B	158	ASP
1	C	7	ASP
1	C	26	LEU
1	C	37	ASN
1	C	44	ASN
1	C	50	LEU
1	C	53	VAL
1	C	75	SER
1	C	78	THR
1	C	111	LEU
1	C	126	THR
1	C	128	SER

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Mol	Chain	Res	Type
1	C	157	LEU
1	C	162	ASN
1	C	167	LEU
1	C	190	THR
1	C	193	ASP
1	C	200	ASN
1	C	264	GLU
1	C	265	ARG
1	C	266	ASN
1	C	287	THR
1	C	295	SER
1	C	305	THR
1	C	311	LYS
1	C	314	LYS
1	C	316	THR
1	C	324	LEU
2	D	22	TYR
2	D	28	ASN
2	D	38	LEU
2	D	66	VAL
2	D	80	LEU
2	D	102	LEU
2	D	105	GLU
2	D	126	LEU
2	D	142	HIS
2	D	150	GLU
1	E	7	ASP
1	E	8	THR
1	E	9	LEU
1	E	10	CYS
1	E	11	ILE
1	E	32	VAL
1	E	37	ASN
1	E	44	ASN
1	E	47	LEU
1	E	50	LEU
1	E	74	GLU
1	E	76	LEU
1	E	91	SER
1	E	111	LEU
1	E	162	ASN
1	E	167	LEU

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Mol	Chain	Res	Type
1	E	190	THR
1	E	193	ASP
1	E	198	TYR
1	E	199	GLN
1	E	205	VAL
1	E	223	ARG
1	E	230	GLU
1	E	264	GLU
1	E	265	ARG
1	E	266	ASN
1	E	279	HIS
1	E	292	ILE
1	E	293	ASN
1	E	294	THR
1	E	295	SER
1	E	305	THR
1	E	311	LYS
1	E	316	THR
1	E	324	LEU
2	F	2	LEU
2	F	9	PHE
2	F	22	TYR
2	F	28	ASN
2	F	38	LEU
2	F	66	VAL
2	F	80	LEU
2	F	106	ARG
2	F	123	ARG
2	F	125	GLN
2	F	126	LEU
2	F	137	CYS
2	F	142	HIS
2	F	150	GLU
2	F	158	ASP
1	G	7	ASP
1	G	9	LEU
1	G	11	ILE
1	G	13	TYR
1	G	21	THR
1	G	37	ASN
1	G	39	LEU
1	G	44	ASN

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Mol	Chain	Res	Type
1	G	50	LEU
1	G	58	LEU
1	G	76	LEU
1	G	107	LEU
1	G	162	ASN
1	G	167	LEU
1	G	190	THR
1	G	193	ASP
1	G	198	TYR
1	G	200	ASN
1	G	240	VAL
1	G	258	ARG
1	G	263	MET
1	G	264	GLU
1	G	265	ARG
1	G	266	ASN
1	G	279	HIS
1	G	294	THR
1	G	295	SER
1	G	305	THR
1	G	316	THR
2	H	22	TYR
2	H	28	ASN
2	H	58	LYS
2	H	84	VAL
2	H	126	LEU
2	H	142	HIS
2	H	150	GLU
1	I	7	ASP
1	I	11	ILE
1	I	26	LEU
1	I	37	ASN
1	I	44	ASN
1	I	49	LYS
1	I	50	LEU
1	I	53	VAL
1	I	67	ILE
1	I	74	GLU
1	I	75	SER
1	I	90	SER
1	I	91	SER
1	I	111	LEU

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Mol	Chain	Res	Type
1	I	118	GLU
1	I	119	ARG
1	I	160	LYS
1	I	167	LEU
1	I	172	ILE
1	I	190	THR
1	I	193	ASP
1	I	264	GLU
1	I	265	ARG
1	I	266	ASN
1	I	279	HIS
1	I	281	CYS
1	I	295	SER
1	I	305	THR
1	I	311	LYS
1	I	319	ARG
1	I	324	LEU
2	J	19	ASP
2	J	22	TYR
2	J	28	ASN
2	J	30	GLN
2	J	32	SER
2	J	38	LEU
2	J	66	VAL
2	J	80	LEU
2	J	125	GLN
2	J	126	LEU
2	J	142	HIS
2	J	150	GLU
1	K	8	THR
1	K	11	ILE
1	K	28	LYS
1	K	37	ASN
1	K	44	ASN
1	K	47	LEU
1	K	50	LEU
1	K	74	GLU
1	K	76	LEU
1	K	77	SER
1	K	91	SER
1	K	93	ASN
1	K	95	THR

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Mol	Chain	Res	Type
1	K	111	LEU
1	K	119	ARG
1	K	142	CYS
1	K	162	ASN
1	K	167	LEU
1	K	190	THR
1	K	193	ASP
1	K	205	VAL
1	K	263	MET
1	K	264	GLU
1	K	265	ARG
1	K	266	ASN
1	K	271	ILE
1	K	279	HIS
1	K	287	THR
1	K	295	SER
1	K	305	THR
1	K	311	LYS
1	K	316	THR
1	K	324	LEU
2	L	22	TYR
2	L	28	ASN
2	L	38	LEU
2	L	66	VAL
2	L	80	LEU
2	L	126	LEU
2	L	142	HIS
2	L	150	GLU
2	L	158	ASP
2	L	159	TYR
2	L	161	LYS
2	L	162	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (94) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	37	ASN
1	A	44	ASN
1	A	132	HIS
1	A	162	ASN
1	A	194	GLN
1	A	195	GLN

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Mol	Chain	Res	Type
1	A	253	ASN
1	A	266	ASN
2	B	27	GLN
2	B	28	ASN
2	B	30	GLN
2	B	125	GLN
2	B	129	ASN
2	B	142	HIS
2	B	146	ASN
1	C	37	ASN
1	C	44	ASN
1	C	132	HIS
1	C	162	ASN
1	C	194	GLN
1	C	195	GLN
1	C	199	GLN
1	C	253	ASN
1	C	266	ASN
2	D	27	GLN
2	D	28	ASN
2	D	30	GLN
2	D	125	GLN
2	D	129	ASN
2	D	146	ASN
1	E	17	ASN
1	E	37	ASN
1	E	44	ASN
1	E	132	HIS
1	E	162	ASN
1	E	194	GLN
1	E	195	GLN
1	E	253	ASN
2	F	27	GLN
2	F	28	ASN
2	F	30	GLN
2	F	95	ASN
2	F	129	ASN
2	F	146	ASN
1	G	14	HIS
1	G	37	ASN
1	G	44	ASN
1	G	132	HIS

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Mol	Chain	Res	Type
1	G	162	ASN
1	G	194	GLN
1	G	195	GLN
1	G	199	GLN
1	G	253	ASN
1	G	266	ASN
1	G	279	HIS
2	H	27	GLN
2	H	28	ASN
2	H	30	GLN
2	H	125	GLN
2	H	129	ASN
2	H	146	ASN
2	H	154	ASN
1	I	37	ASN
1	I	44	ASN
1	I	132	HIS
1	I	144	HIS
1	I	194	GLN
1	I	195	GLN
1	I	253	ASN
1	I	266	ASN
1	I	279	HIS
2	J	27	GLN
2	J	28	ASN
2	J	30	GLN
2	J	95	ASN
2	J	125	GLN
2	J	129	ASN
2	J	146	ASN
1	K	37	ASN
1	K	44	ASN
1	K	93	ASN
1	K	132	HIS
1	K	162	ASN
1	K	194	GLN
1	K	195	GLN
1	K	253	ASN
1	K	266	ASN
1	K	279	HIS
2	L	27	GLN
2	L	28	ASN

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Mol	Chain	Res	Type
2	L	30	GLN
2	L	125	GLN
2	L	129	ASN
2	L	146	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

16 carbohydrates are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	NAG	A	602	1,4	14,14,15	0.52	0	15,19,21	1.06	1 (6%)
4	NAG	A	603	4	14,14,15	0.55	0	15,19,21	1.62	3 (20%)
4	NAG	A	604	1,4	14,14,15	0.54	0	15,19,21	0.58	0
4	NAG	A	605	4	14,14,15	0.44	0	15,19,21	1.02	0
5	NAG	C	602	1,5	14,14,15	0.58	0	15,19,21	1.24	1 (6%)
5	NAG	C	603	5	14,14,15	0.52	0	15,19,21	1.06	1 (6%)
5	BMA	C	604	5	11,11,12	0.25	0	14,15,17	0.60	0
4	NAG	C	605	1,4	14,14,15	0.53	0	15,19,21	0.79	0
4	NAG	C	606	4	14,14,15	0.42	0	15,19,21	2.16	4 (26%)
4	NAG	E	602	1,4	14,14,15	0.53	0	15,19,21	0.59	0
4	NAG	E	603	4	14,14,15	0.55	0	15,19,21	0.69	0
5	NAG	I	601	1,5	14,14,15	0.50	0	15,19,21	1.92	3 (20%)
5	NAG	I	602	5	14,14,15	0.39	0	15,19,21	1.99	3 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	BMA	I	603	5	11,11,12	0.26	0	14,15,17	0.61	0
4	NAG	I	604	1,4	14,14,15	0.52	0	15,19,21	1.94	3 (20%)
4	NAG	I	605	4	14,14,15	0.58	0	15,19,21	1.07	1 (6%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	A	602	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	603	4	-	0/6/23/26	0/1/1/1
4	NAG	A	604	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	605	4	-	0/6/23/26	0/1/1/1
5	NAG	C	602	1,5	-	0/6/23/26	0/1/1/1
5	NAG	C	603	5	-	0/6/23/26	0/1/1/1
5	BMA	C	604	5	-	0/2/19/22	0/1/1/1
4	NAG	C	605	1,4	-	0/6/23/26	0/1/1/1
4	NAG	C	606	4	-	0/6/23/26	0/1/1/1
4	NAG	E	602	1,4	-	0/6/23/26	0/1/1/1
4	NAG	E	603	4	-	0/6/23/26	0/1/1/1
5	NAG	I	601	1,5	-	0/6/23/26	0/1/1/1
5	NAG	I	602	5	-	0/6/23/26	0/1/1/1
5	BMA	I	603	5	-	0/2/19/22	0/1/1/1
4	NAG	I	604	1,4	-	0/6/23/26	0/1/1/1
4	NAG	I	605	4	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	I	601	NAG	C2-N2-C7	-5.56	115.90	123.04
4	A	603	NAG	C2-N2-C7	-4.86	116.80	123.04
5	I	602	NAG	C4-C3-C2	-4.03	104.97	111.23
4	C	606	NAG	C2-N2-C7	-3.82	118.13	123.04
5	C	602	NAG	C2-N2-C7	-3.60	118.42	123.04
4	I	604	NAG	C4-C3-C2	-3.21	106.23	111.23
4	I	604	NAG	C2-N2-C7	-3.10	119.05	123.04
5	I	602	NAG	C2-N2-C7	-2.51	119.81	123.04
4	A	603	NAG	C4-C3-C2	-2.23	107.76	111.23
4	C	606	NAG	C4-C3-C2	-2.19	107.82	111.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	603	NAG	C2-N2-C7	-2.13	120.30	123.04
4	C	606	NAG	C6-C5-C4	-2.05	107.95	113.02
4	A	603	NAG	C1-O5-C5	-2.03	109.67	112.25
4	A	602	NAG	C1-O5-C5	2.07	114.88	112.25
5	I	601	NAG	C4-C3-C2	2.34	114.87	111.23
4	I	605	NAG	C3-C4-C5	2.82	115.11	110.20
5	I	601	NAG	C1-O5-C5	3.27	116.40	112.25
4	I	604	NAG	O4-C4-C3	5.10	121.81	110.34
5	I	602	NAG	C1-O5-C5	5.39	119.08	112.25
4	C	606	NAG	C1-O5-C5	6.54	120.54	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

12 monomers are involved in 29 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	602	NAG	6	0
4	A	603	NAG	3	0
4	A	604	NAG	4	0
4	A	605	NAG	1	0
5	C	602	NAG	3	0
4	C	605	NAG	2	0
4	E	602	NAG	3	0
5	I	601	NAG	1	0
5	I	602	NAG	2	0
5	I	603	BMA	2	0
4	I	604	NAG	3	0
4	I	605	NAG	3	0

5.6 Ligand geometry

16 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	A	601	1	14,14,15	0.53	0	15,19,21	0.59	0
3	NAG	A	606	1	14,14,15	0.52	0	15,19,21	0.80	0
3	NAG	C	601	1	14,14,15	0.54	0	15,19,21	0.59	0
3	NAG	C	607	1	14,14,15	0.53	0	15,19,21	0.60	0
3	NAG	E	601	1	14,14,15	0.54	0	15,19,21	0.58	0
3	NAG	E	604	1	14,14,15	0.52	0	15,19,21	0.65	0
3	NAG	E	605	1	14,14,15	0.53	0	15,19,21	1.17	3 (20%)
3	NAG	F	601	2	14,14,15	0.53	0	15,19,21	0.59	0
3	NAG	G	601	1	14,14,15	0.51	0	15,19,21	0.78	0
3	NAG	G	602	1	14,14,15	0.53	0	15,19,21	0.58	0
3	NAG	G	603	1	14,14,15	0.54	0	15,19,21	0.58	0
3	NAG	K	601	1	14,14,15	0.44	0	15,19,21	2.57	2 (13%)
3	NAG	K	602	1	14,14,15	0.54	0	15,19,21	0.60	0
3	NAG	K	603	1	14,14,15	0.54	0	15,19,21	0.59	0
3	NAG	K	604	1	14,14,15	0.54	0	15,19,21	0.60	0
3	NAG	L	601	2	14,14,15	0.54	0	15,19,21	0.59	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	A	601	1	-	0/6/23/26	0/1/1/1
3	NAG	A	606	1	-	0/6/23/26	0/1/1/1
3	NAG	C	601	1	-	0/6/23/26	0/1/1/1
3	NAG	C	607	1	-	0/6/23/26	0/1/1/1
3	NAG	E	601	1	-	0/6/23/26	0/1/1/1
3	NAG	E	604	1	-	0/6/23/26	0/1/1/1
3	NAG	E	605	1	-	0/6/23/26	0/1/1/1
3	NAG	F	601	2	-	0/6/23/26	0/1/1/1
3	NAG	G	601	1	-	0/6/23/26	0/1/1/1
3	NAG	G	602	1	-	0/6/23/26	0/1/1/1
3	NAG	G	603	1	-	0/6/23/26	0/1/1/1
3	NAG	K	601	1	-	0/6/23/26	0/1/1/1
3	NAG	K	602	1	-	0/6/23/26	0/1/1/1
3	NAG	K	603	1	-	0/6/23/26	0/1/1/1
3	NAG	K	604	1	-	0/6/23/26	0/1/1/1
3	NAG	L	601	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	E	605	NAG	C2-N2-C7	-2.33	120.05	123.04
3	E	605	NAG	C6-C5-C4	-2.31	107.32	113.02
3	K	601	NAG	C4-C3-C2	-2.09	107.98	111.23
3	E	605	NAG	C3-C4-C5	2.22	114.06	110.20
3	K	601	NAG	C1-O5-C5	9.28	124.03	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 27 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	607	NAG	3	0
3	E	601	NAG	2	0
3	G	602	NAG	2	0
3	G	603	NAG	1	0
3	K	602	NAG	4	0
3	K	603	NAG	3	0
3	K	604	NAG	2	0
3	L	601	NAG	10	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2		OWAB(Å ²)	Q < 0.9
1	A	321/333 (96%)	0.57	31 (9%)	10 6	39, 70, 122, 226	0
1	C	321/333 (96%)	0.43	26 (8%)	15 10	36, 67, 116, 196	0
1	E	321/333 (96%)	0.89	47 (14%)	3 2	41, 74, 130, 215	0
1	G	321/333 (96%)	0.73	42 (13%)	5 3	46, 76, 128, 232	0
1	I	321/333 (96%)	0.53	27 (8%)	14 9	37, 70, 120, 228	0
1	K	321/333 (96%)	0.42	27 (8%)	14 9	38, 70, 121, 195	0
2	B	162/181 (89%)	0.87	25 (15%)	3 1	32, 77, 167, 209	0
2	D	162/181 (89%)	1.05	36 (22%)	1 1	34, 72, 186, 246	0
2	F	161/181 (88%)	1.03	35 (21%)	1 1	34, 74, 178, 241	0
2	H	162/181 (89%)	1.21	38 (23%)	1 1	33, 80, 174, 289	0
2	J	162/181 (89%)	0.63	11 (6%)	20 15	32, 69, 165, 200	0
2	L	161/181 (88%)	0.60	15 (9%)	11 7	36, 73, 169, 199	0
All	All	2896/3084 (93%)	0.70	360 (12%)	5 3	32, 72, 157, 289	0

All (360) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	159	TYR	13.1
2	F	128	ASN	10.5
2	D	139	GLU	9.4
2	D	140	PHE	8.2
2	H	31	GLY	8.1
1	C	9	LEU	7.9
2	F	140	PHE	7.9
2	J	159	TYR	7.8
2	D	138	PHE	7.6
1	E	12	GLY	7.5
2	H	32	SER	7.5

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Mol	Chain	Res	Type	RSRZ
2	D	134	GLY	7.3
2	B	139	GLU	7.1
2	H	158	ASP	7.0
1	C	77	SER	6.7
1	C	78	THR	6.6
1	A	78	THR	6.6
2	B	156	THR	6.5
1	G	76	LEU	6.5
2	D	142	HIS	6.4
2	D	158	ASP	6.3
1	K	12	GLY	6.3
2	D	133	ILE	6.2
2	D	132	GLU	6.2
2	B	23	GLY	5.9
2	H	140	PHE	5.9
2	H	154	ASN	5.6
2	H	149	MET	5.6
2	D	154	ASN	5.6
1	E	9	LEU	5.6
1	C	10	CYS	5.4
2	D	129	ASN	5.3
1	C	75	SER	5.3
1	A	126	THR	5.2
2	J	162	TYR	5.1
2	B	149	MET	5.1
1	I	195	GLN	5.1
2	F	155	GLY	5.0
2	H	27	GLN	5.0
1	G	21	THR	5.0
1	I	78	THR	5.0
1	A	162	ASN	4.9
1	K	162	ASN	4.8
2	F	160	PRO	4.7
1	C	76	LEU	4.7
2	F	131	LYS	4.7
2	F	143	LYS	4.7
2	F	158	ASP	4.7
1	E	280	ASP	4.7
2	B	160	PRO	4.6
2	D	141	TYR	4.6
2	H	29	GLU	4.6
1	E	274	SER	4.5

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Mol	Chain	Res	Type	RSRZ
1	C	51	ARG	4.5
1	C	11	ILE	4.5
2	F	141	TYR	4.4
1	G	50	LEU	4.4
2	H	129	ASN	4.4
2	J	38	LEU	4.4
1	A	79	ALA	4.4
1	G	146	GLY	4.4
1	G	14	HIS	4.4
2	D	31	GLY	4.4
2	B	141	TYR	4.4
2	H	20	GLY	4.3
2	F	137	CYS	4.2
2	F	144	CYS	4.2
1	C	195	GLN	4.2
2	B	158	ASP	4.2
2	F	149	MET	4.2
1	A	76	LEU	4.1
1	G	326	ASN	4.1
1	E	136	LYS	4.1
1	E	78	THR	4.1
2	F	127	LYS	4.1
2	F	29	GLU	4.0
2	F	138	PHE	4.0
1	E	149	SER	3.9
1	E	278	VAL	3.9
2	H	128	ASN	3.9
2	H	143	LYS	3.9
1	C	228	ASP	3.9
2	H	141	TYR	3.8
1	G	32	VAL	3.8
1	I	199	GLN	3.8
1	E	146	GLY	3.8
1	E	79	ALA	3.8
1	E	30	VAL	3.8
2	F	139	GLU	3.7
1	E	8	THR	3.7
1	I	92	ASP	3.7
1	G	195	GLN	3.7
1	G	12	GLY	3.7
1	K	116	SER	3.7
2	D	128	ASN	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	9	LEU	3.7
2	D	26	HIS	3.7
2	B	148	CYS	3.7
1	E	148	LYS	3.6
2	F	126	LEU	3.6
1	G	60	LYS	3.6
2	J	29	GLU	3.6
2	B	142	HIS	3.6
1	G	31	THR	3.6
2	D	24	TYR	3.6
1	E	77	SER	3.5
2	D	143	LYS	3.5
1	G	280	ASP	3.5
2	D	126	LEU	3.5
1	K	50	LEU	3.4
2	D	17	MET	3.4
2	D	22	TYR	3.4
1	K	199	GLN	3.4
1	C	159	LYS	3.4
2	D	137	CYS	3.4
2	H	156	THR	3.4
1	A	146	GLY	3.4
1	K	146	GLY	3.4
2	L	142	HIS	3.4
1	E	13	TYR	3.4
1	E	193	ASP	3.4
1	A	17	ASN	3.4
2	F	162	TYR	3.4
2	H	130	ALA	3.4
1	E	281	CYS	3.3
2	D	145	ASP	3.3
1	A	195	GLN	3.3
1	K	149	SER	3.3
2	F	132	GLU	3.3
2	L	132	GLU	3.3
2	D	38	LEU	3.3
2	H	150	GLU	3.3
2	L	140	PHE	3.3
2	F	27	GLN	3.3
2	H	30	GLN	3.3
1	C	12	GLY	3.2
2	L	128	ASN	3.2

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Mol	Chain	Res	Type	RSRZ
2	D	131	LYS	3.2
1	A	95	THR	3.2
2	F	142	HIS	3.2
1	I	17	ASN	3.2
1	I	18	SER	3.2
2	H	126	LEU	3.2
1	A	19	THR	3.2
2	D	150	GLU	3.2
1	A	11	ILE	3.2
2	H	131	LYS	3.2
2	H	19	ASP	3.2
1	A	142	CYS	3.2
1	G	57	HIS	3.2
1	G	29	ASN	3.1
1	E	222	ILE	3.1
1	I	228	ASP	3.1
2	H	33	GLY	3.1
1	E	294	THR	3.1
1	A	279	HIS	3.1
2	F	148	CYS	3.1
2	F	24	TYR	3.1
1	E	75	SER	3.0
1	A	198	TYR	3.0
2	D	146	ASN	3.0
1	K	91	SER	3.0
1	G	19	THR	3.0
2	B	15	THR	3.0
2	F	30	GLN	3.0
1	A	199	GLN	3.0
2	H	138	PHE	3.0
1	K	200	ASN	3.0
1	G	77	SER	3.0
1	K	75	SER	3.0
2	B	140	PHE	3.0
1	E	141	ALA	2.9
1	E	131	ASN	2.9
2	J	26	HIS	2.9
1	G	51	ARG	2.9
1	G	162	ASN	2.9
2	B	126	LEU	2.9
1	G	228	ASP	2.9
1	A	21	THR	2.9

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Mol	Chain	Res	Type	RSRZ
2	D	11	GLU	2.9
1	I	200	ASN	2.9
2	J	148	CYS	2.9
2	L	131	LYS	2.9
2	B	29	GLU	2.8
2	F	156	THR	2.8
1	E	198	TYR	2.8
1	C	50	LEU	2.8
1	I	55	PRO	2.8
2	H	144	CYS	2.8
2	D	157	TYR	2.8
1	G	93	ASN	2.8
1	E	275	ASP	2.8
1	I	146	GLY	2.8
1	E	231	GLY	2.8
1	K	52	GLY	2.8
2	D	1	GLY	2.8
2	L	133	ILE	2.8
2	D	130	ALA	2.8
2	J	160	PRO	2.8
2	F	134	GLY	2.8
1	E	291	ALA	2.7
1	K	164	TYR	2.7
1	K	269	SER	2.7
1	I	51	ARG	2.7
1	I	230	GLU	2.7
1	K	74	GLU	2.7
1	E	76	LEU	2.7
2	F	157	TYR	2.7
1	C	52	GLY	2.7
1	C	294	THR	2.7
2	L	139	GLU	2.7
1	G	137	GLY	2.7
2	F	23	GLY	2.7
2	H	24	TYR	2.7
1	A	116	SER	2.7
2	H	145	ASP	2.6
1	E	19	THR	2.6
2	B	138	PHE	2.6
2	H	146	ASN	2.6
2	H	147	THR	2.6
1	C	198	TYR	2.6

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Mol	Chain	Res	Type	RSRZ
2	B	157	TYR	2.6
1	C	79	ALA	2.6
2	J	144	CYS	2.6
1	A	42	LYS	2.6
2	B	36	ALA	2.6
2	L	147	THR	2.6
1	A	250	ALA	2.6
2	J	141	TYR	2.6
1	A	75	SER	2.6
1	G	83	SER	2.6
1	C	17	ASN	2.6
1	K	92	ASP	2.6
2	B	33	GLY	2.5
2	J	149	MET	2.5
2	D	21	TRP	2.5
2	H	23	GLY	2.5
1	E	196	SER	2.5
2	H	28	ASN	2.5
2	D	39	LYS	2.5
1	A	275	ASP	2.5
1	E	22	VAL	2.5
2	B	18	VAL	2.5
1	E	11	ILE	2.5
1	E	199	GLN	2.5
1	K	28	LYS	2.5
2	D	29	GLU	2.5
2	H	157	TYR	2.5
2	H	26	HIS	2.5
1	G	20	ASP	2.5
2	F	38	LEU	2.5
1	C	60	LYS	2.5
1	I	148	LYS	2.5
2	B	153	LYS	2.5
1	K	143	PRO	2.5
1	G	125	LYS	2.5
2	D	19	ASP	2.5
1	A	163	SER	2.4
2	B	32	SER	2.4
1	E	162	ASN	2.4
1	E	286	GLN	2.4
1	C	279	HIS	2.4
1	G	278	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
2	L	130	ALA	2.4
1	G	193	ASP	2.4
1	A	289	LYS	2.4
2	F	28	ASN	2.4
1	I	8	THR	2.4
1	G	47	LEU	2.4
1	C	158	VAL	2.4
1	C	130	PRO	2.4
2	H	18	VAL	2.4
1	G	197	LEU	2.3
1	K	115	SER	2.3
1	I	149	SER	2.3
1	G	48	CYS	2.3
2	B	35	ALA	2.3
1	C	14	HIS	2.3
1	E	42	LYS	2.3
1	C	268	GLY	2.3
1	K	72	GLU	2.3
1	E	197	LEU	2.3
2	F	129	ASN	2.3
1	A	264	GLU	2.3
1	A	10	CYS	2.3
2	B	147	THR	2.3
1	E	98	PRO	2.3
2	B	144	CYS	2.3
1	E	90	SER	2.3
2	H	139	GLU	2.3
1	A	197	LEU	2.3
1	I	140	ALA	2.3
2	B	16	GLY	2.3
1	C	220	ILE	2.2
1	K	279	HIS	2.2
1	E	46	LYS	2.2
2	H	127	LYS	2.2
1	K	78	THR	2.2
1	K	280	ASP	2.2
1	E	51	ARG	2.2
1	G	89	PRO	2.2
1	I	10	CYS	2.2
2	F	130	ALA	2.2
1	A	51	ARG	2.2
1	K	44	ASN	2.2

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Mol	Chain	Res	Type	RSRZ
1	I	282	ASN	2.2
1	A	136	LYS	2.2
1	E	201	ALA	2.2
2	L	31	GLY	2.2
1	E	277	PRO	2.2
1	I	136	LYS	2.2
1	I	12	GLY	2.2
1	G	16	ASN	2.2
1	G	161	GLY	2.2
1	K	323	GLY	2.2
1	I	145	ALA	2.2
2	J	146	ASN	2.2
1	E	133	ASP	2.1
1	G	150	PHE	2.1
1	I	268	GLY	2.1
1	G	75	SER	2.1
2	H	155	GLY	2.1
2	L	4	GLY	2.1
2	B	143	LYS	2.1
2	L	141	TYR	2.1
2	F	33	GLY	2.1
1	G	18	SER	2.1
1	I	11	ILE	2.1
1	E	195	GLN	2.1
2	D	147	THR	2.1
1	G	17	ASN	2.1
2	H	153	LYS	2.1
1	G	147	ALA	2.1
1	G	267	ALA	2.1
2	H	161	LYS	2.1
2	D	28	ASN	2.1
2	L	129	ASN	2.1
1	E	116	SER	2.1
1	E	295	SER	2.1
1	A	317	LYS	2.1
1	K	90	SER	2.1
2	F	113	SER	2.1
2	L	29	GLU	2.1
1	I	147	ALA	2.1
2	L	35	ALA	2.1
1	G	281	CYS	2.0
2	D	160	PRO	2.0

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Mol	Chain	Res	Type	RSRZ
1	I	20	ASP	2.0
1	C	322	THR	2.0
2	H	133	ILE	2.0
1	A	326	ASN	2.0
1	E	161	GLY	2.0
1	I	112	SER	2.0
1	G	133	ASP	2.0
1	G	273	ILE	2.0
2	F	25	HIS	2.0
1	K	195	GLN	2.0
1	I	126	THR	2.0
1	K	47	LEU	2.0
1	G	241	GLU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	NAG	A	602	14/15	0.88	0.40	2.80	82,113,129,130	0
4	NAG	A	604	14/15	0.78	0.34	0.58	68,108,117,126	0
4	NAG	E	602	14/15	0.82	0.26	0.28	108,129,134,135	0
4	NAG	I	604	14/15	0.83	0.27	0.14	94,114,139,150	0
5	NAG	I	601	14/15	0.81	0.21	-0.80	72,82,95,97	0
5	BMA	C	604	11/12	0.74	0.28	-1.18	89,112,124,151	0
5	NAG	C	602	14/15	0.89	0.12	-1.69	61,76,95,102	0
4	NAG	C	605	14/15	0.90	0.19	-2.85	70,86,98,99	0
5	NAG	C	603	14/15	0.82	0.28	-	55,84,111,120	0
4	NAG	I	605	14/15	0.77	0.31	-	128,134,141,147	0
4	NAG	E	603	14/15	0.75	0.49	-	119,139,166,193	0
4	NAG	A	603	14/15	0.66	0.54	-	120,148,155,174	0
5	NAG	I	602	14/15	0.92	0.32	-	92,117,138,145	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	NAG	A	605	14/15	0.66	0.39	-	124,134,147,148	0
4	NAG	C	606	14/15	0.75	0.34	-	91,106,136,144	0
5	BMA	I	603	11/12	0.50	0.30	-	108,135,142,143	0

6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	NAG	L	601	14/15	0.33	0.55	2.58	132,161,178,187	0
3	NAG	A	601	14/15	0.63	0.34	0.46	53,78,94,104	0
3	NAG	C	607	14/15	0.71	0.40	0.30	95,116,142,146	0
3	NAG	G	601	14/15	0.72	0.32	-	141,158,176,181	0
3	NAG	K	602	14/15	0.62	0.35	-	68,115,138,139	0
3	NAG	E	605	14/15	0.57	0.58	-	134,171,193,199	0
3	NAG	K	604	14/15	0.76	0.49	-	108,133,146,153	0
3	NAG	E	604	14/15	0.72	0.53	-	26,28,30,30	0
3	NAG	K	603	14/15	0.72	0.51	-	84,126,147,153	0
3	NAG	C	601	14/15	0.66	0.49	-	157,180,192,198	0
3	NAG	F	601	14/15	0.62	0.45	-	154,173,188,194	0
3	NAG	E	601	14/15	0.55	0.53	-	117,156,185,194	0
3	NAG	K	601	14/15	0.54	0.35	-	88,113,140,142	0
3	NAG	A	606	14/15	0.53	0.51	-	103,126,141,143	0
3	NAG	G	602	14/15	0.70	0.49	-	171,186,198,202	0
3	NAG	G	603	14/15	0.73	0.43	-	139,163,185,199	0

6.5 Other polymers

There are no such residues in this entry.