



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:05 AM GMT

PDB ID : 3GYR
Title : Structure of Phenoxazinone synthase from Streptomyces antibioticus reveals a new type 2 copper center.
Authors : Smith, A.W.; Camara-Artigas, A.; Wang, M.; Francisco, W.A.; Allen, J.P.
Deposited on : 2009-04-05
Resolution : 2.30 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

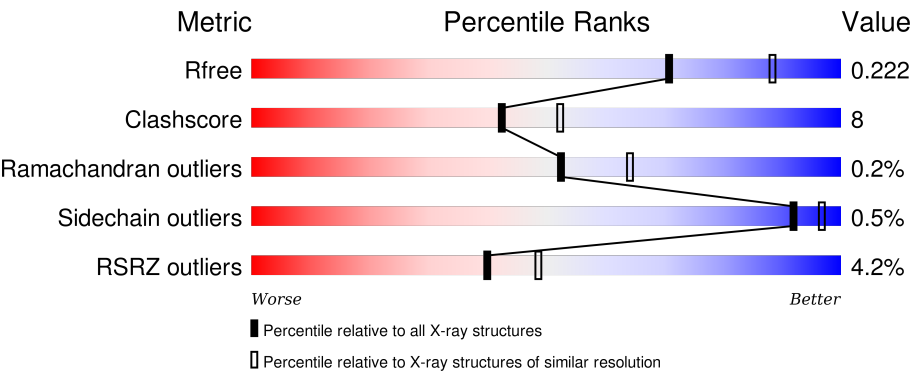
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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	612	<div><div>5%</div><div><div></div><div>78%</div><div>17%</div><div>• •</div></div></div>
1	B	612	<div><div>4%</div><div><div></div><div>83%</div><div>13%</div><div>•</div></div></div>
1	C	612	<div><div>3%</div><div><div></div><div>85%</div><div>11%</div><div>• •</div></div></div>
1	D	612	<div><div>2%</div><div><div></div><div>82%</div><div>13%</div><div>•</div></div></div>
1	E	612	<div><div>5%</div><div><div></div><div>84%</div><div>12%</div><div>•</div></div></div>

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Mol	Chain	Length	Quality of chain
1	F	612	
1	G	612	
1	H	612	
1	I	612	
1	J	612	
1	K	612	
1	L	612	

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
4	GOL	B	5002	-	-	-	X
4	GOL	C	5003	-	-	-	X
4	GOL	D	5004	-	-	-	X
4	GOL	E	5005	-	-	-	X
4	GOL	H	5008	-	-	-	X
4	GOL	K	5011	-	-	-	X
4	GOL	L	5012	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 59241 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 Phenoxazinone synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	587	Total	C	N	O	S	0	0	0
			4560	2886	812	847	15			
1	B	587	Total	C	N	O	S	0	0	0
			4560	2886	812	847	15			
1	C	587	Total	C	N	O	S	0	0	0
			4560	2886	812	847	15			
1	D	587	Total	C	N	O	S	0	0	0
			4560	2886	812	847	15			
1	E	587	Total	C	N	O	S	0	0	0
			4560	2886	812	847	15			
1	F	587	Total	C	N	O	S	0	0	0
			4560	2886	812	847	15			
1	G	587	Total	C	N	O	S	0	0	0
			4560	2886	812	847	15			
1	H	587	Total	C	N	O	S	0	0	0
			4560	2886	812	847	15			
1	I	587	Total	C	N	O	S	0	0	0
			4560	2886	812	847	15			
1	J	587	Total	C	N	O	S	0	0	0
			4560	2886	812	847	15			
1	K	587	Total	C	N	O	S	0	0	0
			4560	2886	812	847	15			
1	L	587	Total	C	N	O	S	0	0	0
			4560	2886	812	847	15			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	496	ARG	ALA	ENGINEERED	UNP Q53692
B	496	ARG	ALA	ENGINEERED	UNP Q53692
C	496	ARG	ALA	ENGINEERED	UNP Q53692
D	496	ARG	ALA	ENGINEERED	UNP Q53692
E	496	ARG	ALA	ENGINEERED	UNP Q53692

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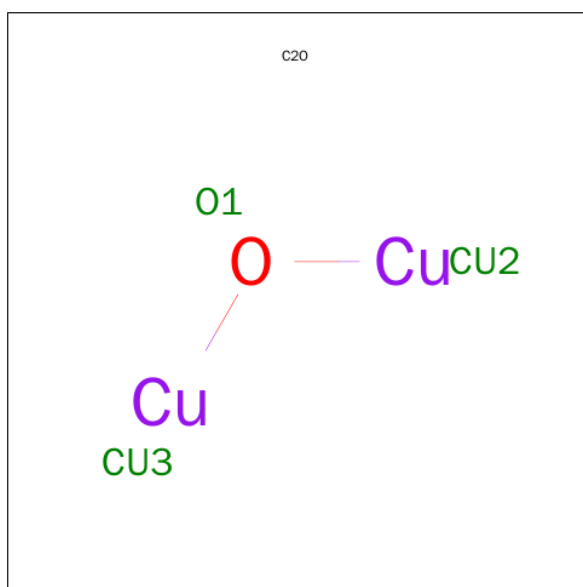
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Chain	Residue	Modelled	Actual	Comment	Reference
F	496	ARG	ALA	ENGINEERED	UNP Q53692
G	496	ARG	ALA	ENGINEERED	UNP Q53692
H	496	ARG	ALA	ENGINEERED	UNP Q53692
I	496	ARG	ALA	ENGINEERED	UNP Q53692
J	496	ARG	ALA	ENGINEERED	UNP Q53692
K	496	ARG	ALA	ENGINEERED	UNP Q53692
L	496	ARG	ALA	ENGINEERED	UNP Q53692

- Molecule 2 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	G	3	Total Cu 3 3	0	0
2	J	3	Total Cu 3 3	0	0
2	D	3	Total Cu 3 3	0	0
2	K	3	Total Cu 3 3	0	0
2	E	3	Total Cu 3 3	0	0
2	H	3	Total Cu 3 3	0	0
2	B	3	Total Cu 3 3	0	0
2	I	3	Total Cu 3 3	0	0
2	C	3	Total Cu 3 3	0	0
2	A	3	Total Cu 3 3	0	0
2	L	3	Total Cu 3 3	0	0
2	F	3	Total Cu 3 3	0	0

- Molecule 3 is CU-O-CU LINKAGE (three-letter code: C2O) (formula: Cu₂O).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	Cu	O	0	0
			3	2	1		
3	B	1	Total	Cu	O	0	0
			3	2	1		
3	C	1	Total	Cu	O	0	0
			3	2	1		
3	D	1	Total	Cu	O	0	0
			3	2	1		
3	E	1	Total	Cu	O	0	0
			3	2	1		
3	F	1	Total	Cu	O	0	0
			3	2	1		
3	G	1	Total	Cu	O	0	0
			3	2	1		
3	H	1	Total	Cu	O	0	0
			3	2	1		
3	I	1	Total	Cu	O	0	0
			3	2	1		
3	J	1	Total	Cu	O	0	0
			3	2	1		
3	K	1	Total	Cu	O	0	0
			3	2	1		
3	L	1	Total	Cu	O	0	0
			3	2	1		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	E	1	Total	C	O	0	0
			6	3	3		
4	F	1	Total	C	O	0	0
			6	3	3		
4	G	1	Total	C	O	0	0
			6	3	3		
4	H	1	Total	C	O	0	0
			6	3	3		
4	I	1	Total	C	O	0	0
			6	3	3		
4	J	1	Total	C	O	0	0
			6	3	3		
4	K	1	Total	C	O	0	0
			6	3	3		
4	L	1	Total	C	O	0	0
			6	3	3		

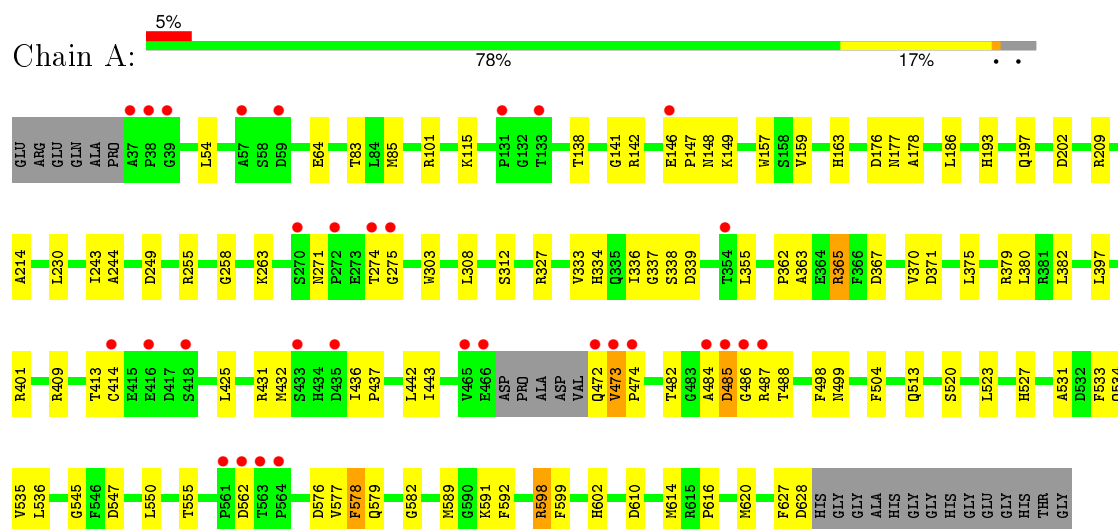
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	354	Total	O	0	0
			354	354		
5	B	362	Total	O	0	0
			362	362		
5	C	398	Total	O	0	0
			398	398		
5	D	386	Total	O	0	0
			386	386		
5	E	357	Total	O	0	0
			357	357		
5	F	361	Total	O	0	0
			361	361		
5	G	359	Total	O	0	0
			359	359		
5	H	376	Total	O	0	0
			376	376		
5	I	330	Total	O	0	0
			330	330		
5	J	388	Total	O	0	0
			388	388		
5	K	359	Total	O	0	0
			359	359		
5	L	347	Total	O	0	0
			347	347		

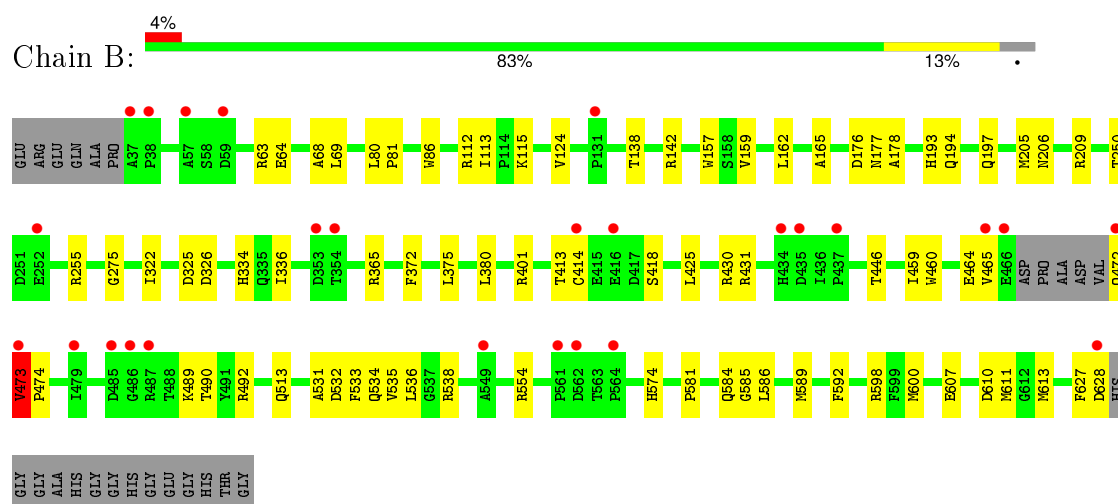
3 Residue-property plots

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.

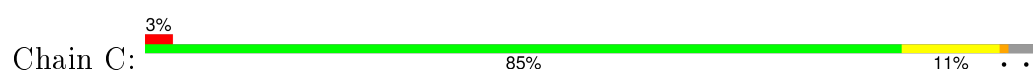
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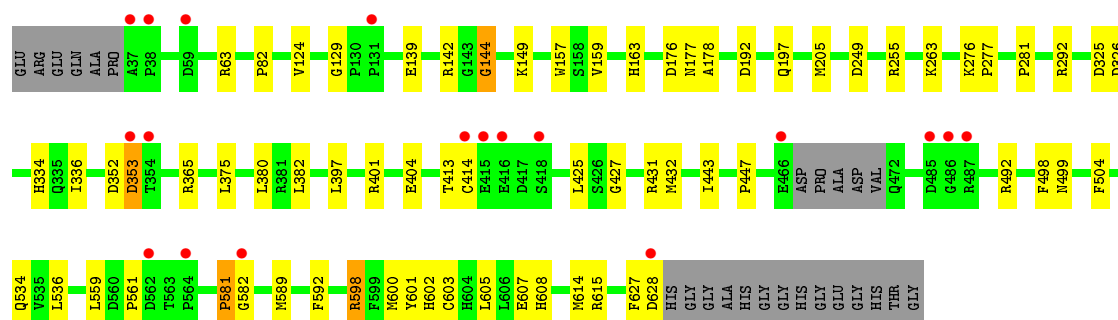


• Molecule 1: Phenoxazinone synthase

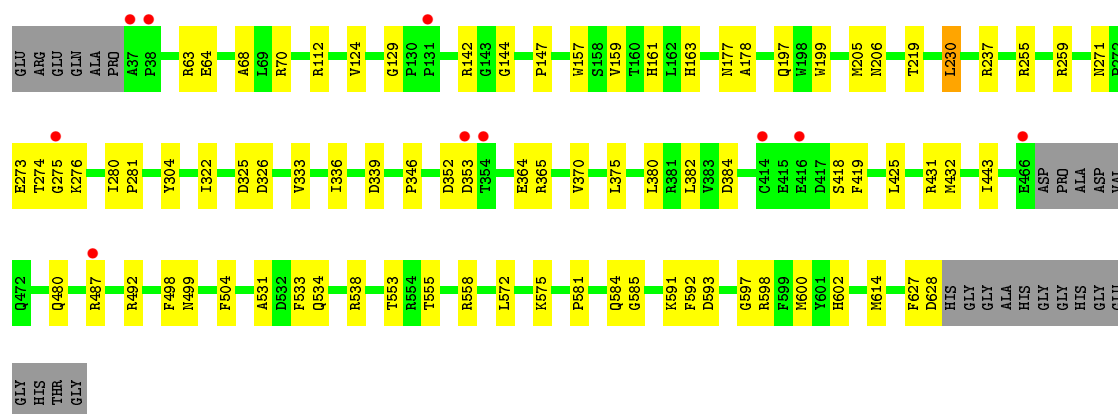
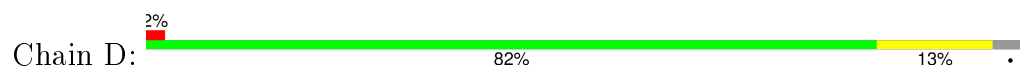


• Molecule 1: Phenoxazinone synthase

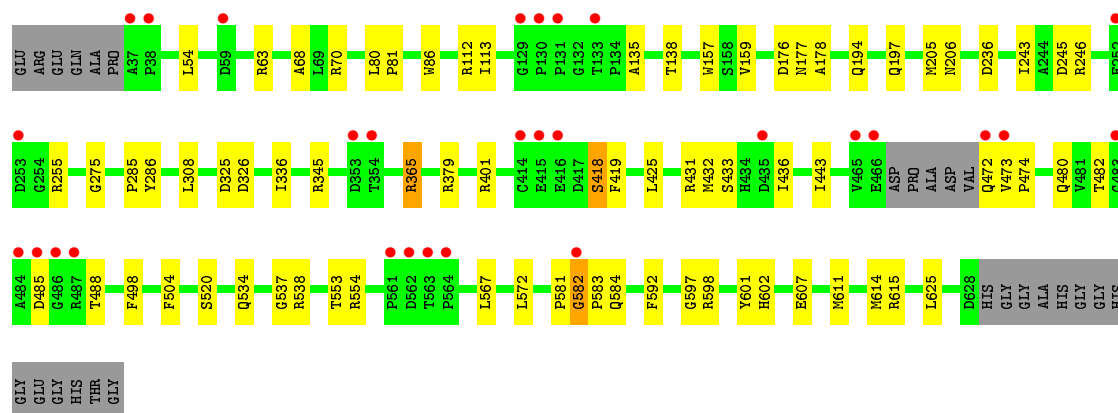
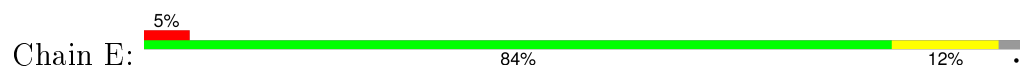




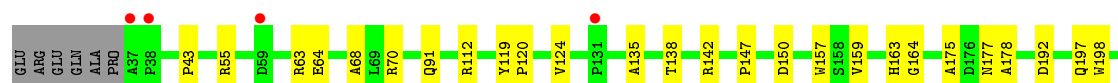
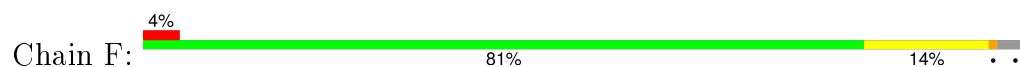
• Molecule 1: Phenoxazinone synthase

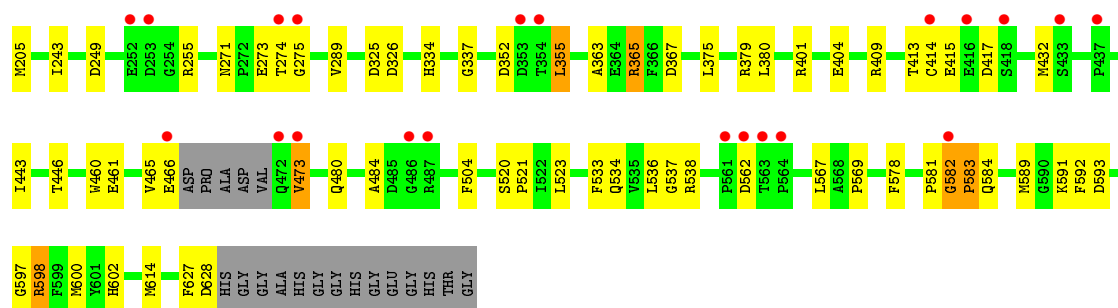


• Molecule 1: Phenoxazinone synthase

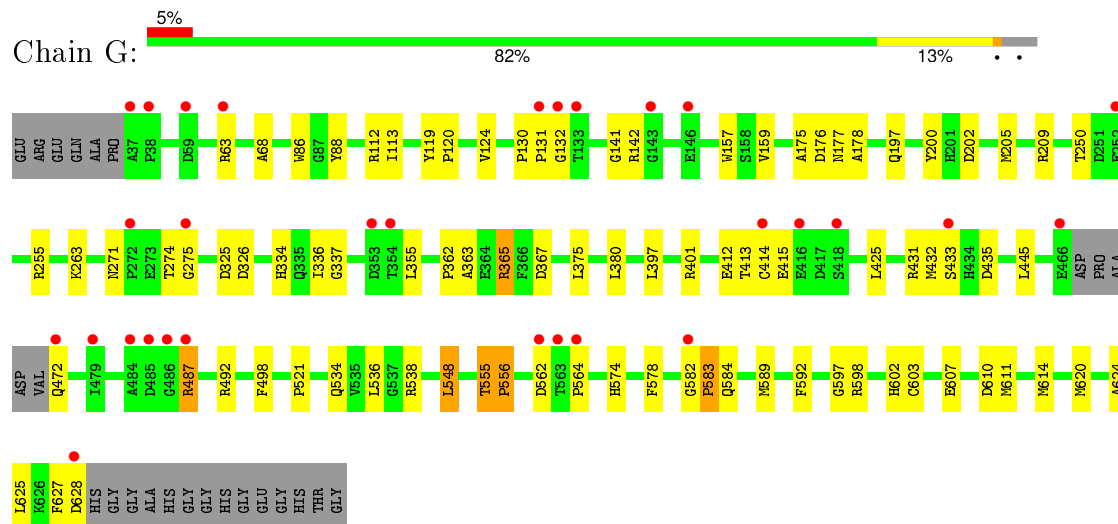


• Molecule 1: Phenoxazinone synthase

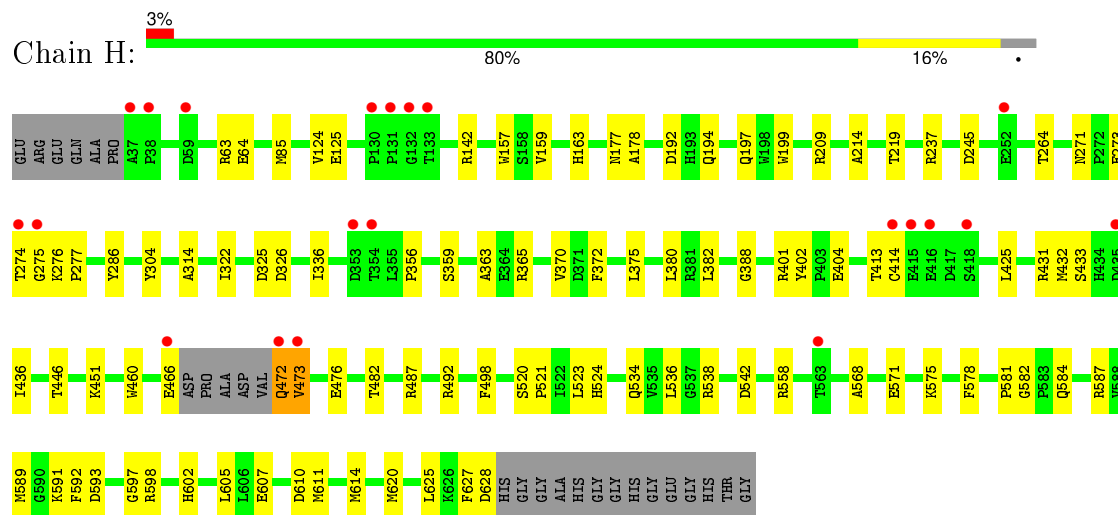




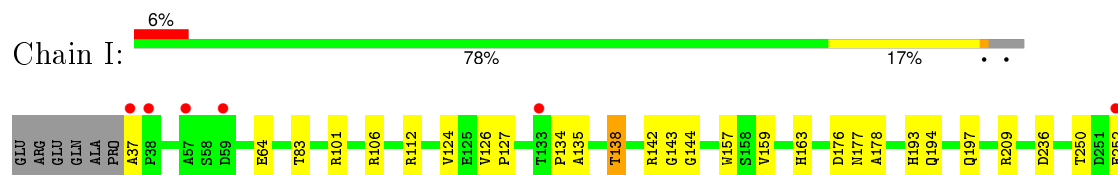
• Molecule 1: Phenoxazinone synthase

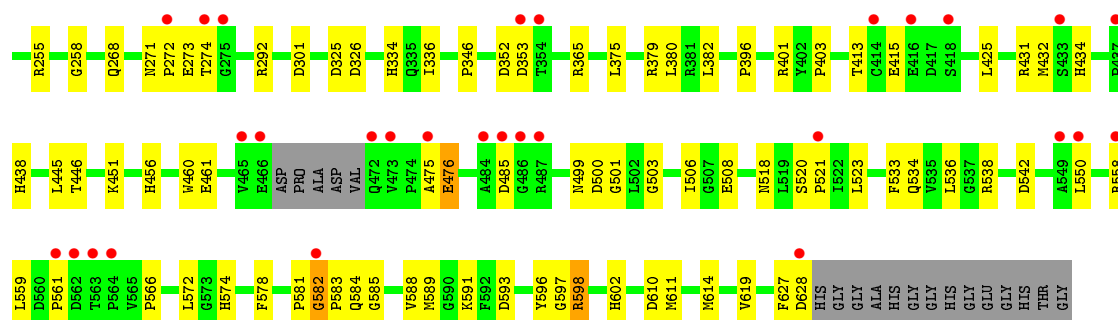


• Molecule 1: Phenoxazinone synthase

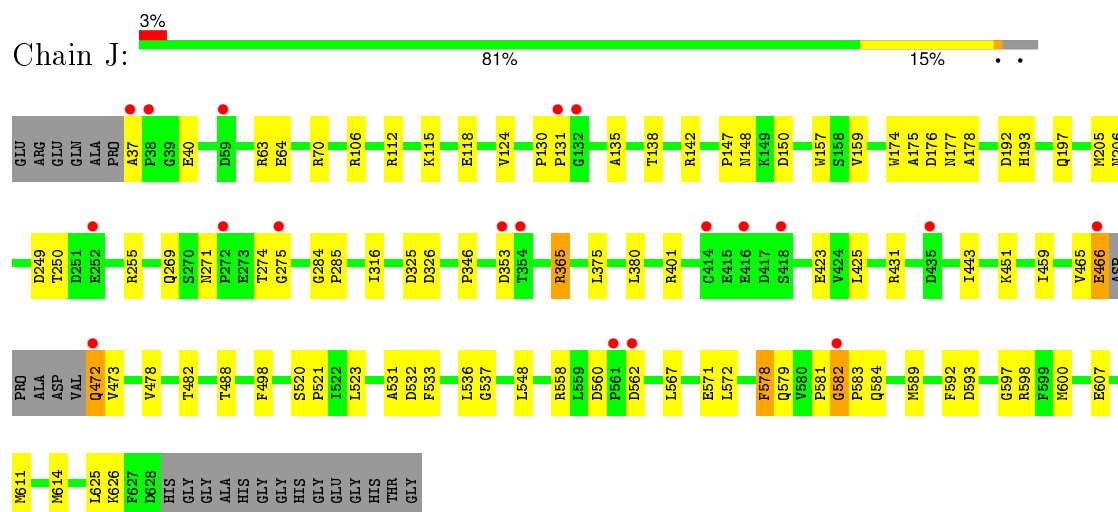


• Molecule 1: Phenoxazinone synthase

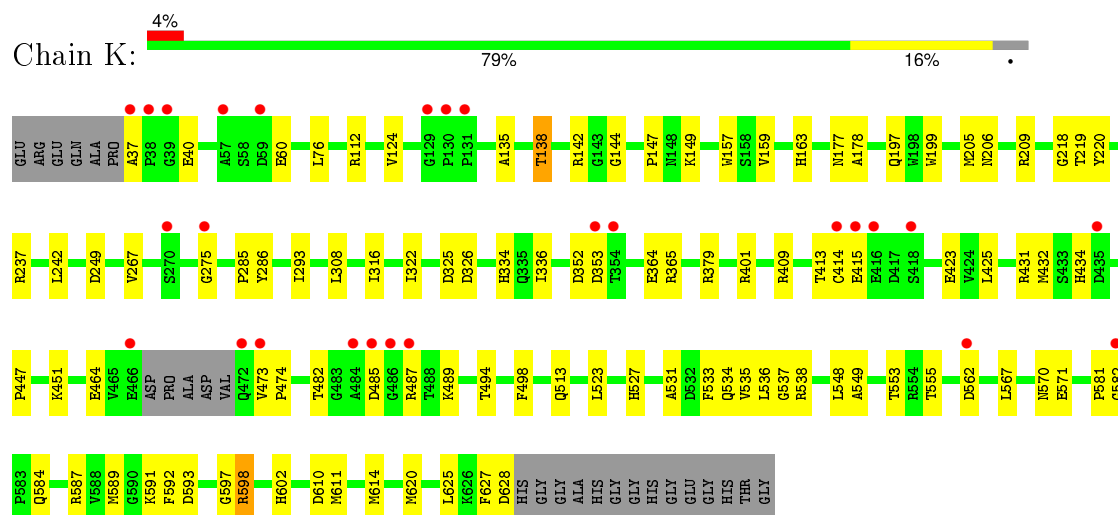




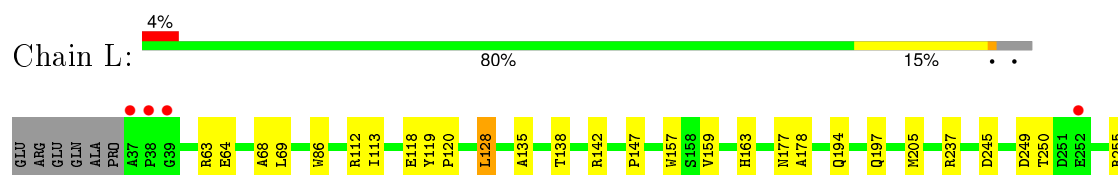
• Molecule 1: Phenoxazinone synthase

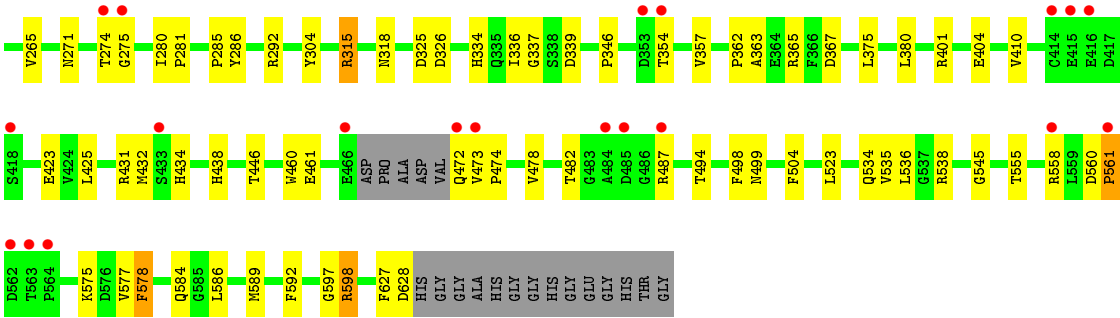


• Molecule 1: Phenoxazinone synthase



• Molecule 1: Phenoxazinone synthase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	109.49Å 163.46Å 164.35Å 117.04° 95.74° 107.23°	Depositor
Resolution (Å)	20.00 – 2.30 20.00 – 2.30	Depositor EDS
% Data completeness (in resolution range)	86.3 (20.00-2.30) 71.9 (20.00-2.30)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.54 (at 2.30Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.165 , 0.222 0.165 , 0.222	Depositor DCC
R_{free} test set	17920 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	29.2	Xtriage
Anisotropy	0.053	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 50.7	EDS
Estimated twinning fraction	0.007 for -h,h+k+l,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 356946 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	59241	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.55% 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: GOL, C2O, CU

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	0.66	0/4697	0.75	4/6423 (0.1%)
1	B	0.65	0/4697	0.74	0/6423
1	C	0.68	1/4697 (0.0%)	0.76	2/6423 (0.0%)
1	D	0.67	0/4697	0.73	2/6423 (0.0%)
1	E	0.67	0/4697	0.74	2/6423 (0.0%)
1	F	0.67	0/4697	0.74	3/6423 (0.0%)
1	G	0.69	1/4697 (0.0%)	0.76	2/6423 (0.0%)
1	H	0.66	0/4697	0.74	2/6423 (0.0%)
1	I	0.67	0/4697	0.74	3/6423 (0.0%)
1	J	0.67	0/4697	0.75	5/6423 (0.1%)
1	K	0.66	0/4697	0.74	2/6423 (0.0%)
1	L	0.65	0/4697	0.74	3/6423 (0.0%)
All	All	0.67	2/56364 (0.0%)	0.74	30/77076 (0.0%)

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	A	0	2
1	B	0	4
1	C	0	5
1	D	0	5
1	E	0	2
1	F	0	4
1	G	0	2
1	H	0	2
1	I	0	1
1	J	0	3
1	K	0	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	L	0	2
All	All	0	37

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	603	CYS	CB-SG	-6.39	1.71	1.82
1	C	603	CYS	CB-SG	-5.81	1.72	1.81

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	365	ARG	NE-CZ-NH2	-9.62	115.49	120.30
1	A	365	ARG	NE-CZ-NH1	6.75	123.68	120.30
1	I	292	ARG	NE-CZ-NH1	6.34	123.47	120.30
1	A	598	ARG	NE-CZ-NH2	-6.15	117.22	120.30
1	C	292	ARG	NE-CZ-NH1	5.97	123.29	120.30
1	G	548	LEU	CA-CB-CG	5.82	128.68	115.30
1	I	292	ARG	NE-CZ-NH2	-5.81	117.40	120.30
1	K	598	ARG	NE-CZ-NH2	-5.76	117.42	120.30
1	C	598	ARG	NE-CZ-NH2	-5.57	117.51	120.30
1	F	365	ARG	NE-CZ-NH2	-5.57	117.52	120.30
1	I	598	ARG	NE-CZ-NH2	-5.51	117.54	120.30
1	L	292	ARG	NE-CZ-NH1	5.48	123.04	120.30
1	F	598	ARG	NE-CZ-NH2	-5.47	117.56	120.30
1	J	106	ARG	NE-CZ-NH1	5.43	123.01	120.30
1	K	308	LEU	CA-CB-CG	5.36	127.63	115.30
1	G	365	ARG	NE-CZ-NH2	-5.34	117.63	120.30
1	F	355	LEU	CA-CB-CG	5.32	127.54	115.30
1	J	106	ARG	NE-CZ-NH2	-5.30	117.65	120.30
1	L	315	ARG	NE-CZ-NH2	-5.29	117.66	120.30
1	D	382	LEU	CB-CG-CD2	-5.28	102.02	111.00
1	E	365	ARG	NE-CZ-NH2	-5.28	117.66	120.30
1	D	384	ASP	CB-CG-OD1	5.12	122.91	118.30
1	L	598	ARG	NE-CZ-NH2	-5.10	117.75	120.30
1	J	365	ARG	NE-CZ-NH2	-5.10	117.75	120.30
1	E	625	LEU	CA-CB-CG	5.05	126.92	115.30
1	J	625	LEU	CA-CB-CG	5.05	126.91	115.30
1	H	401	ARG	NE-CZ-NH2	-5.03	117.79	120.30
1	A	355	LEU	CA-CB-CG	5.02	126.85	115.30
1	H	542	ASP	CB-CG-OD1	5.02	122.82	118.30
1	J	593	ASP	N-CA-CB	-5.01	101.58	110.60

There are no chirality outliers.

All (37) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	275	GLY	Peptide
1	A	592	PHE	Peptide
1	B	275	GLY	Peptide
1	B	581	PRO	Peptide
1	B	592	PHE	Peptide
1	B	600	MET	Peptide
1	C	129	GLY	Peptide
1	C	144	GLY	Peptide
1	C	581	PRO	Peptide
1	C	592	PHE	Peptide
1	C	600	MET	Peptide
1	D	129	GLY	Peptide
1	D	144	GLY	Peptide
1	D	275	GLY	Peptide
1	D	592	PHE	Peptide
1	D	600	MET	Peptide
1	E	275	GLY	Peptide
1	E	592	PHE	Peptide
1	F	275	GLY	Peptide
1	F	562	ASP	Peptide
1	F	592	PHE	Peptide
1	F	600	MET	Peptide
1	G	275	GLY	Peptide
1	G	592	PHE	Peptide
1	H	275	GLY	Peptide
1	H	592	PHE	Peptide
1	I	144	GLY	Peptide
1	J	275	GLY	Peptide
1	J	592	PHE	Peptide
1	J	600	MET	Peptide
1	K	144	GLY	Peptide
1	K	275	GLY	Peptide
1	K	562	ASP	Peptide
1	K	581	PRO	Peptide
1	K	592	PHE	Peptide
1	L	275	GLY	Peptide
1	L	592	PHE	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	4560	0	4408	91	0
1	B	4560	0	4408	74	0
1	C	4560	0	4408	63	0
1	D	4560	0	4408	86	0
1	E	4560	0	4408	72	0
1	F	4560	0	4408	75	0
1	G	4560	0	4408	82	0
1	H	4560	0	4408	83	0
1	I	4560	0	4408	94	0
1	J	4560	0	4408	72	0
1	K	4560	0	4408	85	0
1	L	4560	0	4408	92	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0
2	C	3	0	0	0	0
2	D	3	0	0	0	0
2	E	3	0	0	0	0
2	F	3	0	0	0	0
2	G	3	0	0	0	0
2	H	3	0	0	0	0
2	I	3	0	0	0	0
2	J	3	0	0	0	0
2	K	3	0	0	0	0
2	L	3	0	0	0	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0
3	C	3	0	0	0	0
3	D	3	0	0	0	0
3	E	3	0	0	0	0
3	F	3	0	0	0	0
3	G	3	0	0	0	0
3	H	3	0	0	0	0
3	I	3	0	0	0	0
3	J	3	0	0	0	0
3	K	3	0	0	0	0
3	L	3	0	0	0	0
4	A	6	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	6	0	8	0	0
4	C	6	0	8	0	0
4	D	6	0	8	1	0
4	E	6	0	8	0	0
4	F	6	0	8	0	0
4	G	6	0	8	0	0
4	H	6	0	8	1	0
4	I	6	0	8	0	0
4	J	6	0	8	0	0
4	K	6	0	8	2	0
4	L	6	0	8	0	0
5	A	354	0	0	10	0
5	B	362	0	0	10	0
5	C	398	0	0	11	0
5	D	386	0	0	8	0
5	E	357	0	0	9	0
5	F	361	0	0	9	0
5	G	359	0	0	9	0
5	H	376	0	0	12	0
5	I	330	0	0	14	0
5	J	388	0	0	12	0
5	K	359	0	0	9	0
5	L	347	0	0	10	0
All	All	59241	0	52992	898	0

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 8.

All (898) 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:J:472:GLN:OE1	1:J:472:GLN:N	1.57	1.34
1:L:138:THR:HG22	1:L:401:ARG:NH1	1.42	1.32
1:L:138:THR:CG2	1:L:401:ARG:NH1	2.04	1.20
1:L:555:THR:HG22	5:L:3298:HOH:O	1.49	1.12
1:K:494:THR:HG22	5:K:684:HOH:O	1.52	1.07
1:K:197:GLN:HE21	1:K:219:THR:HG21	1.14	1.06
1:B:473:VAL:HG22	1:B:474:PRO:HD2	1.32	1.06
1:F:138:THR:CG2	1:F:401:ARG:NH1	2.21	1.03
1:F:138:THR:HG22	1:F:401:ARG:NH1	1.74	1.03
1:I:112:ARG:HD3	5:I:1455:HOH:O	1.59	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:138:THR:CG2	1:I:401:ARG:HH11	1.76	0.99
1:B:473:VAL:HG22	1:B:474:PRO:CD	1.93	0.98
1:G:556:PRO:HD2	5:G:4378:HOH:O	1.64	0.97
1:G:132:GLY:O	1:G:397:LEU:HD21	1.63	0.97
1:F:138:THR:HG22	1:F:401:ARG:HH11	1.26	0.96
1:J:138:THR:HG22	1:J:401:ARG:NH1	1.79	0.96
1:G:413:THR:HG21	1:G:415:GLU:HG3	1.48	0.95
1:L:138:THR:HG22	1:L:401:ARG:HH11	1.00	0.95
1:J:138:THR:HG22	1:J:401:ARG:HH11	1.30	0.95
1:G:112:ARG:HD3	5:G:2482:HOH:O	1.67	0.94
1:D:480:GLN:H	1:D:553:THR:HG21	1.31	0.93
1:A:209:ARG:NH1	1:A:610:ASP:HB3	1.84	0.93
1:I:627:PHE:O	1:I:628:ASP:HB2	1.65	0.92
1:A:209:ARG:NH1	1:A:610:ASP:CB	2.32	0.92
1:I:138:THR:HG22	1:I:401:ARG:HH11	1.35	0.91
1:C:427:GLY:HA2	5:C:4358:HOH:O	1.69	0.91
1:C:627:PHE:O	1:C:628:ASP:HB2	1.69	0.91
1:L:138:THR:CG2	1:L:401:ARG:HH11	1.76	0.89
1:A:209:ARG:HH12	1:A:610:ASP:HB3	1.35	0.89
1:B:112:ARG:HD3	5:B:1043:HOH:O	1.71	0.89
1:H:472:GLN:O	1:H:473:VAL:HG23	1.74	0.88
1:G:412:GLU:HG3	5:G:3026:HOH:O	1.71	0.88
1:C:432:MET:H	1:C:534:GLN:HE22	1.22	0.87
1:I:209:ARG:NH1	1:I:610:ASP:HB3	1.89	0.87
1:G:574:HIS:HD2	5:G:2039:HOH:O	1.55	0.87
1:I:138:THR:CG2	1:I:401:ARG:NH1	2.37	0.87
1:L:473:VAL:HB	1:L:474:PRO:HA	1.57	0.87
1:I:413:THR:HG22	1:I:415:GLU:H	1.41	0.85
1:B:334:HIS:HD2	5:B:2420:HOH:O	1.60	0.85
1:G:209:ARG:NH1	1:G:610:ASP:HB3	1.92	0.85
1:G:413:THR:HG22	1:G:414:CYS:H	1.42	0.85
1:C:144:GLY:HA3	5:C:4092:HOH:O	1.77	0.85
1:K:138:THR:HG22	1:K:401:ARG:HH21	1.40	0.85
1:C:432:MET:H	1:C:534:GLN:NE2	1.75	0.84
1:K:432:MET:H	1:K:534:GLN:NE2	1.76	0.84
1:A:432:MET:H	1:A:534:GLN:NE2	1.76	0.84
1:K:138:THR:CG2	1:K:401:ARG:HH21	1.90	0.83
1:F:138:THR:CG2	1:F:401:ARG:HH11	1.88	0.83
1:E:480:GLN:H	1:E:553:THR:HG21	1.43	0.82
1:K:135:ALA:O	1:K:138:THR:HB	1.79	0.82
1:G:413:THR:CG2	1:G:415:GLU:HG3	2.08	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:255:ARG:HG3	1:G:255:ARG:HH11	1.42	0.81
1:A:432:MET:H	1:A:534:GLN:HE22	1.25	0.81
1:H:124:VAL:HG11	1:H:142:ARG:HG2	1.64	0.80
1:I:508:GLU:HG2	1:I:596:TYR:CE1	2.17	0.79
1:C:192:ASP:HB2	5:C:1820:HOH:O	1.82	0.79
1:J:138:THR:CG2	1:J:401:ARG:NH1	2.44	0.79
1:A:334:HIS:HD2	5:A:2857:HOH:O	1.64	0.79
1:G:124:VAL:HG11	1:G:142:ARG:HG2	1.65	0.79
1:D:598:ARG:HH22	1:L:499:ASN:HD21	1.29	0.79
1:J:607:GLU:O	1:J:611:MET:HG3	1.82	0.79
1:E:581:PRO:O	1:E:582:GLY:O	2.01	0.79
1:H:466:GLU:HA	5:H:4158:HOH:O	1.83	0.78
1:F:112:ARG:HD3	5:F:2052:HOH:O	1.81	0.78
1:F:135:ALA:O	1:F:138:THR:HB	1.82	0.78
1:J:558:ARG:HB2	5:J:3620:HOH:O	1.82	0.78
1:G:432:MET:H	1:G:534:GLN:NE2	1.82	0.78
1:H:192:ASP:HB2	5:H:3435:HOH:O	1.83	0.77
1:B:538:ARG:HH11	1:B:584:GLN:HE22	1.32	0.77
1:B:472:GLN:O	1:B:473:VAL:HG12	1.84	0.77
1:H:492:ARG:HD3	5:H:3084:HOH:O	1.84	0.76
1:H:431:ARG:HD2	1:H:534:GLN:NE2	2.01	0.76
1:J:472:GLN:CD	1:J:472:GLN:N	2.39	0.75
1:J:192:ASP:HB2	5:J:3674:HOH:O	1.85	0.75
1:D:553:THR:HG23	5:D:1348:HOH:O	1.85	0.75
1:I:255:ARG:HG3	1:I:255:ARG:HH11	1.51	0.75
1:I:375:LEU:HD13	1:I:380:LEU:HD11	1.69	0.75
1:D:353:ASP:HA	5:D:2019:HOH:O	1.87	0.75
1:B:574:HIS:HD2	5:B:1279:HOH:O	1.70	0.75
1:A:147:PRO:O	1:A:149:LYS:HE2	1.86	0.74
1:L:555:THR:CG2	5:L:3298:HOH:O	2.18	0.74
1:B:209:ARG:NH1	1:B:610:ASP:HB3	2.03	0.74
1:K:432:MET:H	1:K:534:GLN:HE22	1.36	0.73
1:A:197:GLN:O	1:A:365:ARG:HD2	1.88	0.73
1:L:432:MET:H	1:L:534:GLN:HE22	1.36	0.73
1:A:473:VAL:HB	1:A:474:PRO:HD3	1.68	0.73
1:L:118:GLU:HG3	5:L:3413:HOH:O	1.88	0.73
1:G:413:THR:HG22	1:G:414:CYS:N	2.03	0.73
1:G:432:MET:H	1:G:534:GLN:HE22	1.37	0.72
1:K:205:MET:O	1:K:206:ASN:HB2	1.90	0.72
1:A:375:LEU:HD13	1:A:380:LEU:HD11	1.70	0.72
1:D:177:ASN:HD21	1:L:598:ARG:H	1.38	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:63:ARG:HD3	5:H:3738:HOH:O	1.88	0.72
1:F:124:VAL:HG11	1:F:142:ARG:HG2	1.72	0.72
1:I:209:ARG:HD3	1:I:610:ASP:OD2	1.90	0.71
1:I:508:GLU:HG2	1:I:596:TYR:HE1	1.56	0.71
1:L:432:MET:H	1:L:534:GLN:NE2	1.88	0.71
1:E:138:THR:HG22	1:E:401:ARG:HH21	1.54	0.71
1:A:578:PHE:HB3	5:A:3150:HOH:O	1.89	0.71
1:E:236:ASP:HB2	5:E:2752:HOH:O	1.91	0.71
1:L:473:VAL:HG11	1:L:478:VAL:HG11	1.73	0.70
1:G:132:GLY:O	1:G:397:LEU:CD2	2.37	0.70
1:D:142:ARG:HH21	1:D:147:PRO:HD3	1.56	0.70
1:C:536:LEU:HD11	1:C:589:MET:HE3	1.73	0.70
1:D:598:ARG:H	1:L:177:ASN:HD21	1.39	0.70
1:K:591:LYS:HG2	1:K:593:ASP:HB2	1.73	0.70
1:C:536:LEU:HD11	1:C:589:MET:CE	2.21	0.70
1:J:560:ASP:OD1	1:J:562:ASP:HB3	1.91	0.70
1:E:135:ALA:O	1:E:138:THR:HB	1.92	0.70
1:H:375:LEU:HD13	1:H:380:LEU:HD11	1.74	0.70
1:D:602:HIS:HB3	1:D:614:MET:HG3	1.74	0.70
1:E:554:ARG:HH11	1:E:554:ARG:HG2	1.56	0.69
1:J:353:ASP:HA	5:J:1994:HOH:O	1.91	0.69
1:A:177:ASN:HD21	1:I:598:ARG:H	1.41	0.69
1:G:620:MET:SD	1:G:625:LEU:HD12	2.34	0.68
1:F:157:TRP:CE2	1:F:178:ALA:HB3	2.29	0.68
1:A:602:HIS:HB3	1:A:614:MET:HG3	1.75	0.68
1:D:63:ARG:HH12	1:L:63:ARG:NH1	1.92	0.67
1:A:527:HIS:HB2	1:A:577:VAL:HG22	1.76	0.67
1:K:197:GLN:NE2	1:K:219:THR:HG21	1.99	0.67
1:H:472:GLN:O	1:H:473:VAL:CG2	2.41	0.67
1:A:157:TRP:CE2	1:A:178:ALA:HB3	2.28	0.67
1:B:513:GLN:HE21	1:B:536:LEU:HD12	1.60	0.67
1:A:141:GLY:O	1:A:263:LYS:HE3	1.93	0.67
1:H:472:GLN:HA	1:H:472:GLN:NE2	2.07	0.67
1:K:138:THR:CG2	1:K:401:ARG:NH2	2.58	0.67
1:J:451:LYS:HE3	5:J:3397:HOH:O	1.95	0.67
1:F:581:PRO:HG2	1:F:584:GLN:OE1	1.94	0.67
1:A:209:ARG:HH11	1:A:610:ASP:CB	2.06	0.67
1:D:364:GLU:OE2	4:D:5004:GOL:H12	1.95	0.66
1:J:375:LEU:HD13	1:J:380:LEU:HD11	1.77	0.66
1:H:157:TRP:CE2	1:H:178:ALA:HB3	2.30	0.66
1:K:513:GLN:HE21	1:K:536:LEU:HD12	1.60	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:627:PHE:O	1:I:628:ASP:CB	2.43	0.66
1:C:63:ARG:HH22	1:G:63:ARG:NH2	1.94	0.66
1:E:138:THR:CG2	1:E:401:ARG:HH21	2.08	0.66
1:G:627:PHE:O	1:G:628:ASP:HB2	1.96	0.66
1:L:494:THR:HG23	5:L:1773:HOH:O	1.96	0.66
1:E:607:GLU:O	1:E:611:MET:HG3	1.94	0.66
1:C:413:THR:HG22	1:C:414:CYS:H	1.61	0.66
1:G:472:GLN:OE1	1:G:472:GLN:HA	1.94	0.66
1:B:63:ARG:HH11	1:H:63:ARG:NH2	1.94	0.66
1:J:581:PRO:O	1:J:582:GLY:O	2.14	0.65
1:L:461:GLU:O	1:L:494:THR:HG22	1.96	0.65
1:F:446:THR:HG21	1:F:460:TRP:CE2	2.31	0.65
1:B:115:LYS:HE2	5:B:3104:HOH:O	1.95	0.65
1:H:63:ARG:CD	5:H:3738:HOH:O	2.44	0.65
1:B:607:GLU:O	1:B:611:MET:HG3	1.97	0.65
1:A:562:ASP:HB3	5:A:1583:HOH:O	1.96	0.65
1:G:431:ARG:NH1	1:G:534:GLN:HE21	1.95	0.65
1:L:138:THR:HG21	1:L:401:ARG:NH1	2.10	0.65
1:F:192:ASP:HB2	5:F:4347:HOH:O	1.95	0.65
1:L:112:ARG:HD3	5:L:2483:HOH:O	1.97	0.65
1:J:157:TRP:CE2	1:J:178:ALA:HB3	2.31	0.65
1:H:209:ARG:NH1	1:H:610:ASP:HB3	2.12	0.65
1:C:602:HIS:HB3	1:C:614:MET:HG3	1.78	0.65
1:J:255:ARG:HH11	1:J:255:ARG:HG3	1.62	0.65
1:I:521:PRO:HA	1:I:582:GLY:HA3	1.79	0.65
1:I:209:ARG:HH11	1:I:610:ASP:CB	2.09	0.65
1:L:138:THR:HG22	1:L:401:ARG:HH12	1.54	0.65
1:I:124:VAL:HG11	1:I:142:ARG:HG2	1.79	0.65
1:G:209:ARG:HH11	1:G:610:ASP:HB3	1.62	0.64
1:D:333:VAL:HG22	1:D:370:VAL:HG12	1.77	0.64
1:G:209:ARG:HH11	1:G:610:ASP:CB	2.09	0.64
1:E:480:GLN:N	1:E:553:THR:HG21	2.12	0.64
1:E:70:ARG:NH2	5:E:2468:HOH:O	2.31	0.64
1:I:432:MET:H	1:I:534:GLN:NE2	1.96	0.64
1:A:101:ARG:HG3	1:A:193:HIS:O	1.98	0.64
1:I:138:THR:HG22	1:I:401:ARG:NH1	2.05	0.64
1:I:135:ALA:O	1:I:138:THR:HB	1.98	0.64
1:G:607:GLU:O	1:G:611:MET:HG3	1.98	0.64
1:I:209:ARG:HH11	1:I:610:ASP:HB3	1.60	0.64
1:B:209:ARG:HD3	1:B:610:ASP:OD2	1.98	0.64
1:G:209:ARG:NH1	1:G:610:ASP:CB	2.61	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:473:VAL:HB	1:A:474:PRO:CD	2.27	0.63
1:K:197:GLN:HE21	1:K:219:THR:CG2	2.03	0.63
1:K:219:THR:HG22	1:K:220:TYR:H	1.62	0.63
1:K:553:THR:HG23	1:K:555:THR:O	1.99	0.63
1:D:581:PRO:O	1:D:584:GLN:HB3	1.99	0.63
1:L:627:PHE:O	1:L:628:ASP:HB2	1.99	0.63
1:I:209:ARG:NH1	1:I:610:ASP:CB	2.62	0.63
1:H:322:ILE:HD12	1:H:326:ASP:HA	1.79	0.63
1:H:336:ILE:HB	1:H:425:LEU:HD21	1.80	0.62
1:H:431:ARG:HA	1:H:534:GLN:HE22	1.64	0.62
1:B:627:PHE:O	1:B:628:ASP:HB2	1.99	0.62
1:I:456:HIS:CE1	1:I:611:MET:CE	2.82	0.62
1:E:538:ARG:HH11	1:E:584:GLN:HE22	1.47	0.62
1:J:431:ARG:NH1	1:J:572:LEU:O	2.33	0.62
1:H:472:GLN:O	1:H:473:VAL:CB	2.47	0.61
1:J:582:GLY:O	1:J:584:GLN:N	2.32	0.61
1:F:375:LEU:HD13	1:F:380:LEU:HD11	1.80	0.61
1:F:55:ARG:CZ	5:F:3646:HOH:O	2.47	0.61
1:H:271:ASN:O	1:H:274:THR:O	2.18	0.61
1:F:413:THR:HG22	1:F:415:GLU:H	1.66	0.61
1:A:243:ILE:HD13	1:A:308:LEU:HD11	1.83	0.61
1:E:177:ASN:HD21	1:K:598:ARG:H	1.46	0.61
1:K:620:MET:SD	1:K:625:LEU:HD12	2.40	0.61
1:J:138:THR:CG2	1:J:401:ARG:HH11	2.07	0.61
1:I:255:ARG:HG3	1:I:255:ARG:NH1	2.14	0.61
1:D:271:ASN:HD22	1:D:274:THR:H	1.49	0.61
1:E:537:GLY:HA2	1:E:567:LEU:HD21	1.83	0.61
1:J:197:GLN:O	1:J:365:ARG:HD2	2.00	0.61
1:H:413:THR:HG22	1:H:414:CYS:H	1.66	0.61
1:L:375:LEU:HD13	1:L:380:LEU:HD11	1.81	0.61
1:B:325:ASP:O	1:B:326:ASP:HB2	2.01	0.61
1:H:431:ARG:HD2	1:H:534:GLN:HE22	1.66	0.60
1:A:413:THR:HG22	1:A:414:CYS:H	1.63	0.60
1:D:591:LYS:HG2	1:D:593:ASP:HB2	1.83	0.60
1:B:177:ASN:HD21	1:H:598:ARG:H	1.50	0.60
1:I:336:ILE:HB	1:I:425:LEU:HD21	1.83	0.60
1:G:255:ARG:HG3	1:G:255:ARG:NH1	2.15	0.60
1:L:138:THR:CG2	1:L:401:ARG:HH12	2.09	0.60
1:D:271:ASN:HD21	1:D:273:GLU:HB2	1.66	0.60
1:L:346:PRO:HB2	5:L:2770:HOH:O	2.02	0.60
1:L:157:TRP:CE2	1:L:178:ALA:HB3	2.37	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:138:THR:HG22	1:E:401:ARG:HE	1.65	0.60
1:I:134:PRO:HB3	1:I:138:THR:HG21	1.82	0.60
1:C:413:THR:HG22	1:C:414:CYS:N	2.17	0.60
1:E:520:SER:O	1:E:582:GLY:HA2	2.01	0.59
1:C:334:HIS:HE1	5:C:1397:HOH:O	1.85	0.59
1:I:271:ASN:O	1:I:274:THR:O	2.19	0.59
1:C:139:GLU:HG2	5:C:3035:HOH:O	2.02	0.59
1:G:375:LEU:HD13	1:G:380:LEU:HD11	1.83	0.59
1:D:558:ARG:HD2	5:D:3558:HOH:O	2.01	0.59
1:F:142:ARG:HH21	1:F:147:PRO:HD3	1.67	0.59
1:L:536:LEU:HD11	1:L:589:MET:CE	2.32	0.59
1:K:364:GLU:OE2	4:K:5011:GOL:H12	2.02	0.59
1:I:581:PRO:O	1:I:582:GLY:O	2.21	0.59
1:C:157:TRP:CE2	1:C:178:ALA:HB3	2.37	0.59
1:K:571:GLU:O	1:K:571:GLU:HG2	2.03	0.59
1:G:397:LEU:HB2	5:G:1378:HOH:O	2.02	0.59
1:H:520:SER:HB2	1:H:521:PRO:HD2	1.84	0.59
1:F:413:THR:HG22	1:F:414:CYS:N	2.18	0.59
1:B:322:ILE:HD12	1:B:326:ASP:HA	1.83	0.59
1:F:379:ARG:HG2	1:F:409:ARG:HG2	1.84	0.59
1:E:205:MET:CE	1:E:498:PHE:CE1	2.86	0.59
1:D:346:PRO:HG3	1:D:425:LEU:HG	1.85	0.59
1:K:602:HIS:HB3	1:K:614:MET:HG3	1.85	0.58
1:G:431:ARG:NH1	1:G:534:GLN:NE2	2.51	0.58
1:B:209:ARG:HH11	1:B:610:ASP:CB	2.17	0.58
1:D:538:ARG:HH11	1:D:584:GLN:HE22	1.51	0.58
1:D:63:ARG:HH12	1:L:63:ARG:HH11	1.50	0.58
1:J:473:VAL:HG12	1:J:478:VAL:HG11	1.83	0.58
1:B:465:VAL:HG12	1:B:490:THR:HG22	1.86	0.58
1:L:334:HIS:HD2	5:L:3995:HOH:O	1.85	0.58
1:C:177:ASN:HD21	1:G:598:ARG:H	1.51	0.58
1:E:245:ASP:O	1:E:246:ARG:HD3	2.04	0.58
1:A:577:VAL:HG12	1:A:577:VAL:O	2.02	0.58
1:C:197:GLN:O	1:C:365:ARG:HD2	2.02	0.58
1:D:480:GLN:N	1:D:553:THR:HG21	2.12	0.58
1:A:334:HIS:HE1	5:A:1927:HOH:O	1.85	0.58
1:D:142:ARG:HE	1:D:147:PRO:HD3	1.67	0.58
1:D:432:MET:H	1:D:534:GLN:NE2	2.02	0.58
1:D:443:ILE:HD11	1:D:504:PHE:CE2	2.39	0.58
1:D:443:ILE:HD11	1:D:504:PHE:CZ	2.38	0.58
1:F:536:LEU:HD11	1:F:589:MET:HE3	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:271:ASN:HD22	1:L:274:THR:H	1.52	0.58
1:E:432:MET:H	1:E:534:GLN:NE2	2.01	0.58
1:H:607:GLU:O	1:H:611:MET:HG3	2.04	0.58
1:K:582:GLY:N	5:K:661:HOH:O	2.24	0.58
1:A:365:ARG:NH2	1:A:576:ASP:OD1	2.35	0.57
1:E:138:THR:CG2	1:E:401:ARG:NH2	2.67	0.57
1:C:582:GLY:N	5:C:869:HOH:O	2.37	0.57
1:C:276:LYS:HB2	1:C:277:PRO:HD2	1.85	0.57
1:H:451:LYS:HE2	1:H:476:GLU:OE1	2.04	0.57
1:B:177:ASN:HD22	1:H:597:GLY:HA3	1.68	0.57
1:C:352:ASP:CG	1:C:353:ASP:H	2.06	0.57
1:K:413:THR:HG22	1:K:415:GLU:H	1.68	0.57
1:B:473:VAL:CG2	1:B:474:PRO:HD2	2.22	0.57
1:H:523:LEU:C	1:H:523:LEU:HD23	2.23	0.57
1:H:627:PHE:O	1:H:628:ASP:HB3	2.04	0.57
1:J:112:ARG:HD3	5:J:2162:HOH:O	2.05	0.57
1:A:523:LEU:HD21	1:A:579:GLN:HB3	1.86	0.57
1:J:135:ALA:O	1:J:138:THR:HB	2.04	0.57
1:F:581:PRO:O	1:F:582:GLY:O	2.23	0.57
1:F:602:HIS:HB3	1:F:614:MET:HG3	1.87	0.57
1:L:536:LEU:HD11	1:L:589:MET:HE3	1.86	0.57
1:E:472:GLN:OE1	1:E:472:GLN:N	2.38	0.57
1:K:413:THR:HG22	1:K:414:CYS:N	2.20	0.57
1:G:157:TRP:CE2	1:G:178:ALA:HB3	2.40	0.57
1:A:598:ARG:H	1:I:177:ASN:HD21	1.51	0.57
1:D:255:ARG:HH11	1:E:345:ARG:NH1	2.01	0.57
1:H:431:ARG:HH11	1:H:534:GLN:HE21	1.51	0.57
1:E:205:MET:O	1:E:206:ASN:HB2	2.02	0.57
1:E:205:MET:HE3	1:E:498:PHE:CE1	2.40	0.57
1:A:327:ARG:HD2	5:A:2261:HOH:O	2.04	0.57
1:E:194:GLN:NE2	5:E:1962:HOH:O	2.37	0.57
1:C:598:ARG:H	1:G:177:ASN:HD21	1.53	0.57
1:F:197:GLN:O	1:F:365:ARG:HD2	2.03	0.57
1:F:68:ALA:HB1	1:F:112:ARG:HG3	1.87	0.57
1:G:197:GLN:O	1:G:365:ARG:HD2	2.05	0.56
5:I:669:HOH:O	1:J:423:GLU:HG3	2.05	0.56
1:G:209:ARG:HD3	1:G:610:ASP:OD2	2.05	0.56
1:H:402:TYR:HB3	1:H:404:GLU:OE2	2.05	0.56
1:D:177:ASN:ND2	1:L:597:GLY:HA3	2.21	0.56
1:L:271:ASN:O	1:L:274:THR:O	2.23	0.56
1:I:334:HIS:HE1	5:I:692:HOH:O	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:159:VAL:HB	1:K:178:ALA:HA	1.88	0.56
1:J:537:GLY:HA2	1:J:567:LEU:HD21	1.87	0.56
1:E:197:GLN:O	1:E:365:ARG:HD2	2.05	0.56
1:I:143:GLY:HA3	5:I:3277:HOH:O	2.05	0.56
1:K:209:ARG:NH1	1:K:610:ASP:HB3	2.18	0.56
1:B:115:LYS:CE	5:B:3104:HOH:O	2.53	0.56
1:B:177:ASN:ND2	1:H:597:GLY:HA3	2.21	0.56
1:E:325:ASP:O	1:E:326:ASP:HB2	2.05	0.56
1:I:197:GLN:O	1:I:365:ARG:HD2	2.05	0.56
1:E:485:ASP:C	1:E:485:ASP:OD1	2.44	0.56
1:C:432:MET:N	1:C:534:GLN:HE22	1.98	0.55
1:K:611:MET:HG2	5:K:2639:HOH:O	2.06	0.55
1:B:473:VAL:HG22	1:B:474:PRO:HD3	1.84	0.55
1:E:112:ARG:HD3	5:E:1825:HOH:O	2.05	0.55
1:H:276:LYS:HG3	1:H:277:PRO:HD2	1.88	0.55
1:L:197:GLN:O	1:L:365:ARG:HD2	2.06	0.55
1:C:336:ILE:HB	1:C:425:LEU:HD21	1.88	0.55
1:E:138:THR:CG2	1:E:401:ARG:HE	2.20	0.55
1:L:135:ALA:O	1:L:138:THR:HB	2.07	0.55
1:G:555:THR:O	5:G:787:HOH:O	2.18	0.55
1:C:63:ARG:HH22	1:G:63:ARG:HH21	1.54	0.55
1:E:255:ARG:HH11	1:E:255:ARG:HG2	1.71	0.55
1:K:197:GLN:O	1:K:365:ARG:HD2	2.07	0.55
1:K:157:TRP:CE2	1:K:178:ALA:HB3	2.42	0.55
1:I:159:VAL:HB	1:I:178:ALA:HA	1.88	0.55
1:L:523:LEU:HD23	1:L:523:LEU:C	2.27	0.55
1:E:80:LEU:HB3	1:E:81:PRO:HD2	1.89	0.55
1:H:197:GLN:O	1:H:365:ARG:HD2	2.07	0.55
1:E:112:ARG:CD	5:E:1825:HOH:O	2.55	0.55
1:B:413:THR:HG22	1:B:414:CYS:N	2.22	0.55
1:A:85:MET:HB3	1:A:214:ALA:O	2.07	0.55
1:D:336:ILE:HB	1:D:425:LEU:HD11	1.90	0.54
1:A:142:ARG:HD3	1:A:249:ASP:OD2	2.07	0.54
1:A:333:VAL:HG22	1:A:370:VAL:HG12	1.89	0.54
1:F:159:VAL:HB	1:F:178:ALA:HA	1.89	0.54
1:L:473:VAL:HB	1:L:474:PRO:CA	2.32	0.54
1:E:138:THR:HG22	1:E:401:ARG:NH2	2.21	0.54
1:D:627:PHE:O	1:D:628:ASP:HB2	2.07	0.54
1:L:336:ILE:HB	1:L:425:LEU:HD21	1.89	0.54
1:B:472:GLN:N	1:B:472:GLN:CD	2.60	0.54
1:C:352:ASP:OD1	1:C:353:ASP:N	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:115:LYS:HE2	5:A:3659:HOH:O	2.07	0.54
1:C:255:ARG:HH11	1:C:255:ARG:HG3	1.72	0.54
1:A:209:ARG:NH1	1:A:610:ASP:HB2	2.22	0.54
1:E:554:ARG:NH1	1:E:554:ARG:HG2	2.23	0.54
1:E:176:ASP:OD2	1:K:598:ARG:HD2	2.08	0.54
1:K:163:HIS:CE1	1:K:527:HIS:CE1	2.95	0.54
1:D:124:VAL:HG11	1:D:142:ARG:HG2	1.89	0.54
1:D:142:ARG:HH21	1:D:147:PRO:CD	2.21	0.54
1:I:520:SER:O	1:I:582:GLY:HA2	2.08	0.54
1:A:598:ARG:HH12	1:I:499:ASN:HD21	1.56	0.54
1:F:598:ARG:H	1:J:177:ASN:HD21	1.56	0.54
1:B:413:THR:HG22	1:B:414:CYS:H	1.70	0.54
1:H:432:MET:H	1:H:534:GLN:NE2	2.06	0.54
1:H:413:THR:HG22	1:H:414:CYS:N	2.22	0.54
1:F:536:LEU:HD11	1:F:589:MET:CE	2.38	0.54
1:H:602:HIS:HB3	1:H:614:MET:HG3	1.89	0.53
1:E:433:SER:O	1:E:436:ILE:HG22	2.09	0.53
1:K:142:ARG:HD3	1:K:249:ASP:OD2	2.07	0.53
1:I:456:HIS:CE1	1:I:611:MET:HE1	2.43	0.53
1:C:176:ASP:OD1	1:G:598:ARG:HD2	2.07	0.53
1:A:146:GLU:HG2	5:A:1161:HOH:O	2.07	0.53
1:F:627:PHE:O	1:F:628:ASP:HB3	2.08	0.53
1:A:271:ASN:HD22	1:A:274:THR:H	1.55	0.53
1:F:521:PRO:HA	1:F:583:PRO:HD3	1.89	0.53
1:B:334:HIS:HE1	5:B:689:HOH:O	1.90	0.53
1:I:157:TRP:CE2	1:I:178:ALA:HB3	2.43	0.53
1:G:205:MET:HE1	1:G:498:PHE:CE1	2.43	0.53
1:C:325:ASP:O	1:C:326:ASP:HB2	2.09	0.53
1:J:193:HIS:NE2	1:J:532:ASP:OD2	2.28	0.53
1:A:365:ARG:HH22	1:A:576:ASP:CG	2.12	0.53
1:H:523:LEU:HD23	1:H:524:HIS:N	2.24	0.53
1:H:237:ARG:HD3	5:H:970:HOH:O	2.09	0.53
1:E:473:VAL:HG23	1:E:474:PRO:HA	1.91	0.53
1:A:547:ASP:HB3	1:A:550:LEU:HB3	1.90	0.53
1:D:322:ILE:HD12	1:D:326:ASP:HA	1.90	0.53
1:B:63:ARG:HD3	1:H:63:ARG:NH2	2.24	0.53
1:A:255:ARG:HG3	1:A:255:ARG:HH11	1.73	0.53
1:L:404:GLU:CD	1:L:404:GLU:H	2.12	0.53
1:B:176:ASP:O	1:H:597:GLY:HA2	2.09	0.52
1:H:163:HIS:C	1:H:163:HIS:CD2	2.81	0.52
1:F:63:ARG:NH2	1:J:63:ARG:HD3	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:432:MET:H	1:E:534:GLN:HE22	1.57	0.52
1:B:584:GLN:HB2	5:B:1416:HOH:O	2.09	0.52
1:H:356:PRO:HD2	5:H:2523:HOH:O	2.09	0.52
1:D:352:ASP:OD2	1:D:353:ASP:N	2.42	0.52
1:F:521:PRO:HA	1:F:582:GLY:HA3	1.90	0.52
1:A:472:GLN:CD	1:A:472:GLN:O	2.48	0.52
1:F:138:THR:HG21	1:F:401:ARG:NH1	2.21	0.52
1:A:498:PHE:HA	1:A:614:MET:O	2.09	0.52
1:A:513:GLN:HE21	1:A:536:LEU:HD12	1.73	0.52
1:D:177:ASN:HD22	1:L:597:GLY:CA	2.23	0.52
1:F:325:ASP:O	1:F:326:ASP:HB2	2.08	0.52
1:I:602:HIS:HB3	1:I:614:MET:HG3	1.91	0.52
1:C:124:VAL:HG11	1:C:142:ARG:HG2	1.90	0.52
1:K:336:ILE:HB	1:K:425:LEU:HD11	1.92	0.52
1:E:54:LEU:HD11	5:E:3984:HOH:O	2.10	0.52
1:L:472:GLN:HG3	1:L:473:VAL:HG13	1.92	0.52
1:K:112:ARG:HD3	5:K:1644:HOH:O	2.09	0.51
1:G:255:ARG:CG	1:G:255:ARG:HH11	2.15	0.51
1:D:177:ASN:HD22	1:L:597:GLY:HA3	1.74	0.51
1:G:336:ILE:HB	1:G:425:LEU:HD21	1.93	0.51
1:F:355:LEU:HD22	1:F:569:PRO:HG2	1.91	0.51
1:I:301:ASP:OD1	1:I:413:THR:HB	2.10	0.51
1:J:255:ARG:NH1	1:J:255:ARG:HG3	2.25	0.51
1:I:591:LYS:HE2	1:I:593:ASP:OD1	2.11	0.51
1:D:325:ASP:O	1:D:326:ASP:HB2	2.10	0.51
1:F:91:GLN:NE2	5:F:3521:HOH:O	2.42	0.51
1:G:68:ALA:HB1	1:G:112:ARG:HG3	1.93	0.51
1:B:209:ARG:NH1	1:B:610:ASP:CB	2.71	0.51
1:A:591:LYS:HE3	5:A:4191:HOH:O	2.10	0.51
1:J:482:THR:HG1	1:J:488:THR:HG1	1.50	0.51
1:E:431:ARG:NH2	1:E:572:LEU:O	2.42	0.51
1:K:494:THR:CG2	5:K:684:HOH:O	2.30	0.51
1:L:68:ALA:HB1	1:L:112:ARG:HG3	1.93	0.51
1:I:533:PHE:HB3	1:I:588:VAL:HG22	1.92	0.51
1:K:591:LYS:HE2	1:K:593:ASP:OD1	2.10	0.51
1:H:209:ARG:NH1	1:H:610:ASP:CB	2.74	0.51
1:D:581:PRO:HG2	1:D:584:GLN:OE1	2.10	0.51
1:K:598:ARG:NH2	5:K:2199:HOH:O	2.44	0.51
1:C:581:PRO:O	1:C:582:GLY:O	2.28	0.51
1:D:531:ALA:HB3	1:D:533:PHE:CE1	2.46	0.51
1:G:472:GLN:CA	1:G:472:GLN:OE1	2.59	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:536:LEU:HD11	1:A:589:MET:HE3	1.92	0.51
1:B:531:ALA:HB3	1:B:533:PHE:CE1	2.46	0.51
1:K:237:ARG:HD3	5:K:2479:HOH:O	2.11	0.51
1:J:536:LEU:HD11	1:J:589:MET:HE3	1.91	0.51
1:G:538:ARG:HH11	1:G:584:GLN:HE22	1.58	0.50
1:A:163:HIS:CE1	1:A:363:ALA:HB1	2.45	0.50
1:B:598:ARG:H	1:H:177:ASN:HD21	1.57	0.50
1:B:584:GLN:HG2	1:B:585:GLY:N	2.25	0.50
1:I:432:MET:H	1:I:534:GLN:HE22	1.56	0.50
1:D:274:THR:HB	1:D:276:LYS:HD2	1.94	0.50
1:C:176:ASP:O	1:G:597:GLY:HA2	2.11	0.50
1:K:531:ALA:HB3	1:K:533:PHE:CE1	2.46	0.50
1:A:209:ARG:HH11	1:A:610:ASP:CG	2.15	0.50
1:B:536:LEU:HD11	1:B:589:MET:HE3	1.92	0.50
1:D:271:ASN:O	1:D:274:THR:O	2.30	0.50
1:I:346:PRO:HD3	1:I:425:LEU:HB2	1.93	0.50
1:A:186:LEU:HD11	1:I:106:ARG:HG2	1.94	0.50
1:H:325:ASP:O	1:H:326:ASP:HB2	2.12	0.50
1:E:205:MET:HE3	1:E:498:PHE:HE1	1.76	0.50
1:A:337:GLY:N	1:A:367:ASP:HB3	2.27	0.50
1:J:346:PRO:HD3	1:J:425:LEU:HB2	1.94	0.50
1:B:375:LEU:HD13	1:B:380:LEU:HD11	1.93	0.50
1:J:269:GLN:O	5:J:3871:HOH:O	2.18	0.50
1:I:138:THR:HG21	1:I:401:ARG:NH1	2.24	0.50
1:C:159:VAL:HB	1:C:178:ALA:HA	1.94	0.50
1:B:446:THR:HG21	1:B:460:TRP:CE2	2.47	0.50
1:J:205:MET:O	1:J:206:ASN:HB2	2.11	0.50
1:B:205:MET:O	1:B:206:ASN:HB2	2.12	0.50
1:C:499:ASN:ND2	1:G:598:ARG:HH22	2.09	0.50
1:A:271:ASN:O	1:A:274:THR:O	2.29	0.50
1:I:451:LYS:NZ	1:I:476:GLU:OE1	2.35	0.50
1:H:125:GLU:HG2	1:H:264:THR:OG1	2.12	0.50
1:F:177:ASN:HD22	1:J:597:GLY:HA3	1.77	0.50
1:D:627:PHE:O	1:D:628:ASP:CB	2.60	0.50
1:H:587:ARG:NH1	5:H:1191:HOH:O	2.37	0.50
1:L:545:GLY:HA3	1:L:555:THR:O	2.11	0.50
1:G:255:ARG:CG	1:G:255:ARG:NH1	2.73	0.50
1:F:177:ASN:HD21	1:J:598:ARG:H	1.60	0.50
1:K:464:GLU:OE2	1:K:489:LYS:HD3	2.12	0.50
1:L:245:ASP:OD2	1:L:315:ARG:HD2	2.12	0.50
1:J:124:VAL:HG11	1:J:142:ARG:HG2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:70:ARG:NH2	5:F:2951:HOH:O	2.44	0.49
1:H:199:TRP:HA	1:H:219:THR:HA	1.94	0.49
1:K:537:GLY:HA2	1:K:567:LEU:HD21	1.93	0.49
1:B:472:GLN:O	1:B:473:VAL:O	2.30	0.49
1:G:598:ARG:NH2	5:G:1346:HOH:O	2.45	0.49
1:D:197:GLN:O	1:D:365:ARG:HD2	2.12	0.49
1:F:443:ILE:HD12	1:F:443:ILE:N	2.27	0.49
1:B:554:ARG:HG2	1:B:554:ARG:HH11	1.77	0.49
1:F:538:ARG:HH11	1:F:584:GLN:HE22	1.59	0.49
1:D:271:ASN:ND2	1:D:273:GLU:HB2	2.27	0.49
1:F:432:MET:H	1:F:534:GLN:NE2	2.10	0.49
1:I:126:VAL:HG13	1:I:127:PRO:HD2	1.94	0.49
1:D:70:ARG:HD2	5:D:2882:HOH:O	2.12	0.49
1:B:473:VAL:CG2	1:B:474:PRO:CD	2.78	0.49
1:G:620:MET:SD	1:G:625:LEU:CD1	3.01	0.49
1:I:431:ARG:NH1	1:I:572:LEU:O	2.45	0.49
1:D:584:GLN:HG2	1:D:585:GLY:N	2.28	0.49
1:L:362:PRO:O	1:L:363:ALA:HB3	2.13	0.49
1:F:520:SER:O	1:F:582:GLY:HA2	2.10	0.49
1:K:316:ILE:HD11	1:K:523:LEU:HD22	1.94	0.49
1:E:598:ARG:H	1:K:177:ASN:HD21	1.58	0.49
1:D:538:ARG:HH11	1:D:584:GLN:NE2	2.11	0.49
1:K:431:ARG:NH2	1:K:535:VAL:O	2.45	0.49
1:L:128:LEU:HD23	1:L:265:VAL:HG11	1.93	0.49
1:I:83:THR:HG23	1:I:258:GLY:O	2.12	0.49
1:I:500:ASP:HB3	5:I:1771:HOH:O	2.11	0.49
1:G:86:TRP:CD2	1:G:113:ILE:HD13	2.48	0.49
1:K:431:ARG:HD2	1:K:534:GLN:NE2	2.28	0.49
1:A:197:GLN:O	1:A:365:ARG:CD	2.61	0.49
1:G:337:GLY:N	1:G:367:ASP:HB3	2.27	0.49
1:D:597:GLY:HA3	1:L:177:ASN:ND2	2.28	0.49
1:J:70:ARG:HD2	5:J:1838:HOH:O	2.13	0.49
1:F:150:ASP:OD2	1:J:626:LYS:HD2	2.13	0.49
1:I:485:ASP:OD1	1:I:485:ASP:C	2.51	0.49
1:G:397:LEU:HD23	1:G:397:LEU:HA	1.67	0.48
1:L:86:TRP:CD2	1:L:113:ILE:HD13	2.48	0.48
1:D:161:HIS:NE2	1:D:163:HIS:HA	2.28	0.48
1:D:597:GLY:HA3	1:L:177:ASN:HD22	1.77	0.48
1:J:142:ARG:HH21	1:J:147:PRO:HD3	1.77	0.48
1:L:434:HIS:CD2	1:L:438:HIS:CE1	3.01	0.48
1:F:150:ASP:CG	1:J:626:LYS:HD2	2.34	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:209:ARG:HH11	1:B:610:ASP:HB3	1.70	0.48
1:A:159:VAL:HB	1:A:178:ALA:HA	1.95	0.48
1:G:175:ALA:HB3	1:G:205:MET:HE2	1.95	0.48
1:C:149:LYS:HG2	5:C:1112:HOH:O	2.13	0.48
1:C:443:ILE:HD11	1:C:504:PHE:CE2	2.48	0.48
1:B:194:GLN:NE2	5:B:4570:HOH:O	2.41	0.48
1:G:555:THR:HB	1:G:556:PRO:CD	2.43	0.48
1:A:336:ILE:HB	1:A:425:LEU:HD11	1.96	0.48
1:K:219:THR:OG1	1:K:242:LEU:HD21	2.14	0.48
1:B:532:ASP:HB3	5:B:1279:HOH:O	2.13	0.48
1:J:159:VAL:HB	1:J:178:ALA:HA	1.94	0.48
1:D:584:GLN:HB2	5:D:4134:HOH:O	2.14	0.48
1:H:446:THR:HG21	1:H:460:TRP:CE2	2.49	0.48
1:G:124:VAL:CG1	1:G:142:ARG:HG2	2.41	0.48
1:H:209:ARG:HH11	1:H:610:ASP:CB	2.26	0.48
1:E:205:MET:HE1	1:E:498:PHE:CE1	2.48	0.48
1:F:243:ILE:HG22	1:F:289:VAL:HG22	1.96	0.48
1:F:598:ARG:HD2	1:J:176:ASP:OD1	2.13	0.48
1:H:482:THR:HA	1:H:487:ARG:O	2.13	0.48
1:G:355:LEU:HD11	5:G:1116:HOH:O	2.14	0.48
1:J:520:SER:HB2	1:J:521:PRO:HD2	1.95	0.48
1:A:499:ASN:HD21	1:I:598:ARG:HH12	1.61	0.48
1:C:627:PHE:O	1:C:628:ASP:CB	2.53	0.48
1:E:177:ASN:HD22	1:K:597:GLY:HA3	1.77	0.48
1:F:461:GLU:HG2	1:F:504:PHE:CZ	2.48	0.48
1:I:236:ASP:HB2	5:I:1012:HOH:O	2.14	0.48
1:E:63:ARG:NH1	1:K:60:GLU:OE1	2.47	0.48
1:E:601:TYR:CE2	1:E:615:ARG:HB2	2.49	0.48
1:L:69:LEU:HD12	1:L:69:LEU:N	2.29	0.48
1:J:465:VAL:HG12	1:J:466:GLU:N	2.28	0.48
1:K:523:LEU:C	1:K:523:LEU:HD23	2.34	0.47
1:G:334:HIS:HE1	5:G:1009:HOH:O	1.97	0.47
1:I:542:ASP:HA	5:I:4225:HOH:O	2.14	0.47
1:J:578:PHE:HB3	5:J:1556:HOH:O	2.13	0.47
1:A:627:PHE:O	1:A:628:ASP:HB3	2.14	0.47
1:H:194:GLN:NE2	5:H:2938:HOH:O	2.34	0.47
1:J:37:ALA:HB3	1:J:40:GLU:OE1	2.14	0.47
1:D:498:PHE:HA	1:D:614:MET:O	2.14	0.47
1:A:177:ASN:ND2	1:I:598:ARG:H	2.11	0.47
1:I:533:PHE:HB2	1:I:578:PHE:HZ	1.79	0.47
1:B:431:ARG:HA	1:B:534:GLN:HE22	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:443:ILE:HD11	1:E:504:PHE:CZ	2.48	0.47
1:E:554:ARG:NH1	1:E:554:ARG:CG	2.76	0.47
1:D:280:ILE:HB	1:D:281:PRO:CD	2.44	0.47
1:L:472:GLN:C	1:L:473:VAL:HG13	2.34	0.47
1:H:159:VAL:HB	1:H:178:ALA:HA	1.95	0.47
1:A:413:THR:HG22	1:A:414:CYS:N	2.27	0.47
1:E:68:ALA:HB1	1:E:112:ARG:HG3	1.97	0.47
1:B:459:ILE:HG13	1:B:613:MET:HG3	1.96	0.47
1:J:148:ASN:OD1	1:J:150:ASP:HB2	2.13	0.47
1:H:558:ARG:NH1	5:H:1505:HOH:O	2.45	0.47
1:B:492:ARG:HH11	1:B:492:ARG:HG3	1.80	0.47
1:D:142:ARG:NH2	1:D:147:PRO:HD3	2.27	0.47
1:C:498:PHE:HA	1:C:614:MET:O	2.15	0.47
1:K:413:THR:HG22	1:K:415:GLU:N	2.29	0.47
1:A:442:LEU:C	1:A:443:ILE:HD13	2.35	0.47
1:K:431:ARG:HD2	1:K:534:GLN:HE22	1.79	0.47
1:E:553:THR:HG23	5:E:1305:HOH:O	2.13	0.47
1:D:597:GLY:CA	1:L:177:ASN:HD22	2.28	0.47
1:D:499:ASN:ND2	1:L:598:ARG:HH22	2.12	0.47
1:H:498:PHE:HA	1:H:614:MET:O	2.15	0.47
1:F:64:GLU:OE2	1:J:64:GLU:OE2	2.32	0.47
1:J:115:LYS:NZ	5:J:3059:HOH:O	2.35	0.47
1:L:318:ASN:HB3	1:L:357:VAL:HG11	1.97	0.47
1:H:568:ALA:HB3	1:H:571:GLU:HG2	1.96	0.47
1:L:325:ASP:O	1:L:326:ASP:HB2	2.14	0.47
1:C:598:ARG:HD2	1:G:176:ASP:OD2	2.15	0.47
1:I:325:ASP:O	1:I:326:ASP:HB2	2.15	0.47
1:A:545:GLY:HA3	1:A:555:THR:O	2.13	0.47
1:J:498:PHE:HA	1:J:614:MET:O	2.15	0.47
1:E:159:VAL:HB	1:E:178:ALA:HA	1.96	0.47
1:D:280:ILE:HB	1:D:281:PRO:HD2	1.97	0.47
1:I:134:PRO:HG3	1:I:396:PRO:HB2	1.97	0.47
1:G:555:THR:HB	1:G:556:PRO:HD3	1.97	0.47
1:H:124:VAL:CG1	1:H:142:ARG:HG2	2.41	0.47
1:C:63:ARG:NH2	1:G:63:ARG:NH2	2.63	0.47
1:D:68:ALA:HB1	1:D:112:ARG:HG3	1.97	0.47
1:D:159:VAL:HB	1:D:178:ALA:HA	1.97	0.47
1:E:243:ILE:HD13	1:E:308:LEU:HD11	1.97	0.47
1:C:492:ARG:NH1	5:C:2755:HOH:O	2.48	0.46
1:K:485:ASP:OD1	1:K:487:ARG:HB3	2.14	0.46
1:K:538:ARG:HH11	1:K:584:GLN:HE22	1.62	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:250:THR:HA	1:G:255:ARG:O	2.16	0.46
1:E:138:THR:CG2	1:E:401:ARG:NE	2.78	0.46
1:F:163:HIS:CE1	1:F:363:ALA:HB1	2.51	0.46
1:F:523:LEU:HD23	1:F:523:LEU:C	2.36	0.46
1:K:197:GLN:O	1:K:365:ARG:CD	2.64	0.46
1:I:255:ARG:CG	1:I:255:ARG:NH1	2.78	0.46
1:G:620:MET:HE2	1:G:624:ALA:HB3	1.97	0.46
1:H:591:LYS:HG2	1:H:593:ASP:HB2	1.97	0.46
1:H:538:ARG:HH11	1:H:584:GLN:HE22	1.62	0.46
1:F:413:THR:HG22	1:F:414:CYS:H	1.79	0.46
1:K:482:THR:HA	1:K:487:ARG:O	2.15	0.46
1:L:285:PRO:HG2	1:L:286:TYR:CE1	2.50	0.46
1:G:562:ASP:O	1:G:564:PRO:HD3	2.15	0.46
1:D:487:ARG:CZ	1:D:487:ARG:HB2	2.45	0.46
1:E:538:ARG:HH11	1:E:584:GLN:NE2	2.12	0.46
1:D:499:ASN:HD21	1:L:598:ARG:HH22	1.62	0.46
1:F:473:VAL:HG11	1:F:480:GLN:HE22	1.81	0.46
1:F:142:ARG:NH2	1:F:147:PRO:HD3	2.31	0.46
1:K:485:ASP:OD1	1:K:487:ARG:CB	2.64	0.46
1:B:138:THR:OG1	1:B:401:ARG:NH1	2.49	0.46
1:A:431:ARG:NH2	1:A:535:VAL:O	2.48	0.46
1:H:359:SER:HB3	4:H:5008:GOL:H31	1.97	0.46
1:C:447:PRO:HG3	5:C:4138:HOH:O	2.16	0.46
1:B:69:LEU:N	1:B:69:LEU:HD12	2.31	0.46
1:I:163:HIS:CD2	1:I:163:HIS:C	2.87	0.46
1:K:163:HIS:CD2	1:K:163:HIS:C	2.89	0.46
1:H:163:HIS:CE1	1:H:363:ALA:HB1	2.51	0.46
1:H:433:SER:HB3	1:H:436:ILE:HG13	1.98	0.46
1:E:336:ILE:HB	1:E:425:LEU:HD21	1.96	0.46
1:G:119:TYR:HA	1:G:120:PRO:HD3	1.76	0.46
1:G:431:ARG:HA	1:G:534:GLN:HE22	1.81	0.46
1:B:193:HIS:NE2	1:B:532:ASP:OD2	2.44	0.46
1:L:318:ASN:HB3	1:L:357:VAL:CG1	2.46	0.46
1:A:64:GLU:OE2	1:I:64:GLU:OE2	2.34	0.46
1:D:602:HIS:HB3	1:D:614:MET:HA	1.97	0.46
1:E:157:TRP:CE2	1:E:178:ALA:HB3	2.51	0.46
1:B:336:ILE:HB	1:B:425:LEU:HD21	1.97	0.46
1:J:271:ASN:O	1:J:274:THR:O	2.34	0.46
1:C:601:TYR:CE2	1:C:615:ARG:HB2	2.51	0.46
1:B:554:ARG:HG2	1:B:554:ARG:NH1	2.31	0.45
1:K:473:VAL:HB	1:K:474:PRO:HA	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:436:ILE:HG13	1:A:437:PRO:HD2	1.98	0.45
1:F:465:VAL:O	1:F:466:GLU:HG3	2.16	0.45
1:F:255:ARG:HH11	1:F:255:ARG:HG3	1.81	0.45
1:I:124:VAL:CG1	1:I:142:ARG:HG2	2.46	0.45
1:C:139:GLU:O	1:C:263:LYS:NZ	2.48	0.45
1:J:579:GLN:HG3	5:J:688:HOH:O	2.16	0.45
1:G:487:ARG:CZ	1:G:487:ARG:HB2	2.46	0.45
1:H:382:LEU:HD12	1:H:382:LEU:HA	1.62	0.45
1:L:337:GLY:N	1:L:367:ASP:HB3	2.30	0.45
1:A:620:MET:HG2	1:I:157:TRP:CH2	2.52	0.45
1:E:379:ARG:NH2	5:E:1663:HOH:O	2.49	0.45
1:L:578:PHE:HB3	5:L:1257:HOH:O	2.16	0.45
1:H:388:GLY:HA3	5:H:2013:HOH:O	2.15	0.45
1:D:205:MET:O	1:D:206:ASN:HB2	2.17	0.45
1:F:334:HIS:HE1	5:F:1640:HOH:O	2.00	0.45
1:K:219:THR:HG22	1:K:220:TYR:N	2.29	0.45
1:F:466:GLU:N	5:F:1806:HOH:O	2.49	0.45
1:L:446:THR:HG21	1:L:460:TRP:CE2	2.51	0.45
1:L:339:ASP:HB2	1:L:575:LYS:HA	1.97	0.45
1:A:484:ALA:C	1:A:486:GLY:H	2.20	0.45
1:H:85:MET:HB3	1:H:214:ALA:O	2.16	0.45
1:F:197:GLN:O	1:F:365:ARG:CD	2.65	0.45
1:L:69:LEU:HD12	1:L:69:LEU:H	1.81	0.45
1:D:64:GLU:OE2	1:L:64:GLU:OE2	2.35	0.45
1:B:162:LEU:HG	1:B:165:ALA:HB2	1.98	0.45
1:D:237:ARG:HD3	5:D:2130:HOH:O	2.16	0.45
1:E:138:THR:HG22	1:E:401:ARG:NE	2.31	0.45
1:G:337:GLY:CA	1:G:367:ASP:HB3	2.46	0.45
1:K:334:HIS:HE1	5:K:672:HOH:O	2.00	0.45
1:C:375:LEU:HD13	1:C:380:LEU:HD11	1.99	0.45
1:C:382:LEU:HA	1:C:382:LEU:HD12	1.80	0.45
1:A:138:THR:O	1:A:401:ARG:HD2	2.17	0.45
1:J:325:ASP:O	1:J:326:ASP:HB2	2.16	0.45
1:D:259:ARG:HD2	5:D:1433:HOH:O	2.16	0.45
5:J:654:HOH:O	1:K:423:GLU:HG2	2.17	0.45
1:K:627:PHE:O	1:K:628:ASP:HB3	2.17	0.45
1:J:175:ALA:HB3	1:J:205:MET:CE	2.47	0.44
1:L:205:MET:HE3	1:L:498:PHE:CE1	2.52	0.44
1:B:535:VAL:HG13	1:B:586:LEU:HD11	1.99	0.44
1:C:404:GLU:CD	1:C:404:GLU:H	2.21	0.44
1:I:379:ARG:HD2	5:I:4231:HOH:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:250:THR:HA	1:I:255:ARG:O	2.17	0.44
1:B:63:ARG:HH11	1:H:63:ARG:HH21	1.65	0.44
1:C:397:LEU:HB2	5:C:1942:HOH:O	2.16	0.44
1:K:199:TRP:HB2	1:K:218:GLY:O	2.18	0.44
1:E:70:ARG:HD2	5:E:2588:HOH:O	2.17	0.44
1:J:465:VAL:CG1	1:J:466:GLU:N	2.81	0.44
1:I:538:ARG:HH11	1:I:584:GLN:HE22	1.66	0.44
1:E:482:THR:HG1	1:E:488:THR:HG1	1.64	0.44
1:A:599:PHE:O	1:A:616:PRO:HA	2.18	0.44
1:A:148:ASN:C	1:A:148:ASN:OD1	2.56	0.44
1:L:334:HIS:HE1	5:L:684:HOH:O	2.00	0.44
1:D:432:MET:H	1:D:534:GLN:HE22	1.63	0.44
1:A:362:PRO:O	1:A:363:ALA:HB3	2.16	0.44
1:E:443:ILE:CD1	1:E:504:PHE:HZ	2.31	0.44
1:A:531:ALA:HB3	1:A:533:PHE:CE1	2.53	0.44
1:D:339:ASP:HB2	1:D:575:LYS:HA	1.98	0.44
1:F:591:LYS:HE2	1:F:593:ASP:OD1	2.18	0.44
1:L:545:GLY:CA	1:L:555:THR:HG23	2.47	0.44
1:A:159:VAL:O	1:A:202:ASP:HA	2.18	0.44
1:A:338:SER:O	1:A:339:ASP:C	2.56	0.44
1:H:472:GLN:O	1:H:473:VAL:HB	2.16	0.44
1:C:536:LEU:HD11	1:C:589:MET:HE2	1.98	0.44
1:D:63:ARG:NH1	1:L:63:ARG:HH11	2.13	0.44
1:I:271:ASN:ND2	1:I:273:GLU:H	2.15	0.44
1:B:431:ARG:NE	1:B:534:GLN:NE2	2.65	0.44
1:I:566:PRO:HA	5:I:3613:HOH:O	2.18	0.44
1:H:370:VAL:HG11	1:H:372:PHE:CZ	2.53	0.44
1:J:316:ILE:HD11	1:J:523:LEU:HD22	1.99	0.44
1:A:504:PHE:CD1	1:A:504:PHE:N	2.85	0.44
1:I:456:HIS:CE1	1:I:611:MET:HE2	2.51	0.44
1:I:533:PHE:HB2	1:I:578:PHE:CZ	2.53	0.44
1:A:545:GLY:HA2	1:A:555:THR:HG23	2.00	0.44
1:I:446:THR:HG21	1:I:460:TRP:CE2	2.52	0.44
1:G:141:GLY:O	1:G:263:LYS:HE3	2.18	0.44
1:F:537:GLY:HA2	1:F:567:LEU:HD21	2.00	0.44
1:H:620:MET:SD	1:H:625:LEU:HD12	2.57	0.44
1:J:548:LEU:N	1:J:548:LEU:HD23	2.33	0.44
1:H:271:ASN:HD22	1:H:274:THR:H	1.66	0.43
1:B:176:ASP:OD2	1:H:598:ARG:HD2	2.18	0.43
1:A:443:ILE:HD13	1:A:443:ILE:N	2.33	0.43
1:J:271:ASN:HD22	1:J:274:THR:H	1.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:255:ARG:HG3	1:L:255:ARG:HH11	1.83	0.43
1:I:559:LEU:O	1:I:561:PRO:HD3	2.17	0.43
1:K:322:ILE:HD12	1:K:326:ASP:HA	2.00	0.43
1:G:88:TYR:CD2	1:G:200:TYR:HE1	2.36	0.43
1:E:498:PHE:HA	1:E:614:MET:O	2.19	0.43
1:L:535:VAL:HG13	1:L:586:LEU:HD11	1.99	0.43
1:B:472:GLN:C	1:B:473:VAL:O	2.56	0.43
1:L:205:MET:CE	1:L:498:PHE:CE1	3.00	0.43
1:A:255:ARG:HG3	1:A:255:ARG:NH1	2.33	0.43
1:C:163:HIS:C	1:C:163:HIS:CD2	2.91	0.43
1:K:447:PRO:HG2	1:K:548:LEU:HD11	2.00	0.43
1:I:536:LEU:HD11	1:I:589:MET:HB2	2.01	0.43
1:E:582:GLY:O	1:E:584:GLN:N	2.52	0.43
1:B:177:ASN:HD22	1:H:597:GLY:CA	2.32	0.43
1:K:498:PHE:HA	1:K:614:MET:O	2.19	0.43
1:D:431:ARG:HA	1:D:534:GLN:HE22	1.84	0.43
1:L:250:THR:HA	1:L:255:ARG:O	2.18	0.43
1:B:430:ARG:CZ	5:B:3569:HOH:O	2.67	0.43
1:A:54:LEU:HD11	5:A:4289:HOH:O	2.18	0.43
1:I:255:ARG:NE	1:J:423:GLU:OE1	2.51	0.43
1:J:250:THR:HA	1:J:255:ARG:O	2.17	0.43
1:L:142:ARG:HD2	1:L:249:ASP:OD2	2.19	0.43
1:L:194:GLN:NE2	5:L:1236:HOH:O	2.52	0.43
1:B:464:GLU:OE2	1:B:489:LYS:HE2	2.19	0.43
1:G:582:GLY:O	1:G:583:PRO:C	2.56	0.43
1:K:267:VAL:HG22	1:K:267:VAL:O	2.19	0.43
1:D:177:ASN:ND2	1:L:598:ARG:H	2.12	0.43
1:E:602:HIS:HB3	1:E:614:MET:HG3	2.01	0.43
1:D:230:LEU:HD21	1:D:425:LEU:HD22	2.00	0.43
1:F:177:ASN:HD22	1:J:597:GLY:CA	2.31	0.43
1:H:314:ALA:HA	1:H:605:LEU:HD22	2.01	0.43
1:I:475:ALA:H	1:I:550:LEU:HD21	1.84	0.43
1:F:602:HIS:HB3	1:F:614:MET:HA	2.01	0.43
1:D:418:SER:O	1:D:419:PHE:C	2.57	0.43
1:I:252:GLU:HG3	5:I:2806:HOH:O	2.18	0.43
1:B:197:GLN:O	1:B:365:ARG:HD2	2.18	0.43
1:A:147:PRO:O	1:A:149:LYS:CE	2.64	0.42
1:A:176:ASP:O	1:I:597:GLY:HA2	2.19	0.42
1:J:142:ARG:HD3	1:J:249:ASP:OD1	2.19	0.42
1:D:199:TRP:HA	1:D:219:THR:HA	2.00	0.42
1:C:281:PRO:HA	1:C:607:GLU:HG2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:531:ALA:HB3	1:J:533:PHE:CE1	2.54	0.42
1:I:574:HIS:CD2	5:I:1319:HOH:O	2.72	0.42
1:D:112:ARG:HD3	5:D:984:HOH:O	2.18	0.42
1:H:591:LYS:HE3	1:H:593:ASP:OD1	2.19	0.42
1:A:485:ASP:OD2	1:A:487:ARG:HG2	2.19	0.42
1:I:268:GLN:NE2	1:I:272:PRO:HD3	2.33	0.42
1:I:101:ARG:HG3	1:I:193:HIS:O	2.18	0.42
1:A:379:ARG:HG2	1:A:409:ARG:HG2	2.01	0.42
1:J:560:ASP:C	1:J:562:ASP:H	2.21	0.42
1:D:271:ASN:ND2	1:D:273:GLU:H	2.17	0.42
1:G:433:SER:OG	1:G:435:ASP:HB2	2.19	0.42
1:J:118:GLU:HB3	5:J:2503:HOH:O	2.19	0.42
1:F:119:TYR:HA	1:F:120:PRO:HD3	1.90	0.42
5:K:1301:HOH:O	1:L:423:GLU:HG2	2.18	0.42
1:B:68:ALA:HB1	1:B:112:ARG:HG3	2.02	0.42
1:E:255:ARG:HH11	1:E:255:ARG:CG	2.33	0.42
1:B:64:GLU:OE2	1:H:64:GLU:OE2	2.37	0.42
1:G:536:LEU:HD11	1:G:589:MET:HB2	2.01	0.42
1:C:431:ARG:HA	1:C:534:GLN:HE22	1.85	0.42
1:L:159:VAL:HB	1:L:178:ALA:HA	2.01	0.42
1:H:581:PRO:HG2	1:H:584:GLN:OE1	2.19	0.42
1:A:83:THR:HG23	1:A:258:GLY:O	2.18	0.42
1:L:560:ASP:HA	1:L:561:PRO:HD3	1.90	0.42
1:I:37:ALA:N	5:I:1486:HOH:O	2.52	0.42
1:F:404:GLU:CD	1:F:404:GLU:H	2.23	0.42
1:I:523:LEU:HD23	1:I:523:LEU:C	2.40	0.42
1:D:177:ASN:ND2	1:L:597:GLY:CA	2.82	0.42
1:I:584:GLN:HG2	1:I:585:GLY:N	2.34	0.42
1:A:520:SER:O	1:A:582:GLY:HA3	2.19	0.42
1:F:417:ASP:HB2	5:F:3791:HOH:O	2.19	0.42
1:I:403:PRO:HB3	5:I:2701:HOH:O	2.18	0.42
1:H:536:LEU:HD11	1:H:589:MET:HE3	2.02	0.42
1:G:492:ARG:HG3	1:G:492:ARG:NH1	2.34	0.42
1:J:284:GLY:HA2	1:J:285:PRO:HD3	1.87	0.42
1:A:598:ARG:NH2	5:A:2528:HOH:O	2.42	0.42
1:K:142:ARG:HE	1:K:147:PRO:HD3	1.84	0.42
1:G:498:PHE:HA	1:G:614:MET:O	2.20	0.42
1:A:244:ALA:HA	1:A:312:SER:OG	2.20	0.42
1:H:245:ASP:HA	1:H:286:TYR:O	2.19	0.42
1:I:382:LEU:HD12	1:I:382:LEU:HA	1.81	0.42
1:I:461:GLU:OE1	1:I:503:GLY:HA3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:443:ILE:HG23	1:J:459:ILE:HG23	2.01	0.42
1:L:119:TYR:HA	1:L:120:PRO:HD3	1.81	0.42
1:L:375:LEU:O	1:L:410:VAL:HB	2.20	0.42
1:K:285:PRO:HG2	1:K:286:TYR:CE1	2.55	0.42
1:K:434:HIS:HD2	1:K:589:MET:HE1	1.85	0.42
1:B:157:TRP:CE2	1:B:178:ALA:HB3	2.54	0.42
1:I:506:ILE:O	1:I:619:VAL:HA	2.19	0.42
1:G:401:ARG:HH11	1:G:401:ARG:HG3	1.85	0.42
1:D:431:ARG:HH22	1:D:572:LEU:HB3	1.85	0.42
1:C:276:LYS:HB2	1:C:277:PRO:CD	2.50	0.42
1:B:159:VAL:HB	1:B:178:ALA:HA	2.01	0.42
1:F:352:ASP:HB2	5:F:1612:HOH:O	2.20	0.42
1:G:362:PRO:O	1:G:363:ALA:HB3	2.20	0.42
1:A:176:ASP:OD2	1:I:598:ARG:HD2	2.20	0.41
1:B:124:VAL:HG11	1:B:142:ARG:HG2	2.01	0.41
1:K:451:LYS:HD3	1:K:549:ALA:O	2.19	0.41
1:B:80:LEU:HB3	1:B:81:PRO:HD2	2.02	0.41
1:L:280:ILE:HB	1:L:281:PRO:HD2	2.01	0.41
1:I:434:HIS:CD2	1:I:438:HIS:CE1	3.08	0.41
1:D:492:ARG:HE	1:D:492:ARG:HB2	1.50	0.41
1:G:159:VAL:O	1:G:202:ASP:HA	2.20	0.41
1:K:379:ARG:HG2	1:K:409:ARG:HG2	2.02	0.41
1:F:337:GLY:N	1:F:367:ASP:HB3	2.35	0.41
1:C:142:ARG:HD3	1:C:249:ASP:OD2	2.20	0.41
1:F:164:GLY:HA3	1:F:198:TRP:CD1	2.55	0.41
1:A:382:LEU:HD12	1:A:382:LEU:HA	1.82	0.41
1:D:598:ARG:H	1:L:177:ASN:ND2	2.14	0.41
1:C:82:PRO:HD3	1:D:230:LEU:HD13	2.03	0.41
1:A:482:THR:HG1	1:A:488:THR:HG1	1.68	0.41
1:D:553:THR:OG1	1:D:555:THR:O	2.37	0.41
1:G:602:HIS:HB3	1:G:614:MET:HG3	2.02	0.41
1:F:271:ASN:HD22	1:F:274:THR:H	1.68	0.41
1:J:130:PRO:HA	1:J:131:PRO:HD3	1.96	0.41
1:L:482:THR:HA	1:L:487:ARG:O	2.21	0.41
1:J:571:GLU:O	1:J:571:GLU:HG3	2.20	0.41
1:I:138:THR:O	1:I:401:ARG:HD2	2.20	0.41
1:A:149:LYS:HD3	1:A:149:LYS:HA	1.90	0.41
1:D:63:ARG:NH1	1:L:63:ARG:NH1	2.66	0.41
1:B:536:LEU:HD11	1:B:589:MET:CE	2.50	0.41
1:H:209:ARG:NH2	5:H:4371:HOH:O	2.52	0.41
1:H:271:ASN:HD21	1:H:273:GLU:HB2	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:521:PRO:HA	1:G:583:PRO:HD3	2.03	0.41
1:K:37:ALA:HB3	1:K:40:GLU:OE1	2.21	0.41
1:C:197:GLN:O	1:C:365:ARG:CD	2.67	0.41
1:F:597:GLY:HA3	1:J:177:ASN:ND2	2.35	0.41
1:H:237:ARG:HD2	1:H:304:TYR:CZ	2.55	0.41
1:A:536:LEU:HD11	1:A:589:MET:CE	2.51	0.41
1:L:255:ARG:HG3	1:L:255:ARG:NH1	2.35	0.41
1:L:163:HIS:HE2	1:L:577:VAL:HG23	1.86	0.41
1:E:418:SER:O	1:E:419:PHE:C	2.58	0.41
1:A:230:LEU:HA	1:A:230:LEU:HD23	1.93	0.41
1:E:177:ASN:ND2	1:K:598:ARG:H	2.16	0.41
1:C:177:ASN:HD22	1:G:597:GLY:HA3	1.85	0.41
1:J:174:TRP:CD1	1:J:176:ASP:HB2	2.55	0.41
1:L:142:ARG:HH21	1:L:147:PRO:HD3	1.86	0.41
1:K:587:ARG:HH11	1:K:587:ARG:HD2	1.75	0.41
1:K:138:THR:HG21	1:K:401:ARG:NH2	2.35	0.41
1:C:536:LEU:CD1	1:C:589:MET:CE	2.95	0.41
1:F:582:GLY:O	1:F:583:PRO:C	2.58	0.41
1:C:205:MET:HE3	1:C:498:PHE:CE1	2.56	0.41
1:B:627:PHE:O	1:B:628:ASP:CB	2.67	0.41
1:D:443:ILE:CD1	1:D:504:PHE:HZ	2.34	0.41
1:K:413:THR:CG2	1:K:414:CYS:N	2.84	0.41
1:B:372:PHE:HE1	1:B:380:LEU:HD12	1.86	0.41
1:A:303:TRP:CZ3	1:A:371:ASP:HB2	2.56	0.41
1:K:76:LEU:HA	1:K:76:LEU:HD23	1.93	0.41
1:I:445:LEU:HB2	1:I:518:ASN:HA	2.02	0.41
1:C:605:LEU:HD12	1:C:608:HIS:CE1	2.56	0.41
1:E:86:TRP:CD2	1:E:113:ILE:HD13	2.56	0.41
1:G:325:ASP:O	1:G:326:ASP:HB2	2.21	0.41
1:J:142:ARG:HD2	1:J:249:ASP:OD2	2.21	0.41
1:F:271:ASN:ND2	1:F:273:GLU:H	2.19	0.41
1:I:194:GLN:NE2	5:I:3156:HOH:O	2.52	0.41
1:D:375:LEU:HD13	1:D:380:LEU:HD11	2.02	0.41
1:E:520:SER:O	1:E:582:GLY:CA	2.66	0.40
1:F:142:ARG:HD3	1:F:249:ASP:OD2	2.21	0.40
1:H:520:SER:O	1:H:582:GLY:HA3	2.22	0.40
1:L:504:PHE:N	1:L:504:PHE:CD1	2.88	0.40
1:G:620:MET:HE2	1:G:624:ALA:CB	2.51	0.40
1:K:124:VAL:HG11	1:K:142:ARG:HG2	2.02	0.40
1:C:142:ARG:HD3	1:C:249:ASP:OD1	2.20	0.40
1:D:157:TRP:CE2	1:D:178:ALA:HB3	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:538:ARG:HH11	1:L:584:GLN:HE22	1.69	0.40
1:L:237:ARG:HD2	1:L:304:TYR:CZ	2.56	0.40
1:B:250:THR:HA	1:B:255:ARG:O	2.21	0.40
1:F:533:PHE:HB2	1:F:578:PHE:HZ	1.86	0.40
1:I:352:ASP:OD2	1:I:353:ASP:N	2.55	0.40
1:G:130:PRO:HA	1:G:131:PRO:HD3	1.79	0.40
1:F:581:PRO:C	1:F:582:GLY:O	2.60	0.40
1:K:209:ARG:NH1	1:K:610:ASP:CB	2.84	0.40
1:E:597:GLY:CA	1:K:177:ASN:HD22	2.34	0.40
1:C:443:ILE:HD11	1:C:504:PHE:HE2	1.84	0.40
1:G:271:ASN:O	1:G:274:THR:O	2.39	0.40
1:C:559:LEU:O	1:C:561:PRO:HD3	2.20	0.40
1:E:581:PRO:C	1:E:582:GLY:O	2.59	0.40
1:K:513:GLN:NE2	1:K:536:LEU:HD12	2.32	0.40
1:D:304:TYR:HB2	1:D:370:VAL:HG23	2.03	0.40
1:K:570:ASN:OD1	4:K:5011:GOL:H32	2.21	0.40
1:K:325:ASP:O	1:K:326:ASP:HB2	2.21	0.40
1:F:43:PRO:HB3	1:F:404:GLU:HG3	2.03	0.40
1:H:575:LYS:HB2	1:H:578:PHE:HE1	1.86	0.40
1:E:285:PRO:HG2	1:E:286:TYR:CE1	2.56	0.40
1:D:431:ARG:NH2	1:D:572:LEU:O	2.55	0.40
1:A:598:ARG:HD2	1:I:176:ASP:OD2	2.22	0.40
1:K:76:LEU:HB3	1:K:293:ILE:HD12	2.03	0.40
1:F:175:ALA:HB3	1:F:205:MET:HE2	2.03	0.40
1:C:401:ARG:HD3	5:C:2373:HOH:O	2.22	0.40
1:B:86:TRP:CD2	1:B:113:ILE:HD13	2.56	0.40
1:K:352:ASP:CG	1:K:353:ASP:H	2.24	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	583/612 (95%)	558 (96%)	23 (4%)	2 (0%)	46	57
1	B	583/612 (95%)	560 (96%)	22 (4%)	1 (0%)	52	64
1	C	583/612 (95%)	557 (96%)	26 (4%)	0	100	100
1	D	583/612 (95%)	561 (96%)	22 (4%)	0	100	100
1	E	583/612 (95%)	558 (96%)	23 (4%)	2 (0%)	46	57
1	F	583/612 (95%)	556 (95%)	24 (4%)	3 (0%)	34	41
1	G	583/612 (95%)	556 (95%)	24 (4%)	3 (0%)	34	41
1	H	583/612 (95%)	564 (97%)	18 (3%)	1 (0%)	52	64
1	I	583/612 (95%)	546 (94%)	34 (6%)	3 (0%)	34	41
1	J	583/612 (95%)	552 (95%)	29 (5%)	2 (0%)	46	57
1	K	583/612 (95%)	560 (96%)	23 (4%)	0	100	100
1	L	583/612 (95%)	558 (96%)	25 (4%)	0	100	100
All	All	6996/7344 (95%)	6686 (96%)	293 (4%)	17 (0%)	52	64

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	582	GLY
1	G	555	THR
1	G	556	PRO
1	G	583	PRO
1	H	473	VAL
1	A	473	VAL
1	A	485	ASP
1	F	582	GLY
1	F	583	PRO
1	I	582	GLY
1	J	582	GLY
1	J	583	PRO
1	E	583	PRO
1	B	473	VAL
1	F	484	ALA
1	I	583	PRO
1	I	501	GLY

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	484/499 (97%)	482 (100%)	2 (0%)	93	97
1	B	484/499 (97%)	482 (100%)	2 (0%)	93	97
1	C	484/499 (97%)	483 (100%)	1 (0%)	95	98
1	D	484/499 (97%)	483 (100%)	1 (0%)	95	98
1	E	484/499 (97%)	483 (100%)	1 (0%)	95	98
1	F	484/499 (97%)	483 (100%)	1 (0%)	95	98
1	G	484/499 (97%)	480 (99%)	4 (1%)	86	94
1	H	484/499 (97%)	483 (100%)	1 (0%)	95	98
1	I	484/499 (97%)	481 (99%)	3 (1%)	90	96
1	J	484/499 (97%)	481 (99%)	3 (1%)	90	96
1	K	484/499 (97%)	482 (100%)	2 (0%)	93	97
1	L	484/499 (97%)	478 (99%)	6 (1%)	78	89
All	All	5808/5988 (97%)	5781 (100%)	27 (0%)	92	97

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	397	LEU
1	A	578	PHE
1	B	418	SER
1	B	473	VAL
1	C	353	ASP
1	D	230	LEU
1	E	418	SER
1	F	473	VAL
1	G	445	LEU
1	G	487	ARG
1	G	548	LEU
1	G	578	PHE
1	H	472	GLN
1	I	138	THR

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Mol	Chain	Res	Type
1	I	476	GLU
1	I	558	ARG
1	J	466	GLU
1	J	472	GLN
1	J	578	PHE
1	K	138	THR
1	K	149	LYS
1	L	128	LEU
1	L	354	THR
1	L	431	ARG
1	L	558	ARG
1	L	561	PRO
1	L	578	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (108) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	91	GLN
1	A	177	ASN
1	A	191	ASN
1	A	271	ASN
1	A	334	HIS
1	A	499	ASN
1	A	513	GLN
1	A	534	GLN
1	B	91	GLN
1	B	177	ASN
1	B	191	ASN
1	B	271	ASN
1	B	318	ASN
1	B	334	HIS
1	B	456	HIS
1	B	499	ASN
1	B	513	GLN
1	B	534	GLN
1	B	574	HIS
1	B	584	GLN
1	C	91	GLN
1	C	177	ASN
1	C	191	ASN
1	C	271	ASN
1	C	318	ASN

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Mol	Chain	Res	Type
1	C	334	HIS
1	C	499	ASN
1	C	534	GLN
1	D	177	ASN
1	D	191	ASN
1	D	271	ASN
1	D	334	HIS
1	D	499	ASN
1	D	513	GLN
1	D	534	GLN
1	D	584	GLN
1	E	91	GLN
1	E	177	ASN
1	E	191	ASN
1	E	271	ASN
1	E	318	ASN
1	E	334	HIS
1	E	456	HIS
1	E	472	GLN
1	E	534	GLN
1	E	584	GLN
1	F	177	ASN
1	F	191	ASN
1	F	271	ASN
1	F	334	HIS
1	F	456	HIS
1	F	513	GLN
1	F	534	GLN
1	G	177	ASN
1	G	191	ASN
1	G	271	ASN
1	G	318	ASN
1	G	334	HIS
1	G	534	GLN
1	G	574	HIS
1	G	584	GLN
1	H	177	ASN
1	H	191	ASN
1	H	271	ASN
1	H	318	ASN
1	H	334	HIS
1	H	472	GLN

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Mol	Chain	Res	Type
1	H	499	ASN
1	H	534	GLN
1	I	177	ASN
1	I	191	ASN
1	I	271	ASN
1	I	334	HIS
1	I	456	HIS
1	I	499	ASN
1	I	513	GLN
1	I	534	GLN
1	I	574	HIS
1	I	584	GLN
1	J	177	ASN
1	J	191	ASN
1	J	271	ASN
1	J	334	HIS
1	J	472	GLN
1	J	499	ASN
1	J	513	GLN
1	J	534	GLN
1	J	584	GLN
1	K	177	ASN
1	K	191	ASN
1	K	197	GLN
1	K	206	ASN
1	K	271	ASN
1	K	334	HIS
1	K	513	GLN
1	K	534	GLN
1	K	584	GLN
1	L	91	GLN
1	L	177	ASN
1	L	191	ASN
1	L	194	GLN
1	L	271	ASN
1	L	318	ASN
1	L	334	HIS
1	L	499	ASN
1	L	513	GLN
1	L	534	GLN
1	L	584	GLN

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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 60 ligands modelled in this entry, 36 are monoatomic - leaving 24 for Mogul analysis.

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	C2O	A	1002	1	0,2,2	0.00	-	0,1,1	0.00	-
4	GOL	A	5001	-	5,5,5	0.38	0	5,5,5	0.93	0
3	C2O	B	1002	1	0,2,2	0.00	-	0,1,1	0.00	-
4	GOL	B	5002	-	5,5,5	0.32	0	5,5,5	0.71	0
3	C2O	C	1002	1	0,2,2	0.00	-	0,1,1	0.00	-
4	GOL	C	5003	-	5,5,5	0.42	0	5,5,5	1.07	0
3	C2O	D	1002	1	0,2,2	0.00	-	0,1,1	0.00	-
4	GOL	D	5004	-	5,5,5	0.36	0	5,5,5	0.79	0
3	C2O	E	1002	1	0,2,2	0.00	-	0,1,1	0.00	-
4	GOL	E	5005	-	5,5,5	0.31	0	5,5,5	0.69	0
3	C2O	F	1002	1	0,2,2	0.00	-	0,1,1	0.00	-
4	GOL	F	5006	-	5,5,5	0.18	0	5,5,5	0.72	0
3	C2O	G	1002	1	0,2,2	0.00	-	0,1,1	0.00	-
4	GOL	G	5007	-	5,5,5	0.16	0	5,5,5	0.54	0
3	C2O	H	1002	1	0,2,2	0.00	-	0,1,1	0.00	-
4	GOL	H	5008	-	5,5,5	0.32	0	5,5,5	0.78	0
3	C2O	I	1002	1	0,2,2	0.00	-	0,1,1	0.00	-
4	GOL	I	5009	-	5,5,5	0.24	0	5,5,5	0.89	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	C2O	J	1002	1	0,2,2	0.00	-	0,1,1	0.00	-
4	GOL	J	5010	-	5,5,5	0.20	0	5,5,5	0.51	0
3	C2O	K	1002	1	0,2,2	0.00	-	0,1,1	0.00	-
4	GOL	K	5011	-	5,5,5	0.33	0	5,5,5	1.18	0
3	C2O	L	1002	1	0,2,2	0.00	-	0,1,1	0.00	-
4	GOL	L	5012	-	5,5,5	0.44	0	5,5,5	0.91	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	C2O	A	1002	1	-	0/0/0/0	0/0/0/0
4	GOL	A	5001	-	-	0/4/4/4	0/0/0/0
3	C2O	B	1002	1	-	0/0/0/0	0/0/0/0
4	GOL	B	5002	-	-	0/4/4/4	0/0/0/0
3	C2O	C	1002	1	-	0/0/0/0	0/0/0/0
4	GOL	C	5003	-	-	0/4/4/4	0/0/0/0
3	C2O	D	1002	1	-	0/0/0/0	0/0/0/0
4	GOL	D	5004	-	-	0/4/4/4	0/0/0/0
3	C2O	E	1002	1	-	0/0/0/0	0/0/0/0
4	GOL	E	5005	-	-	0/4/4/4	0/0/0/0
3	C2O	F	1002	1	-	0/0/0/0	0/0/0/0
4	GOL	F	5006	-	-	0/4/4/4	0/0/0/0
3	C2O	G	1002	1	-	0/0/0/0	0/0/0/0
4	GOL	G	5007	-	-	0/4/4/4	0/0/0/0
3	C2O	H	1002	1	-	0/0/0/0	0/0/0/0
4	GOL	H	5008	-	-	0/4/4/4	0/0/0/0
3	C2O	I	1002	1	-	0/0/0/0	0/0/0/0
4	GOL	I	5009	-	-	0/4/4/4	0/0/0/0
3	C2O	J	1002	1	-	0/0/0/0	0/0/0/0
4	GOL	J	5010	-	-	0/4/4/4	0/0/0/0
3	C2O	K	1002	1	-	0/0/0/0	0/0/0/0
4	GOL	K	5011	-	-	0/4/4/4	0/0/0/0
3	C2O	L	1002	1	-	0/0/0/0	0/0/0/0
4	GOL	L	5012	-	-	0/4/4/4	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	5004	GOL	1	0
4	H	5008	GOL	1	0
4	K	5011	GOL	2	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	587/612 (95%)	-0.22	31 (5%)	30	39	15, 26, 51, 68	2 (0%)
1	B	587/612 (95%)	-0.23	26 (4%)	38	47	14, 25, 47, 69	4 (0%)
1	C	587/612 (95%)	-0.33	18 (3%)	52	62	14, 22, 46, 67	0
1	D	587/612 (95%)	-0.38	10 (1%)	73	79	14, 22, 44, 66	0
1	E	587/612 (95%)	-0.30	29 (4%)	33	42	14, 23, 47, 71	1 (0%)
1	F	587/612 (95%)	-0.23	25 (4%)	39	48	14, 23, 47, 69	3 (0%)
1	G	587/612 (95%)	-0.29	30 (5%)	32	41	14, 24, 47, 70	1 (0%)
1	H	587/612 (95%)	-0.29	21 (3%)	46	55	15, 24, 45, 70	2 (0%)
1	I	587/612 (95%)	-0.10	35 (5%)	25	33	15, 25, 53, 74	2 (0%)
1	J	587/612 (95%)	-0.30	19 (3%)	51	60	15, 23, 45, 61	2 (0%)
1	K	587/612 (95%)	-0.23	26 (4%)	38	47	15, 25, 49, 68	1 (0%)
1	L	587/612 (95%)	-0.23	24 (4%)	41	50	16, 25, 50, 71	1 (0%)
All	All	7044/7344 (95%)	-0.26	294 (4%)	40	49	14, 24, 48, 74	19 (0%)

All (294) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	472	GLN	33.0
1	L	472	GLN	23.5
1	H	473	VAL	18.1
1	F	472	GLN	17.4
1	I	473	VAL	16.9
1	B	472	GLN	16.4
1	F	473	VAL	15.8
1	J	472	GLN	12.6
1	K	473	VAL	12.5
1	H	472	GLN	11.8
1	A	472	GLN	11.6

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Mol	Chain	Res	Type	RSRZ
1	B	473	VAL	10.9
1	E	472	GLN	9.6
1	L	38	PRO	7.9
1	C	38	PRO	7.0
1	D	38	PRO	7.0
1	L	37	ALA	6.2
1	J	38	PRO	6.1
1	B	414	CYS	5.8
1	F	414	CYS	5.8
1	H	414	CYS	5.7
1	E	38	PRO	5.7
1	L	563	THR	5.6
1	G	416	GLU	5.6
1	G	414	CYS	5.5
1	H	37	ALA	5.4
1	K	414	CYS	5.4
1	E	487	ARG	5.4
1	L	416	GLU	5.3
1	K	38	PRO	5.3
1	I	38	PRO	5.2
1	I	37	ALA	5.2
1	H	38	PRO	5.1
1	A	37	ALA	5.1
1	A	473	VAL	4.9
1	K	131	PRO	4.8
1	E	414	CYS	4.8
1	C	414	CYS	4.8
1	I	416	GLU	4.8
1	J	131	PRO	4.7
1	C	37	ALA	4.7
1	I	414	CYS	4.7
1	F	466	GLU	4.6
1	G	37	ALA	4.6
1	I	484	ALA	4.6
1	K	487	ARG	4.6
1	A	38	PRO	4.5
1	J	414	CYS	4.5
1	L	414	CYS	4.5
1	D	414	CYS	4.5
1	B	37	ALA	4.5
1	J	37	ALA	4.5
1	F	562	ASP	4.4

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Mol	Chain	Res	Type	RSRZ
1	A	414	CYS	4.4
1	I	487	ARG	4.4
1	K	37	ALA	4.3
1	L	487	ARG	4.3
1	C	416	GLU	4.3
1	A	484	ALA	4.3
1	I	275	GLY	4.3
1	L	466	GLU	4.2
1	F	582	GLY	4.2
1	B	487	ARG	4.2
1	A	563	THR	4.1
1	F	416	GLU	4.1
1	C	131	PRO	4.1
1	K	275	GLY	4.1
1	B	38	PRO	4.1
1	D	37	ALA	4.0
1	H	131	PRO	4.0
1	C	59	ASP	4.0
1	E	466	GLU	4.0
1	J	354	THR	4.0
1	A	416	GLU	4.0
1	K	129	GLY	4.0
1	F	275	GLY	4.0
1	I	562	ASP	3.8
1	L	415	GLU	3.8
1	K	353	ASP	3.8
1	E	582	GLY	3.8
1	I	354	THR	3.8
1	A	466	GLU	3.8
1	L	562	ASP	3.7
1	K	354	THR	3.7
1	E	37	ALA	3.7
1	G	487	ARG	3.7
1	G	485	ASP	3.6
1	D	354	THR	3.6
1	I	564	PRO	3.6
1	B	131	PRO	3.6
1	D	131	PRO	3.6
1	J	582	GLY	3.6
1	D	416	GLU	3.5
1	G	418	SER	3.5
1	G	562	ASP	3.5

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Mol	Chain	Res	Type	RSRZ
1	K	59	ASP	3.5
1	B	416	GLU	3.5
1	H	416	GLU	3.5
1	G	582	GLY	3.5
1	C	466	GLU	3.5
1	B	466	GLU	3.5
1	I	485	ASP	3.5
1	F	274	THR	3.4
1	I	465	VAL	3.4
1	D	466	GLU	3.4
1	E	131	PRO	3.4
1	A	354	THR	3.4
1	F	37	ALA	3.4
1	B	59	ASP	3.4
1	I	466	GLU	3.3
1	K	416	GLU	3.3
1	A	59	ASP	3.3
1	J	466	GLU	3.3
1	L	252	GLU	3.3
1	G	252	GLU	3.3
1	A	275	GLY	3.3
1	F	487	ARG	3.3
1	F	353	ASP	3.3
1	A	131	PRO	3.3
1	C	582	GLY	3.3
1	L	433	SER	3.3
1	B	437	PRO	3.2
1	A	562	ASP	3.2
1	I	353	ASP	3.2
1	A	418	SER	3.2
1	H	354	THR	3.2
1	A	487	ARG	3.2
1	I	563	THR	3.2
1	E	485	ASP	3.1
1	A	486	GLY	3.1
1	K	582	GLY	3.1
1	K	484	ALA	3.1
1	G	353	ASP	3.1
1	J	275	GLY	3.1
1	F	38	PRO	3.1
1	H	275	GLY	3.1
1	L	274	THR	3.0

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Mol	Chain	Res	Type	RSRZ
1	H	59	ASP	3.0
1	H	418	SER	3.0
1	E	416	GLU	3.0
1	H	274	THR	3.0
1	A	433	SER	3.0
1	E	435	ASP	3.0
1	G	466	GLU	3.0
1	I	59	ASP	3.0
1	K	472	GLN	3.0
1	C	487	ARG	3.0
1	L	564	PRO	3.0
1	E	252	GLU	3.0
1	F	131	PRO	3.0
1	I	475	ALA	3.0
1	J	353	ASP	2.9
1	D	487	ARG	2.9
1	C	486	GLY	2.9
1	A	485	ASP	2.9
1	J	416	GLU	2.9
1	B	354	THR	2.9
1	G	132	GLY	2.9
1	B	562	ASP	2.9
1	E	486	GLY	2.9
1	J	562	ASP	2.9
1	L	418	SER	2.9
1	E	465	VAL	2.8
1	J	418	SER	2.8
1	G	131	PRO	2.8
1	F	354	THR	2.8
1	K	485	ASP	2.8
1	L	39	GLY	2.8
1	C	564	PRO	2.8
1	K	57	ALA	2.8
1	C	418	SER	2.8
1	I	628	ASP	2.8
1	L	485	ASP	2.8
1	J	561	PRO	2.8
1	E	473	VAL	2.8
1	A	57	ALA	2.8
1	G	354	THR	2.8
1	K	415	GLU	2.8
1	B	465	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
1	D	275	GLY	2.7
1	F	418	SER	2.7
1	H	415	GLU	2.7
1	G	59	ASP	2.7
1	E	415	GLU	2.7
1	H	132	GLY	2.7
1	E	563	THR	2.7
1	L	275	GLY	2.7
1	I	558	ARG	2.7
1	E	562	ASP	2.7
1	L	353	ASP	2.7
1	I	133	THR	2.7
1	A	435	ASP	2.7
1	C	354	THR	2.6
1	I	252	GLU	2.6
1	E	59	ASP	2.6
1	F	253	ASP	2.6
1	K	270	SER	2.6
1	A	146	GLU	2.6
1	F	563	THR	2.6
1	C	353	ASP	2.6
1	A	564	PRO	2.6
1	L	354	THR	2.6
1	F	252	GLU	2.6
1	B	57	ALA	2.6
1	I	561	PRO	2.6
1	C	562	ASP	2.6
1	D	353	ASP	2.5
1	L	484	ALA	2.5
1	B	435	ASP	2.5
1	A	465	VAL	2.5
1	F	486	GLY	2.5
1	G	38	PRO	2.5
1	G	486	GLY	2.5
1	I	550	LEU	2.5
1	F	437	PRO	2.5
1	F	561	PRO	2.5
1	F	59	ASP	2.5
1	I	418	SER	2.4
1	K	39	GLY	2.4
1	K	130	PRO	2.4
1	K	418	SER	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	561	PRO	2.4
1	G	564	PRO	2.4
1	K	466	GLU	2.4
1	A	39	GLY	2.4
1	H	133	THR	2.4
1	G	272	PRO	2.4
1	C	485	ASP	2.4
1	G	479	ILE	2.4
1	E	354	THR	2.4
1	I	274	THR	2.4
1	E	561	PRO	2.4
1	K	486	GLY	2.4
1	B	549	ALA	2.3
1	L	561	PRO	2.3
1	J	59	ASP	2.3
1	B	628	ASP	2.3
1	E	353	ASP	2.3
1	F	564	PRO	2.3
1	I	582	GLY	2.3
1	C	415	GLU	2.3
1	G	146	GLU	2.3
1	B	353	ASP	2.3
1	H	353	ASP	2.3
1	G	63	ARG	2.3
1	I	486	GLY	2.3
1	A	133	THR	2.3
1	A	274	THR	2.3
1	I	549	ALA	2.3
1	A	270	SER	2.3
1	I	437	PRO	2.2
1	G	484	ALA	2.2
1	G	563	THR	2.2
1	H	466	GLU	2.2
1	E	129	GLY	2.2
1	E	483	GLY	2.2
1	A	561	PRO	2.2
1	B	485	ASP	2.2
1	H	563	THR	2.2
1	L	473	VAL	2.2
1	H	130	PRO	2.2
1	B	479	ILE	2.2
1	K	562	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	J	252	GLU	2.2
1	E	484	ALA	2.2
1	B	486	GLY	2.1
1	E	253	ASP	2.1
1	J	132	GLY	2.1
1	A	272	PRO	2.1
1	I	272	PRO	2.1
1	I	433	SER	2.1
1	G	472	GLN	2.1
1	G	143	GLY	2.1
1	G	275	GLY	2.1
1	B	252	GLU	2.1
1	C	628	ASP	2.1
1	G	628	ASP	2.1
1	L	558	ARG	2.1
1	I	57	ALA	2.1
1	H	252	GLU	2.1
1	G	133	THR	2.1
1	J	272	PRO	2.1
1	J	435	ASP	2.0
1	B	434	HIS	2.0
1	B	564	PRO	2.0
1	E	564	PRO	2.0
1	H	435	ASP	2.0
1	K	435	ASP	2.0
1	F	433	SER	2.0
1	G	433	SER	2.0
1	E	133	THR	2.0
1	A	474	PRO	2.0
1	E	130	PRO	2.0
1	I	521	PRO	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

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(Å ²)	Q<0.9
4	GOL	K	5011	6/6	0.84	0.18	5.44	29,41,42,43	0
4	GOL	C	5003	6/6	0.90	0.17	4.99	26,28,32,34	0
4	GOL	E	5005	6/6	0.85	0.15	3.09	35,40,43,43	0
4	GOL	B	5002	6/6	0.89	0.16	2.75	33,39,42,42	0
4	GOL	D	5004	6/6	0.85	0.17	2.70	34,36,38,38	0
4	GOL	L	5012	6/6	0.86	0.15	2.06	34,37,39,39	0
4	GOL	H	5008	6/6	0.90	0.14	2.05	26,33,35,36	0
4	GOL	F	5006	6/6	0.91	0.12	1.88	38,39,41,43	0
4	GOL	A	5001	6/6	0.90	0.13	1.65	25,32,38,39	0
4	GOL	I	5009	6/6	0.91	0.15	1.45	28,36,39,40	0
4	GOL	J	5010	6/6	0.94	0.11	0.73	27,35,35,37	0
4	GOL	G	5007	6/6	0.94	0.11	0.58	30,39,41,42	0
3	C2O	C	1002	3/3	0.96	0.09	-0.09	29,29,39,41	0
3	C2O	F	1002	3/3	0.96	0.09	-0.32	38,38,39,48	0
3	C2O	K	1002	3/3	0.95	0.09	-0.75	42,42,45,46	0
3	C2O	A	1002	3/3	0.94	0.08	-0.92	41,41,44,52	0
3	C2O	H	1002	3/3	0.96	0.07	-0.94	38,38,40,45	0
3	C2O	L	1002	3/3	0.96	0.07	-1.05	39,39,41,46	0
3	C2O	J	1002	3/3	0.95	0.07	-1.38	29,29,38,43	0
3	C2O	B	1002	3/3	0.95	0.07	-1.51	40,40,41,48	0
3	C2O	E	1002	3/3	0.97	0.06	-1.59	32,32,40,40	0
2	CU	E	1000	1/1	0.99	0.06	-2.07	45,45,45,45	0
2	CU	F	1004	1/1	0.99	0.06	-2.32	42,42,42,42	0
2	CU	H	1000	1/1	0.99	0.04	-2.38	49,49,49,49	0
3	C2O	G	1002	3/3	0.97	0.06	-2.39	41,41,42,49	0
2	CU	F	1000	1/1	1.00	0.03	-2.40	42,42,42,42	0
3	C2O	D	1002	3/3	0.98	0.05	-2.40	30,30,39,41	0
2	CU	L	1000	1/1	1.00	0.05	-2.46	43,43,43,43	0
2	CU	I	1000	1/1	1.00	0.02	-2.50	46,46,46,46	0
2	CU	C	1004	1/1	1.00	0.04	-2.86	39,39,39,39	0
3	C2O	I	1002	3/3	0.96	0.05	-3.07	37,37,46,47	0
2	CU	I	1004	1/1	0.99	0.03	-3.12	43,43,43,43	0
2	CU	B	1000	1/1	1.00	0.03	-3.26	43,43,43,43	0
2	CU	H	1004	1/1	0.99	0.04	-3.38	43,43,43,43	0
2	CU	J	1004	1/1	0.99	0.04	-3.40	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	CU	D	1004	1/1	0.99	0.05	-3.60	38,38,38,38	0
2	CU	J	1000	1/1	0.99	0.03	-3.88	40,40,40,40	0
2	CU	C	1000	1/1	0.99	0.02	-3.96	43,43,43,43	0
2	CU	A	1004	1/1	0.99	0.04	-3.97	41,41,41,41	0
2	CU	A	1000	1/1	1.00	0.04	-4.03	50,50,50,50	0
2	CU	D	1000	1/1	1.00	0.03	-4.09	37,37,37,37	0
2	CU	L	1004	1/1	0.98	0.03	-4.67	43,43,43,43	0
2	CU	K	1004	1/1	0.99	0.04	-4.94	40,40,40,40	0
2	CU	G	1000	1/1	1.00	0.03	-	43,43,43,43	0
2	CU	A	1005	1/1	0.98	0.02	-	43,43,43,43	0
2	CU	E	1005	1/1	0.99	0.03	-	42,42,42,42	0
2	CU	C	1005	1/1	0.98	0.02	-	37,37,37,37	0
2	CU	B	1004	1/1	0.99	0.04	-	40,40,40,40	0
2	CU	G	1005	1/1	0.99	0.03	-	39,39,39,39	0
2	CU	K	1005	1/1	0.99	0.02	-	42,42,42,42	0
2	CU	D	1005	1/1	0.98	0.04	-	38,38,38,38	0
2	CU	B	1005	1/1	1.00	0.07	-	37,37,37,37	0
2	CU	F	1005	1/1	0.99	0.03	-	38,38,38,38	0
2	CU	I	1005	1/1	0.99	0.04	-	42,42,42,42	0
2	CU	G	1004	1/1	0.99	0.04	-	43,43,43,43	0
2	CU	L	1005	1/1	0.96	0.03	-	41,41,41,41	0
2	CU	H	1005	1/1	1.00	0.03	-	36,36,36,36	0
2	CU	E	1004	1/1	1.00	0.03	-	41,41,41,41	0
2	CU	K	1000	1/1	0.99	0.03	-	43,43,43,43	0
2	CU	J	1005	1/1	0.98	0.02	-	39,39,39,39	0

6.5 Other polymers [i](#)

There are no such residues in this entry.