



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 10:28 PM GMT

PDB ID : 1TU0
Title : Aspartate Transcarbamoylase Catalytic Chain Mutant E50A Complex with Phosphonoacetamide
Authors : Stieglitz, K.; Stec, B.; Baker, D.P.; Kantrowitz, E.R.
Deposited on : 2004-06-23
Resolution : 2.55 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

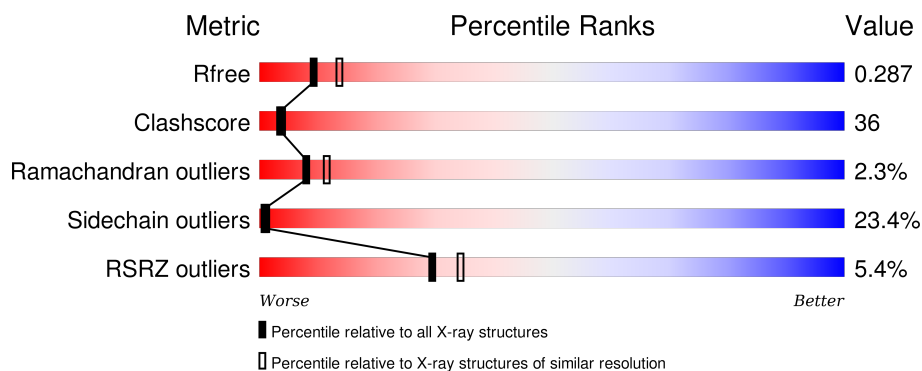
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 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	4549 (2.58-2.50)
Clashscore	102246	5292 (2.58-2.50)
Ramachandran outliers	100387	5194 (2.58-2.50)
Sidechain outliers	100360	5196 (2.58-2.50)
RSRZ outliers	91569	4561 (2.58-2.50)

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	310	<div> <div>4%</div> <div>39%</div> <div>47%</div> <div>13%</div> <div>.</div> </div>
1	C	310	<div> <div>4%</div> <div>49%</div> <div>39%</div> <div>11%</div> <div>.</div> </div>
2	B	153	<div> <div>8%</div> <div>24%</div> <div>52%</div> <div>20%</div> <div>5%</div> </div>
2	D	153	<div> <div>8%</div> <div>33%</div> <div>45%</div> <div>20%</div> <div>.</div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	PCT	C	1312	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7596 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 Aspartate carbamoyltransferase catalytic chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	310	Total	C	N	O	S	0	0	0
			2411	1525	423	454	9			
1	C	310	Total	C	N	O	S	0	0	0
			2411	1525	423	454	9			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	50	ALA	GLU	ENGINEERED	UNP P0A786
C	50	ALA	GLU	ENGINEERED	UNP P0A786

- Molecule 2 is a protein called Aspartate carbamoyltransferase regulatory chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	153	Total	C	N	O	S	0	0	0
			1201	752	213	230	6			
2	D	153	Total	C	N	O	S	0	0	0
			1201	752	213	230	6			

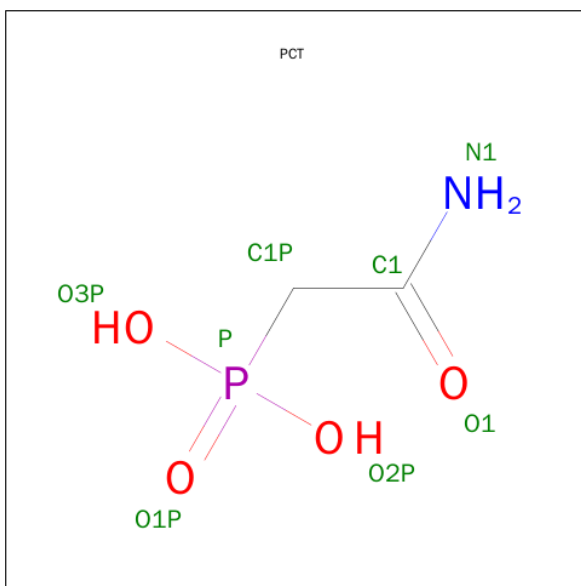
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	MET	-	INITIATING METHIONINE	UNP P0A7F3
D	1	MET	-	INITIATING METHIONINE	UNP P0A7F3

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Zn	0	0
			1	1		
3	D	1	Total	Zn	0	0
			1	1		

- Molecule 4 is PHOSPHONOACETAMIDE (three-letter code: PCT) (formula: $C_2H_6NO_4P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			8	2	1	4	1		
4	C	1	Total	C	N	O	P	0	0
			8	2	1	4	1		

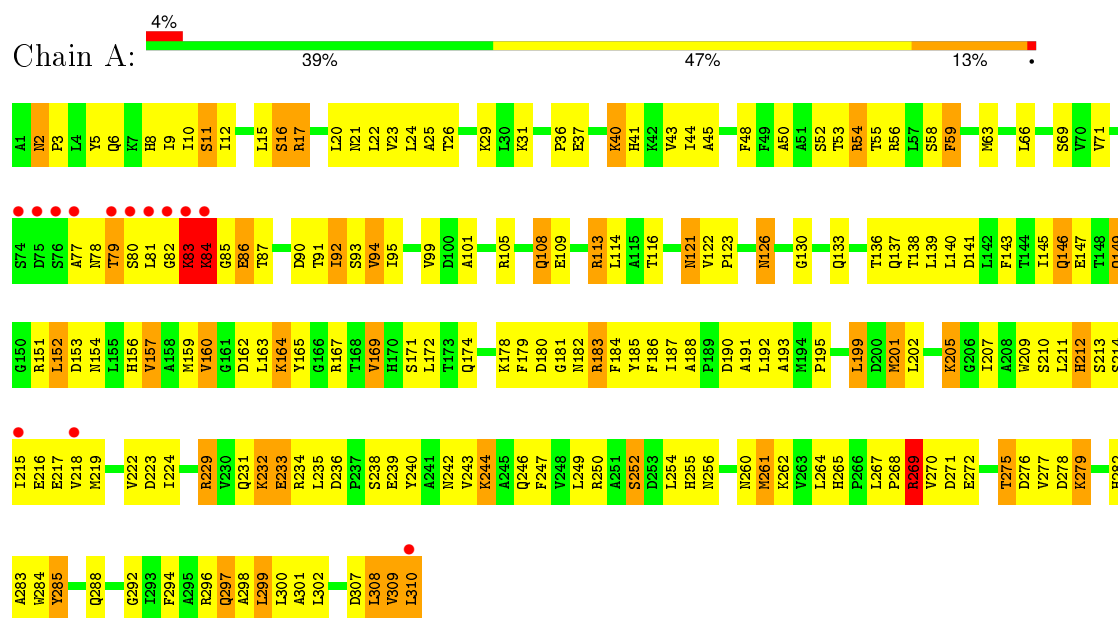
- Molecule 5 is water.

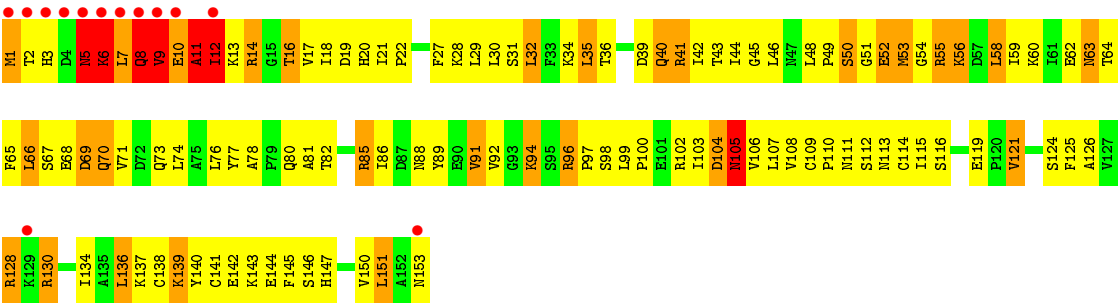
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	119	Total	O	0	0
			119	119		
5	B	53	Total	O	0	0
			53	53		
5	C	131	Total	O	0	0
			131	131		
5	D	51	Total	O	0	0
			51	51		

3 Residue-property plots

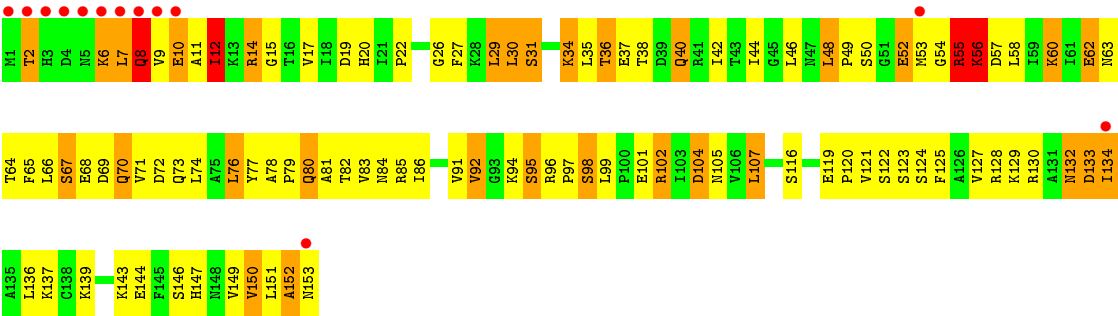
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 ($\text{RSRZ} > 2$). 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: Aspartate carbamoyltransferase catalytic chain





● Molecule 2: Aspartate carbamoyltransferase regulatory chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants a, b, c, α , β , γ	122.20 Å 122.20 Å 142.70 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 2.55 61.10 – 2.55	Depositor EDS
% Data completeness (in resolution range)	94.0 (30.00-2.55) 97.8 (61.10-2.55)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.27 (at 2.55 Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.211 , 0.279 0.212 , 0.287	Depositor DCC
R_{free} test set	1990 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	22.5	Xtriage
Anisotropy	0.409	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 388.0	EDS
Estimated twinning fraction	0.043 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	1 of 39799 reflections (0.003%)	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	7596	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.98% 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: ZN, PCT

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	0.49	2/2457 (0.1%)	1.03	11/3334 (0.3%)
1	C	0.44	3/2457 (0.1%)	1.06	12/3334 (0.4%)
2	B	1.34	8/1219 (0.7%)	1.21	12/1647 (0.7%)
2	D	0.76	6/1219 (0.5%)	1.11	15/1647 (0.9%)
All	All	0.73	19/7352 (0.3%)	1.08	50/9962 (0.5%)

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	3
1	C	0	1
2	B	0	3
2	D	0	2
All	All	0	9

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	105	ASN	N-CA	20.81	1.88	1.46
2	B	8	GLN	C-N	-17.65	0.93	1.34
2	B	105	ASN	C-N	17.59	1.74	1.34
2	B	9	VAL	C-N	17.00	1.73	1.34
2	D	152	ALA	C-N	15.67	1.70	1.34
1	A	309	VAL	C-N	15.44	1.69	1.34
2	B	153	ASN	C-OXT	15.42	1.52	1.23
2	B	5	ASN	C-N	14.48	1.67	1.34
2	B	11	ALA	C-N	-14.32	1.01	1.34
2	D	56	LYS	C-N	10.17	1.57	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	75	ASP	C-N	-9.97	1.11	1.34
2	D	8	GLN	C-N	8.80	1.54	1.34
2	D	7	LEU	C-N	-8.45	1.14	1.34
1	C	51	ALA	C-N	-7.63	1.16	1.34
1	C	309	VAL	C-N	6.91	1.50	1.34
1	A	77	ALA	C-N	5.56	1.46	1.34
2	B	12	ILE	C-N	5.27	1.46	1.34
2	D	133	ASP	C-N	5.27	1.46	1.34
2	D	55	ARG	C-N	-5.26	1.22	1.34

All (50) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	309	VAL	O-C-N	-18.13	93.69	122.70
2	B	8	GLN	O-C-N	17.52	150.73	122.70
2	B	8	GLN	CA-C-N	-16.20	81.57	117.20
2	D	8	GLN	O-C-N	13.04	143.56	122.70
1	C	309	VAL	CA-C-N	11.46	142.41	117.20
1	A	269	ARG	CD-NE-CZ	10.35	138.09	123.60
1	C	74	SER	C-N-CA	10.15	147.07	121.70
2	D	8	GLN	CA-C-N	-9.81	95.61	117.20
2	D	104	ASP	C-N-CA	9.17	144.64	121.70
1	A	79	THR	C-N-CA	8.98	144.14	121.70
1	C	51	ALA	O-C-N	-8.44	109.20	122.70
1	A	309	VAL	O-C-N	-8.30	109.42	122.70
2	B	12	ILE	O-C-N	8.11	135.68	122.70
1	C	51	ALA	C-N-CA	8.05	141.83	121.70
2	D	152	ALA	O-C-N	7.80	135.19	122.70
1	A	269	ARG	NE-CZ-NH1	-7.75	116.42	120.30
2	D	56	LYS	O-C-N	7.52	134.72	122.70
1	C	309	VAL	C-N-CA	7.29	139.93	121.70
1	A	84	LYS	CB-CA-C	7.16	124.73	110.40
1	A	269	ARG	NE-CZ-NH2	7.11	123.86	120.30
2	B	8	GLN	C-N-CA	-7.04	104.11	121.70
2	D	11	ALA	C-N-CA	6.50	137.95	121.70
2	B	12	ILE	CA-C-N	-6.44	103.03	117.20
2	B	6	LYS	CA-C-N	-6.41	103.10	117.20
2	B	105	ASN	C-N-CA	-6.40	105.70	121.70
1	A	84	LYS	O-C-N	-6.33	112.43	123.20
1	C	73	PHE	CB-CG-CD2	6.23	125.16	120.80
2	D	152	ALA	CA-C-N	-6.12	103.73	117.20
2	D	104	ASP	O-C-N	-6.12	112.91	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	77	ALA	O-C-N	6.08	132.42	122.70
2	D	133	ASP	O-C-N	-6.07	112.99	122.70
2	D	56	LYS	CA-C-N	-6.03	103.93	117.20
2	D	12	ILE	O-C-N	6.03	132.35	122.70
2	D	105	ASN	O-C-N	5.92	132.17	122.70
2	D	105	ASN	C-N-CA	-5.90	106.95	121.70
1	A	85	GLY	N-CA-C	5.84	127.69	113.10
2	B	128	ARG	NE-CZ-NH1	5.82	123.21	120.30
2	B	6	LYS	O-C-N	5.79	131.96	122.70
1	A	84	LYS	CA-C-N	5.69	127.58	116.20
2	B	105	ASN	O-C-N	5.66	131.75	122.70
2	D	152	ALA	C-N-CA	-5.66	107.56	121.70
1	C	51	ALA	CA-C-N	5.54	129.39	117.20
1	C	77	ALA	C-N-CA	5.54	135.54	121.70
1	C	98	TYR	CB-CG-CD2	-5.47	117.72	121.00
1	C	75	ASP	O-C-N	-5.37	114.11	122.70
1	A	84	LYS	N-CA-CB	5.28	120.11	110.60
2	B	5	ASN	C-N-CA	5.21	134.74	121.70
1	C	75	ASP	N-CA-C	5.20	125.03	111.00
2	B	104	ASP	C-N-CA	5.10	134.45	121.70
2	D	133	ASP	CB-CG-OD2	5.08	122.87	118.30

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	83	LYS	Mainchain
1	A	84	LYS	Mainchain,Peptide
2	B	11	ALA	Mainchain
2	B	128	ARG	Mainchain
2	B	8	GLN	Mainchain
1	C	73	PHE	Mainchain
2	D	132	ASN	Mainchain
2	D	133	ASP	Mainchain

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	2411	0	2420	177	0
1	C	2411	0	2418	116	0
2	B	1201	0	1215	133	5
2	D	1201	0	1215	111	0
3	B	1	0	0	0	0
3	D	1	0	0	0	0
4	A	8	0	4	1	0
4	C	8	0	4	6	0
5	A	119	0	0	9	0
5	B	53	0	0	11	0
5	C	131	0	0	6	5
5	D	51	0	0	9	0
All	All	7596	0	7276	525	5

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 36.

All (525) 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:A:309:VAL:C	1:A:310:LEU:N	1.69	1.45
2:D:152:ALA:C	2:D:153:ASN:N	1.70	1.42
2:B:9:VAL:C	2:B:10:GLU:N	1.73	1.42
2:B:105:ASN:C	2:B:106:VAL:N	1.74	1.39
2:B:105:ASN:CA	2:B:105:ASN:N	1.88	1.36
2:B:9:VAL:HG12	2:B:10:GLU:N	1.59	1.15
2:B:17:VAL:HG22	2:B:60:LYS:HG2	1.43	1.00
2:B:9:VAL:CG1	2:B:10:GLU:N	2.29	0.95
1:A:29:LYS:NZ	1:A:310:LEU:HB2	1.84	0.93
2:B:30:LEU:HA	2:B:35:LEU:HD12	1.52	0.90
1:C:236:ASP:HB3	1:C:239:GLU:HB3	1.52	0.89
2:B:12:ILE:HG22	2:B:62:GLU:OE2	1.76	0.86
2:D:146:SER:HB3	2:D:149:VAL:HG23	1.59	0.85
1:A:29:LYS:NZ	1:A:310:LEU:CB	2.40	0.85
2:B:49:PRO:HB2	5:B:206:HOH:O	1.77	0.85
2:D:130:ARG:HD2	5:D:204:HOH:O	1.77	0.84
2:D:136:LEU:HD12	2:D:150:VAL:HG21	1.59	0.83
1:A:187:ILE:HG12	1:A:212:HIS:HB2	1.60	0.83
1:C:54:ARG:HB3	4:C:1312:PCT:O1P	1.79	0.82
2:B:107:LEU:HD22	2:B:150:VAL:HG12	1.58	0.82
1:C:205:LYS:HB3	1:C:207:ILE:HD12	1.63	0.81
1:A:29:LYS:HZ1	1:A:310:LEU:HB2	1.45	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:183:ARG:HH22	1:A:210:SER:H	1.30	0.80
1:A:183:ARG:HH12	1:A:210:SER:HB3	1.47	0.79
1:A:159:MET:HE3	1:A:172:LEU:HB3	1.64	0.79
2:B:66:LEU:HD12	2:B:71:VAL:HG23	1.64	0.79
2:B:30:LEU:HD11	2:B:44:ILE:HG12	1.63	0.79
1:C:292:GLY:O	1:C:296:ARG:HG3	1.83	0.79
1:A:265:HIS:H	1:A:288:GLN:HE22	1.29	0.78
2:B:42:ILE:HB	2:D:46:LEU:HB2	1.63	0.78
2:B:107:LEU:HD13	2:B:136:LEU:HD13	1.66	0.78
2:B:85:ARG:O	2:B:86:ILE:HD13	1.84	0.77
1:C:12:ILE:HD13	1:C:135:PRO:HA	1.66	0.77
2:B:46:LEU:HB2	2:D:42:ILE:HB	1.67	0.77
1:A:113:ARG:O	1:A:116:THR:HB	1.83	0.77
1:A:234:ARG:O	1:A:235:LEU:HD23	1.85	0.77
1:A:201:MET:HG2	1:A:202:LEU:HD23	1.68	0.76
2:B:80:GLN:HB2	5:B:184:HOH:O	1.86	0.75
2:D:152:ALA:C	2:D:153:ASN:CA	2.55	0.74
2:D:66:LEU:H	2:D:85:ARG:HH12	1.34	0.74
1:A:154:ASN:HA	1:A:181:GLY:O	1.87	0.74
2:B:105:ASN:C	2:B:106:VAL:CA	2.56	0.74
1:C:24:LEU:HD22	1:C:143:PHE:HB2	1.68	0.74
1:A:183:ARG:HH22	1:A:210:SER:N	1.85	0.74
2:B:99:LEU:HD12	2:B:100:PRO:HD2	1.68	0.74
2:B:50:SER:H	2:B:55:ARG:HA	1.51	0.73
1:C:52:SER:HB2	4:C:1312:PCT:P	2.28	0.73
1:A:90:ASP:O	1:A:94:VAL:HG13	1.88	0.73
1:A:229:ARG:HH11	1:A:229:ARG:HB3	1.53	0.73
1:C:219:MET:HE3	1:C:254:LEU:HA	1.70	0.73
1:A:160:VAL:HG13	1:A:187:ILE:HB	1.69	0.73
2:D:22:PRO:HD3	2:D:80:GLN:OE1	1.89	0.73
1:A:292:GLY:O	1:A:296:ARG:HG3	1.89	0.72
1:A:50:ALA:HB3	1:A:105:ARG:HG2	1.70	0.72
1:A:153:ASP:OD2	1:A:179:PHE:HB3	1.89	0.72
1:A:29:LYS:HZ3	1:A:310:LEU:CB	2.00	0.72
1:A:153:ASP:HB3	1:A:154:ASN:ND2	2.04	0.72
2:D:76:LEU:HD12	2:D:151:LEU:HD21	1.72	0.71
1:C:301:ALA:O	1:C:305:ASN:HB2	1.90	0.71
1:A:307:ASP:OD1	1:A:308:LEU:HD22	1.89	0.71
1:A:223:ASP:O	1:A:261:MET:HA	1.91	0.71
2:D:152:ALA:CA	2:D:153:ASN:N	2.54	0.71
2:B:12:ILE:HG21	2:B:62:GLU:HB2	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:163:LEU:HG	1:A:188:ALA:HB2	1.72	0.71
1:C:184:PHE:HB2	1:C:209:TRP:HB3	1.72	0.71
2:B:28:LYS:O	2:B:32:LEU:HB2	1.90	0.71
1:C:231:GLN:O	1:C:234:ARG:HB2	1.91	0.70
1:A:285:TYR:HA	1:A:288:GLN:HE21	1.56	0.70
2:D:36:THR:HG23	5:D:160:HOH:O	1.92	0.70
2:D:52:GLU:OE1	2:D:53:MET:HG3	1.92	0.70
2:B:50:SER:OG	2:B:56:LYS:HD2	1.91	0.69
1:A:298:ALA:O	1:A:301:ALA:HB3	1.92	0.69
2:B:3:HIS:O	2:B:9:VAL:HB	1.93	0.69
2:B:22:PRO:HG3	5:B:184:HOH:O	1.91	0.69
1:A:66:LEU:HD11	1:A:297:GLN:HG2	1.74	0.69
2:B:14:ARG:HD2	2:B:63:ASN:HA	1.75	0.69
2:D:124:SER:HB3	2:D:139:LYS:HB2	1.75	0.68
2:D:104:ASP:HA	2:D:123:SER:O	1.93	0.68
2:D:50:SER:HB2	2:D:56:LYS:HG2	1.75	0.68
2:B:16:THR:HG22	2:B:64:THR:O	1.94	0.68
1:C:243:VAL:HA	1:C:246:GLN:NE2	2.08	0.68
1:C:59:PHE:O	1:C:63:MET:HG3	1.93	0.67
2:D:10:GLU:HG3	5:D:198:HOH:O	1.94	0.67
2:D:102:ARG:HD2	2:D:124:SER:OG	1.95	0.67
2:D:147:HIS:HA	2:D:150:VAL:HG23	1.75	0.67
1:C:163:LEU:HG	1:C:188:ALA:HB2	1.75	0.67
1:C:3:PRO:HG2	1:C:22:LEU:HD22	1.77	0.66
2:B:71:VAL:O	2:B:97:PRO:HB3	1.95	0.66
2:D:22:PRO:HA	2:D:53:MET:SD	2.35	0.66
2:B:147:HIS:O	2:B:151:LEU:HB2	1.95	0.66
2:D:34:LYS:HE3	2:D:34:LYS:H	1.59	0.66
1:C:1:ALA:HB2	1:C:306:ARG:NH2	2.11	0.66
2:D:34:LYS:HA	5:D:160:HOH:O	1.94	0.66
2:D:14:ARG:HA	2:D:86:ILE:O	1.96	0.65
2:B:134:ILE:H	2:B:147:HIS:CD2	2.15	0.65
2:B:104:ASP:OD1	2:B:124:SER:HB2	1.96	0.65
1:A:108:GLN:HG2	2:B:115:ILE:HA	1.79	0.65
1:A:45:ALA:HB2	1:A:99:VAL:HG11	1.79	0.65
2:B:21:ILE:O	2:B:56:LYS:HB2	1.96	0.65
2:B:20:HIS:HB3	5:B:194:HOH:O	1.97	0.64
1:A:159:MET:HE1	1:A:169:VAL:O	1.96	0.64
2:D:49:PRO:HA	2:D:54:GLY:O	1.97	0.64
1:C:52:SER:HB2	4:C:1312:PCT:O2P	1.98	0.64
2:D:56:LYS:HE3	2:D:58:LEU:HD12	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:201:MET:O	1:A:205:LYS:HB2	1.97	0.64
1:A:229:ARG:NH1	1:A:229:ARG:HB3	2.12	0.64
1:A:29:LYS:HZ3	1:A:310:LEU:HB3	1.62	0.63
2:B:9:VAL:C	2:B:10:GLU:CA	2.65	0.63
1:A:29:LYS:HZ1	1:A:310:LEU:CB	2.05	0.63
1:A:186:PHE:O	1:A:211:LEU:HD23	1.98	0.63
1:A:78:ASN:HA	1:A:83:LYS:HB3	1.81	0.63
2:B:111:ASN:HD22	2:B:114:CYS:HB2	1.62	0.62
1:A:11:SER:HB2	1:A:133:GLN:HG3	1.82	0.62
1:C:199:LEU:HD22	1:C:209:TRP:CH2	2.34	0.62
1:C:160:VAL:O	1:C:228:THR:HG23	2.00	0.62
1:C:81:LEU:HD22	1:C:86:GLU:OE1	2.00	0.62
1:A:275:THR:O	1:A:278:ASP:HB2	2.00	0.62
1:C:175:ALA:O	1:C:178:LYS:HB2	1.99	0.62
2:D:17:VAL:HG22	2:D:60:LYS:HG2	1.82	0.62
1:C:231:GLN:HB3	1:C:233:GLU:OE1	1.99	0.62
2:D:27:PHE:O	2:D:30:LEU:HD12	1.99	0.62
2:D:67:SER:HB3	2:D:70:GLN:NE2	2.15	0.62
1:A:275:THR:HG23	5:A:1419:HOH:O	1.99	0.61
2:B:18:ILE:HG22	2:B:21:ILE:HD11	1.82	0.61
2:B:65:PHE:CD2	2:B:85:ARG:HG2	2.34	0.61
1:C:125:LEU:HD23	1:C:299:LEU:HD23	1.81	0.61
2:D:147:HIS:O	2:D:151:LEU:HD12	2.00	0.61
2:B:65:PHE:HD2	2:B:85:ARG:HG2	1.65	0.61
2:B:11:ALA:O	2:B:12:ILE:O	2.18	0.61
1:A:187:ILE:HD13	1:A:214:SER:O	2.01	0.60
1:A:164:LYS:HG3	1:A:193:ALA:O	2.01	0.60
2:D:10:GLU:HG2	2:D:10:GLU:O	2.01	0.60
2:B:114:CYS:SG	2:B:116:SER:HB3	2.41	0.60
1:C:187:ILE:HG12	1:C:212:HIS:HB2	1.83	0.60
1:C:145:ILE:O	1:C:149:GLN:HB2	2.00	0.60
1:A:164:LYS:HE2	1:A:165:TYR:CZ	2.37	0.60
1:C:76:SER:HA	1:C:79:THR:OG1	2.01	0.60
2:B:9:VAL:CA	2:B:10:GLU:N	2.63	0.60
2:B:85:ARG:HH11	2:B:85:ARG:HB3	1.66	0.60
1:A:52:SER:HB2	1:A:105:ARG:NH1	2.16	0.60
2:D:70:GLN:O	2:D:73:GLN:HB2	2.00	0.60
1:C:244:LYS:HG3	1:C:245:ALA:N	2.16	0.59
1:A:108:GLN:HG3	2:B:113:ASN:O	2.02	0.59
1:C:131:SER:HB2	5:C:1333:HOH:O	2.01	0.59
2:D:102:ARG:HA	2:D:125:PHE:O	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:86:GLU:HG2	1:C:91:THR:OG1	2.03	0.59
1:C:81:LEU:HD13	1:C:91:THR:OG1	2.02	0.59
1:A:31:LYS:HE2	1:A:147:GLU:OE1	2.03	0.59
1:A:31:LYS:HE3	5:A:1367:HOH:O	2.02	0.59
1:A:59:PHE:HZ	1:A:136:THR:HG21	1.67	0.59
2:D:7:LEU:O	2:D:8:GLN:O	2.20	0.59
2:D:34:LYS:HB3	2:D:37:GLU:HG3	1.85	0.58
1:C:144:THR:O	1:C:148:THR:HG23	2.03	0.58
1:C:31:LYS:NZ	1:C:291:ASN:HD21	2.00	0.58
1:C:170:HIS:O	1:C:174:GLN:HG3	2.03	0.58
2:D:73:GLN:CG	5:D:203:HOH:O	2.52	0.58
1:A:240:TYR:O	1:A:244:LYS:HB2	2.04	0.58
1:C:81:LEU:HB2	1:C:86:GLU:CB	2.34	0.58
2:B:41:ARG:HA	2:D:46:LEU:O	2.04	0.58
1:A:249:LEU:HD12	1:A:250:ARG:H	1.68	0.57
2:B:54:GLY:O	2:B:55:ARG:HG3	2.05	0.57
2:D:72:ASP:HB3	2:D:98:SER:O	2.04	0.57
1:A:232:LYS:HG3	1:A:233:GLU:N	2.19	0.57
1:C:287:GLN:HG3	5:C:1421:HOH:O	2.03	0.57
2:B:143:LYS:HE2	5:B:168:HOH:O	2.03	0.57
2:D:85:ARG:HH11	2:D:85:ARG:HG2	1.68	0.57
2:D:34:LYS:HE3	2:D:34:LYS:N	2.20	0.57
2:B:105:ASN:CA	2:B:106:VAL:N	2.66	0.56
2:B:43:THR:HB	2:B:60:LYS:HB2	1.86	0.56
2:B:55:ARG:HH21	2:B:55:ARG:HB2	1.70	0.56
2:B:27:PHE:HE1	2:D:30:LEU:HD13	1.70	0.56
1:C:189:PRO:HG2	1:C:192:LEU:HB2	1.88	0.56
2:B:66:LEU:HD11	2:B:70:GLN:HB2	1.86	0.56
2:B:102:ARG:HH11	2:B:102:ARG:HB2	1.70	0.56
1:A:66:LEU:CD1	1:A:297:GLN:HG2	2.34	0.56
2:B:66:LEU:HD13	2:B:70:GLN:HG3	1.87	0.56
2:B:107:LEU:CD1	2:B:136:LEU:HD13	2.34	0.56
1:A:58:SER:OG	1:A:296:ARG:HD2	2.06	0.56
1:C:261:MET:HG3	5:C:1321:HOH:O	2.05	0.56
2:B:50:SER:CB	2:B:56:LYS:HD2	2.36	0.56
2:B:52:GLU:HG2	2:B:53:MET:HG2	1.88	0.56
1:C:201:MET:O	1:C:201:MET:HG2	2.06	0.56
2:D:26:GLY:HA3	2:D:57:ASP:OD1	2.05	0.55
1:C:81:LEU:HB2	1:C:86:GLU:HB3	1.86	0.55
1:A:8:HIS:CE1	1:A:123:PRO:HA	2.41	0.55
2:B:14:ARG:HA	2:B:86:ILE:O	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:82:GLY:N	5:A:1423:HOH:O	2.36	0.55
2:D:78:ALA:HB1	2:D:81:ALA:HB2	1.88	0.55
2:B:86:ILE:HD11	2:B:91:VAL:HG13	1.88	0.55
1:C:226:TYR:OH	1:C:266:PRO:HG3	2.07	0.55
2:B:138:CYS:HB3	2:B:141:CYS:SG	2.46	0.55
1:C:156:HIS:HD2	1:C:183:ARG:HB2	1.72	0.54
2:D:71:VAL:HG13	2:D:83:VAL:HG21	1.89	0.54
2:D:146:SER:HB3	2:D:149:VAL:CG2	2.35	0.54
2:B:14:ARG:HG3	2:B:63:ASN:ND2	2.23	0.54
1:C:143:PHE:O	1:C:147:GLU:HB3	2.08	0.54
1:C:258:LYS:O	1:C:282:HIS:HE1	1.90	0.54
1:A:23:VAL:HG11	1:A:139:LEU:HD13	1.89	0.54
2:D:12:ILE:N	5:D:198:HOH:O	2.39	0.54
1:A:121:ASN:HA	5:A:1329:HOH:O	2.07	0.54
2:B:78:ALA:HB1	2:B:81:ALA:HB2	1.89	0.54
1:A:29:LYS:NZ	1:A:310:LEU:HB3	2.17	0.54
1:A:16:SER:O	1:A:20:LEU:HG	2.08	0.54
1:A:261:MET:CE	1:A:282:HIS:HB3	2.38	0.54
1:A:184:PHE:HE1	1:A:207:ILE:HG21	1.72	0.54
2:D:14:ARG:HG2	2:D:15:GLY:N	2.23	0.54
2:D:50:SER:O	2:D:54:GLY:HA2	2.08	0.53
1:C:219:MET:HE3	1:C:254:LEU:HD23	1.90	0.53
1:A:199:LEU:HG	1:A:209:TRP:CH2	2.42	0.53
2:B:9:VAL:CG1	2:B:10:GLU:HG2	2.38	0.53
1:A:160:VAL:HG12	1:A:187:ILE:O	2.08	0.53
2:D:14:ARG:HD3	2:D:63:ASN:HA	1.91	0.53
1:A:48:PHE:CD1	1:A:56:ARG:HG3	2.43	0.53
2:B:12:ILE:CG2	2:B:62:GLU:OE2	2.53	0.53
1:A:8:HIS:O	1:A:9:ILE:HD13	2.09	0.53
1:A:114:LEU:HD12	2:B:121:VAL:HG21	1.89	0.53
1:A:52:SER:HB2	1:A:105:ARG:HH11	1.74	0.53
2:D:73:GLN:HG3	5:D:203:HOH:O	2.07	0.53
1:A:15:LEU:O	1:A:178:LYS:HE2	2.08	0.53
2:D:116:SER:HA	2:D:121:VAL:HG21	1.89	0.53
1:A:81:LEU:HG	1:A:86:GLU:HB3	1.91	0.53
2:D:67:SER:O	2:D:70:GLN:HB2	2.08	0.53
2:B:76:LEU:HD21	2:B:134:ILE:HD12	1.90	0.53
2:D:27:PHE:HA	2:D:30:LEU:HD11	1.89	0.53
2:D:79:PRO:HD2	5:D:195:HOH:O	2.08	0.53
1:A:269:ARG:HA	1:A:272:GLU:OE1	2.09	0.53
1:A:16:SER:HB3	5:A:1328:HOH:O	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:269:ARG:HH21	1:C:273:ILE:HG22	1.73	0.53
1:C:277:VAL:O	1:C:280:THR:HG23	2.08	0.53
1:C:184:PHE:O	1:C:209:TRP:HA	2.09	0.52
1:A:80:SER:C	1:A:81:LEU:HD12	2.30	0.52
2:D:137:LYS:HB2	2:D:144:GLU:OE2	2.09	0.52
1:A:262:LYS:HD2	1:A:284:TRP:CG	2.43	0.52
1:A:54:ARG:HD2	4:A:1311:PCT:H1P2	1.90	0.52
1:A:141:ASP:O	1:A:145:ILE:HG13	2.09	0.52
1:C:216:GLU:HG2	1:C:217:GLU:N	2.23	0.52
1:C:209:TRP:HZ3	1:C:211:LEU:HD21	1.74	0.52
1:C:194:MET:CE	1:C:198:ILE:HG21	2.37	0.52
1:A:12:ILE:HA	1:A:15:LEU:HD12	1.90	0.52
1:C:156:HIS:CD2	1:C:183:ARG:HB2	2.45	0.52
1:A:81:LEU:HA	1:A:86:GLU:HB3	1.92	0.52
2:B:17:VAL:HG12	2:B:17:VAL:O	2.09	0.52
1:C:59:PHE:O	1:C:62:SER:HB2	2.10	0.52
1:C:52:SER:CB	4:C:1312:PCT:O2P	2.57	0.52
2:D:96:ARG:CD	2:D:97:PRO:HD2	2.39	0.52
1:A:45:ALA:HA	1:A:71:VAL:O	2.08	0.52
2:B:130:ARG:HD2	5:B:179:HOH:O	2.08	0.52
1:A:5:TYR:O	1:A:6:GLN:HB2	2.10	0.52
1:A:91:THR:O	1:A:95:ILE:HG12	2.09	0.52
2:B:52:GLU:CG	2:B:53:MET:HG2	2.40	0.52
1:A:232:LYS:HB2	1:A:240:TYR:CD1	2.45	0.52
1:A:2:ASN:ND2	1:A:5:TYR:HB2	2.25	0.51
2:D:107:LEU:HD12	2:D:125:PHE:CD1	2.45	0.51
1:C:219:MET:CE	1:C:254:LEU:HD23	2.40	0.51
1:A:43:VAL:O	1:A:99:VAL:HB	2.10	0.51
1:A:162:ASP:OD2	1:A:165:TYR:HB2	2.10	0.51
2:B:7:LEU:HD12	2:D:10:GLU:HB2	1.93	0.51
2:D:40:GLN:HG2	2:D:62:GLU:O	2.10	0.51
1:C:118:PHE:HA	5:C:1434:HOH:O	2.10	0.51
2:D:48:LEU:O	2:D:54:GLY:O	2.29	0.51
1:C:1:ALA:HB2	1:C:306:ARG:CZ	2.40	0.51
1:A:83:LYS:C	1:A:83:LYS:HE2	2.31	0.51
1:C:230:VAL:O	1:C:240:TYR:HE2	1.92	0.51
2:B:52:GLU:OE2	2:B:53:MET:HE1	2.11	0.51
1:A:239:GLU:O	1:A:242:ASN:HB2	2.10	0.51
1:C:205:LYS:HB3	1:C:207:ILE:CD1	2.39	0.50
1:A:261:MET:HE2	1:A:282:HIS:HB3	1.92	0.50
1:C:174:GLN:O	1:C:177:ALA:HB3	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:239:GLU:O	1:C:243:VAL:HG22	2.10	0.50
1:A:262:LYS:HD2	1:A:284:TRP:CD2	2.46	0.50
2:B:110:PRO:HD2	2:B:145:PHE:CE1	2.46	0.50
1:A:83:LYS:HE2	1:A:83:LYS:O	2.10	0.50
1:C:31:LYS:HD2	1:C:294:PHE:CE2	2.47	0.50
1:A:308:LEU:H	1:A:308:LEU:HD13	1.77	0.50
1:C:269:ARG:NH2	1:C:273:ILE:HG22	2.27	0.50
2:D:99:LEU:HD21	2:D:134:ILE:HG21	1.91	0.50
1:A:309:VAL:HG12	1:A:309:VAL:O	2.12	0.50
2:B:20:HIS:HA	2:B:56:LYS:HG3	1.93	0.50
1:A:191:ALA:O	1:A:192:LEU:HD23	2.11	0.50
1:C:218:VAL:O	1:C:222:VAL:HG13	2.12	0.50
2:D:53:MET:HE1	2:D:80:GLN:HE22	1.77	0.50
2:D:20:HIS:O	2:D:80:GLN:OE1	2.30	0.50
1:A:81:LEU:HD21	1:A:86:GLU:OE2	2.11	0.50
2:B:8:GLN:C	2:B:9:VAL:HG23	2.33	0.49
1:A:149:GLN:HE22	1:A:224:ILE:CD1	2.25	0.49
1:A:149:GLN:NE2	1:A:224:ILE:HG12	2.27	0.49
2:B:12:ILE:CG2	2:B:62:GLU:HB2	2.42	0.49
2:D:76:LEU:CD1	2:D:151:LEU:HD11	2.43	0.49
2:B:111:ASN:ND2	2:B:114:CYS:HB2	2.26	0.49
2:B:9:VAL:HG13	2:B:10:GLU:HG2	1.94	0.49
2:B:88:ASN:O	2:B:89:TYR:HB2	2.11	0.49
1:A:183:ARG:HH12	1:A:210:SER:CB	2.23	0.49
2:B:19:ASP:O	2:B:20:HIS:HB2	2.12	0.49
1:A:187:ILE:HD13	1:A:215:ILE:HA	1.94	0.49
1:C:239:GLU:HG2	1:C:239:GLU:O	2.13	0.49
2:D:99:LEU:HD11	2:D:134:ILE:HD12	1.95	0.49
1:C:126:ASN:HD21	1:C:129:ASP:CG	2.16	0.49
1:A:29:LYS:HZ3	1:A:310:LEU:HB2	1.62	0.49
1:A:249:LEU:HD12	1:A:250:ARG:N	2.28	0.49
2:B:86:ILE:CD1	2:B:91:VAL:HA	2.43	0.49
1:A:232:LYS:HB2	1:A:240:TYR:CG	2.48	0.48
1:C:24:LEU:CD2	1:C:143:PHE:HB2	2.41	0.48
2:D:12:ILE:HG21	2:D:62:GLU:HG3	1.95	0.48
1:C:270:VAL:HG13	1:C:271:ASP:H	1.78	0.48
1:C:40:LYS:O	1:C:41:HIS:HB2	2.13	0.48
1:C:160:VAL:HG22	1:C:187:ILE:HB	1.95	0.48
1:C:262:LYS:HE3	1:C:284:TRP:CE3	2.48	0.48
1:A:215:ILE:HD12	5:A:1369:HOH:O	2.13	0.48
1:A:81:LEU:HG	1:A:86:GLU:CB	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:186:PHE:HB2	1:A:211:LEU:CD2	2.43	0.48
2:D:53:MET:CE	2:D:80:GLN:HE22	2.27	0.48
1:C:232:LYS:HA	1:C:240:TYR:CD2	2.49	0.48
1:C:75:ASP:O	1:C:77:ALA:N	2.45	0.48
1:A:212:HIS:CD2	1:A:218:VAL:HB	2.48	0.48
2:B:107:LEU:HD22	2:B:150:VAL:CG1	2.38	0.48
1:A:81:LEU:HD23	1:A:86:GLU:HG2	1.95	0.48
2:D:67:SER:HB3	2:D:70:GLN:HE22	1.78	0.48
1:C:8:HIS:CE1	1:C:123:PRO:HA	2.48	0.48
2:B:94:LYS:HG2	2:B:94:LYS:O	2.13	0.48
1:A:80:SER:O	1:A:81:LEU:HD12	2.14	0.47
1:A:24:LEU:HD23	1:A:143:PHE:HA	1.96	0.47
1:C:235:LEU:HB2	1:C:239:GLU:OE2	2.14	0.47
2:B:50:SER:HB2	2:B:56:LYS:H	1.79	0.47
1:A:236:ASP:HB3	1:A:239:GLU:H	1.79	0.47
2:D:107:LEU:HD11	2:D:136:LEU:HD13	1.96	0.47
1:A:187:ILE:O	1:A:187:ILE:HG22	2.13	0.47
1:A:201:MET:HG2	1:A:202:LEU:N	2.29	0.47
2:D:17:VAL:HG22	2:D:60:LYS:CG	2.43	0.47
2:D:19:ASP:HB3	2:D:82:THR:HB	1.96	0.47
2:B:7:LEU:CD1	2:D:10:GLU:HB2	2.43	0.47
1:C:265:HIS:HA	1:C:266:PRO:HD3	1.73	0.47
1:A:10:ILE:HA	1:A:126:ASN:HB2	1.95	0.47
2:D:107:LEU:HB3	2:D:125:PHE:CE1	2.49	0.47
2:B:108:VAL:O	2:B:110:PRO:HD3	2.14	0.47
1:A:59:PHE:CZ	1:A:136:THR:HG21	2.48	0.47
2:B:98:SER:HA	5:B:181:HOH:O	2.13	0.47
2:B:70:GLN:HA	2:B:73:GLN:HG2	1.96	0.47
1:A:285:TYR:HA	1:A:288:GLN:NE2	2.26	0.47
2:D:48:LEU:O	2:D:55:ARG:HA	2.15	0.47
2:B:109:CYS:SG	2:B:111:ASN:HB3	2.55	0.47
1:A:31:LYS:HD2	1:A:294:PHE:CE2	2.50	0.47
1:A:157:VAL:HG13	1:A:224:ILE:HB	1.95	0.47
2:B:29:LEU:HD21	2:B:77:TYR:HB2	1.96	0.47
2:B:8:GLN:C	2:B:9:VAL:CG2	2.81	0.47
1:A:214:SER:O	1:A:217:GLU:HB3	2.15	0.47
1:A:146:GLN:HG3	1:A:147:GLU:N	2.30	0.47
2:B:30:LEU:HD23	2:B:35:LEU:CD1	2.45	0.46
2:B:46:LEU:HD12	2:D:44:ILE:HD11	1.96	0.46
2:B:80:GLN:OE1	2:B:80:GLN:HA	2.15	0.46
2:D:35:LEU:O	2:D:38:THR:HG22	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:234:ARG:HG3	1:C:234:ARG:HH21	1.79	0.46
1:C:106:HIS:CG	1:C:107:PRO:HD2	2.50	0.46
1:A:137:GLN:O	1:A:140:LEU:HG	2.16	0.46
1:C:305:ASN:HB3	1:C:308:LEU:HD22	1.97	0.46
2:B:138:CYS:O	2:B:142:GLU:HA	2.14	0.46
2:D:129:LYS:HE2	2:D:134:ILE:HD13	1.96	0.46
1:A:215:ILE:HD11	1:A:247:PHE:HA	1.97	0.46
1:A:186:PHE:HB2	1:A:211:LEU:HD23	1.98	0.46
2:B:49:PRO:HA	2:B:55:ARG:HG2	1.98	0.46
2:B:139:LYS:HD3	2:B:140:TYR:CZ	2.51	0.46
1:A:184:PHE:CE1	1:A:207:ILE:HG21	2.51	0.46
2:D:99:LEU:CD1	2:D:134:ILE:HD12	2.46	0.46
1:C:81:LEU:HD11	1:C:91:THR:HG21	1.98	0.46
2:B:102:ARG:HB2	2:B:102:ARG:NH1	2.29	0.46
1:A:185:TYR:CG	1:A:218:VAL:HG21	2.50	0.45
2:D:52:GLU:HG3	2:D:53:MET:N	2.30	0.45
2:B:68:GLU:HA	2:B:68:GLU:OE2	2.16	0.45
1:C:31:LYS:HZ3	1:C:291:ASN:HD21	1.62	0.45
2:B:125:PHE:HB3	2:B:136:LEU:HB3	1.98	0.45
1:A:183:ARG:HG2	1:A:183:ARG:HH21	1.81	0.45
1:A:269:ARG:NH1	1:A:278:ASP:OD2	2.49	0.45
1:C:219:MET:CE	1:C:254:LEU:HA	2.44	0.45
2:D:79:PRO:HG3	5:D:181:HOH:O	2.15	0.45
1:A:267:LEU:HB3	1:A:268:PRO:HA	1.97	0.45
1:A:44:ILE:HD12	1:A:63:MET:HG2	1.98	0.45
1:A:212:HIS:CD2	1:A:217:GLU:HG2	2.52	0.45
2:B:11:ALA:O	2:B:12:ILE:C	2.51	0.45
2:B:19:ASP:OD1	2:B:56:LYS:NZ	2.50	0.45
2:B:82:THR:OG1	2:B:96:ARG:NH1	2.50	0.45
1:A:307:ASP:OD1	1:A:308:LEU:N	2.50	0.45
2:B:39:ASP:OD1	2:B:39:ASP:N	2.50	0.45
1:C:130:GLY:O	1:C:167:ARG:NH2	2.50	0.45
1:C:45:ALA:HA	1:C:71:VAL:O	2.17	0.45
1:A:190:ASP:OD1	1:A:191:ALA:N	2.50	0.44
1:A:308:LEU:HD13	1:A:308:LEU:N	2.32	0.44
1:A:252:SER:O	1:A:255:HIS:ND1	2.50	0.44
1:C:54:ARG:HD2	4:C:1312:PCT:H1P2	2.00	0.44
2:D:71:VAL:HG13	2:D:83:VAL:CG2	2.47	0.44
2:D:83:VAL:HB	2:D:95:SER:HB3	1.98	0.44
1:A:92:ILE:HG22	1:A:93:SER:N	2.32	0.44
2:B:39:ASP:O	2:D:55:ARG:HD3	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:261:MET:HE3	1:C:261:MET:HB3	1.88	0.44
1:A:40:LYS:O	1:A:41:HIS:HB2	2.18	0.44
1:C:180:ASP:OD1	1:C:180:ASP:N	2.50	0.44
2:D:76:LEU:HD13	2:D:151:LEU:HD11	1.98	0.44
1:C:31:LYS:HD2	1:C:294:PHE:CD2	2.53	0.44
2:D:29:LEU:N	2:D:29:LEU:HD23	2.32	0.44
1:C:94:VAL:O	1:C:97:THR:HG23	2.18	0.44
2:B:19:ASP:OD1	2:B:20:HIS:N	2.49	0.44
2:B:86:ILE:CD1	2:B:91:VAL:HG13	2.47	0.44
1:A:153:ASP:OD2	1:A:180:ASP:N	2.50	0.44
1:C:256:ASN:OD1	1:C:256:ASN:N	2.50	0.44
1:A:182:ASN:O	1:A:207:ILE:HG23	2.18	0.44
2:D:48:LEU:HB2	2:D:56:LYS:HG3	1.99	0.44
2:B:40:GLN:HB3	2:B:40:GLN:HE21	1.61	0.44
1:A:130:GLY:O	1:A:167:ARG:NH2	2.50	0.44
1:A:25:ALA:HA	5:A:1396:HOH:O	2.18	0.44
1:A:232:LYS:O	1:A:235:LEU:O	2.36	0.44
1:A:202:LEU:HD23	1:A:202:LEU:N	2.32	0.44
1:A:136:THR:HG22	1:A:299:LEU:HD12	2.00	0.43
2:D:17:VAL:CG2	2:D:86:ILE:HD12	2.48	0.43
1:C:302:LEU:HD23	1:C:308:LEU:HD23	2.00	0.43
1:C:234:ARG:HG3	1:C:234:ARG:NH2	2.32	0.43
1:A:48:PHE:CE1	1:A:56:ARG:HG3	2.54	0.43
2:B:58:LEU:HG	2:B:59:ILE:N	2.29	0.43
2:D:92:VAL:HG13	2:D:92:VAL:O	2.17	0.43
1:C:137:GLN:NE2	1:C:140:LEU:HD22	2.33	0.43
1:C:3:PRO:HD2	1:C:22:LEU:HD22	2.00	0.43
2:B:80:GLN:O	2:B:96:ARG:NH1	2.50	0.43
2:B:99:LEU:CD1	2:B:100:PRO:HD2	2.41	0.43
1:A:222:VAL:HG23	1:A:261:MET:HG3	2.00	0.43
2:B:5:ASN:HB2	5:B:202:HOH:O	2.18	0.43
2:B:147:HIS:O	2:B:151:LEU:HD23	2.18	0.43
2:B:55:ARG:HB2	2:B:55:ARG:NH2	2.33	0.43
2:B:67:SER:OG	2:B:70:GLN:HG2	2.19	0.43
1:A:265:HIS:N	1:A:288:GLN:HE22	2.07	0.43
1:A:36:PRO:HA	1:A:66:LEU:HA	2.00	0.43
2:D:27:PHE:O	2:D:31:SER:OG	2.30	0.43
2:B:70:GLN:O	2:B:73:GLN:HB2	2.19	0.43
1:A:26:THR:HB	1:A:298:ALA:HB1	2.00	0.43
2:D:99:LEU:HD21	2:D:134:ILE:CG2	2.48	0.43
1:A:277:VAL:O	1:A:283:ALA:HB2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2:ASN:ND2	1:A:302:LEU:O	2.50	0.43
1:C:41:HIS:HD2	5:C:1427:HOH:O	2.00	0.43
2:D:20:HIS:HD2	2:D:82:THR:OG1	2.01	0.43
1:A:52:SER:OG	1:A:55:THR:HB	2.18	0.43
2:D:96:ARG:HA	2:D:96:ARG:HD3	1.83	0.43
2:D:136:LEU:HD12	2:D:150:VAL:CG2	2.40	0.42
1:A:229:ARG:HG3	1:A:272:GLU:OE1	2.19	0.42
1:C:262:LYS:HE3	1:C:284:TRP:CZ3	2.55	0.42
1:A:3:PRO:HG2	1:A:22:LEU:HD22	2.00	0.42
2:D:119:GLU:HB3	2:D:120:PRO:HD2	2.01	0.42
2:B:18:ILE:CG2	2:B:21:ILE:HD11	2.48	0.42
2:D:58:LEU:HD21	2:D:60:LYS:NZ	2.33	0.42
1:C:8:HIS:ND1	1:C:123:PRO:HA	2.33	0.42
1:A:159:MET:HE1	1:A:169:VAL:HA	2.00	0.42
2:D:65:PHE:CD2	2:D:85:ARG:HD3	2.54	0.42
1:C:35:GLN:HB3	1:C:38:LEU:HB2	2.02	0.42
2:B:108:VAL:N	5:B:159:HOH:O	2.50	0.42
1:C:174:GLN:HG2	1:C:201:MET:CE	2.50	0.42
1:A:199:LEU:HA	1:A:199:LEU:HD12	1.83	0.42
1:C:2:ASN:OD1	1:C:302:LEU:HB3	2.20	0.42
2:B:50:SER:O	2:B:52:GLU:N	2.49	0.42
1:A:187:ILE:CD1	1:A:215:ILE:HA	2.50	0.42
1:A:235:LEU:HD22	1:A:239:GLU:OE2	2.20	0.42
1:C:270:VAL:HG13	1:C:271:ASP:N	2.34	0.42
2:B:49:PRO:HA	2:B:55:ARG:CG	2.49	0.42
1:A:159:MET:CE	1:A:172:LEU:HB3	2.42	0.42
1:A:202:LEU:HA	1:A:207:ILE:HD12	2.02	0.42
1:A:223:ASP:HA	1:A:260:ASN:ND2	2.34	0.42
1:A:2:ASN:HD22	1:A:5:TYR:HB2	1.85	0.42
1:C:185:TYR:CD2	1:C:218:VAL:HG21	2.55	0.42
2:B:126:ALA:HB2	5:B:156:HOH:O	2.19	0.42
2:B:1:MET:SD	2:B:17:VAL:HG11	2.60	0.42
1:A:187:ILE:HD11	1:A:218:VAL:CG1	2.50	0.42
2:B:76:LEU:HD23	2:B:76:LEU:HA	1.61	0.42
1:C:174:GLN:HG2	1:C:201:MET:HE3	2.02	0.42
1:A:276:ASP:HA	1:A:279:LYS:HE3	2.02	0.42
2:D:22:PRO:HD3	2:D:80:GLN:CD	2.40	0.41
2:D:99:LEU:HG	2:D:127:VAL:HG11	2.01	0.41
1:A:270:VAL:HG12	1:A:271:ASP:CG	2.40	0.41
1:A:195:PRO:HA	5:A:1354:HOH:O	2.20	0.41
2:B:110:PRO:CD	2:B:150:VAL:HG22	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:306:ARG:HG2	1:C:306:ARG:NH2	2.35	0.41
1:C:269:ARG:HH12	1:C:278:ASP:CG	2.21	0.41
2:D:146:SER:O	2:D:150:VAL:HG23	2.20	0.41
2:B:48:LEU:HB3	2:B:49:PRO:HD2	2.01	0.41
1:C:52:SER:OG	4:C:1312:PCT:O2P	2.37	0.41
2:B:22:PRO:HA	5:B:193:HOH:O	2.19	0.41
1:A:270:VAL:HG12	1:A:271:ASP:N	2.35	0.41
2:D:66:LEU:O	2:D:85:ARG:NH2	2.50	0.41
2:D:85:ARG:O	2:D:86:ILE:HG13	2.20	0.41
1:A:101:ALA:HA	1:A:122:VAL:HG13	2.02	0.41
1:A:138:THR:HA	1:A:141:ASP:OD2	2.21	0.41
2:B:5:ASN:O	2:B:6:LYS:HB2	2.20	0.41
2:D:2:THR:HG22	2:D:2:THR:O	2.19	0.41
1:C:162:ASP:CG	1:C:192:LEU:HD13	2.40	0.41
1:C:35:GLN:HA	5:C:1337:HOH:O	2.20	0.41
2:D:147:HIS:CA	2:D:150:VAL:HG23	2.47	0.41
2:B:50:SER:HB3	2:B:54:GLY:N	2.35	0.41
2:D:116:SER:HA	2:D:121:VAL:CG2	2.50	0.41
2:D:38:THR:HG23	2:D:42:ILE:HD11	2.03	0.41
1:A:156:HIS:HB3	1:A:222:VAL:HA	2.03	0.41
1:A:87:THR:HB	2:B:119:GLU:OE2	2.21	0.41
2:B:30:LEU:HD23	2:B:35:LEU:HD12	2.03	0.41
2:D:76:LEU:HD22	2:D:76:LEU:HA	1.84	0.41
2:B:86:ILE:HD12	2:B:91:VAL:HA	2.02	0.41
2:B:14:ARG:HG3	2:B:63:ASN:HD22	1.86	0.41
2:D:58:LEU:HD21	2:D:60:LYS:HZ3	1.85	0.41
1:A:53:THR:HG22	1:A:54:ARG:N	2.35	0.41
1:C:104:MET:O	1:C:104:MET:HG3	2.20	0.41
1:A:152:LEU:HD12	1:A:152:LEU:HA	1.80	0.41
2:D:76:LEU:CD1	2:D:151:LEU:HD21	2.46	0.41
1:A:160:VAL:HG11	1:A:215:ILE:HG12	2.03	0.41
2:D:77:TYR:O	2:D:79:PRO:HD3	2.20	0.41
1:A:44:ILE:HD13	1:A:300:LEU:HD22	2.02	0.41
2:D:143:LYS:HA	2:D:143:LYS:HD3	1.72	0.41
2:B:45:GLY:HA3	2:B:48:LEU:HD11	2.02	0.40
1:A:17:ARG:O	1:A:21:ASN:OD1	2.39	0.40
1:C:236:ASP:HB3	1:C:239:GLU:CB	2.37	0.40
1:C:199:LEU:HD22	1:C:209:TRP:CZ3	2.57	0.40
1:C:223:ASP:O	1:C:261:MET:HA	2.20	0.40
2:D:84:ASN:OD1	2:D:94:LYS:HG3	2.21	0.40
2:D:6:LYS:HD2	2:D:6:LYS:HA	1.30	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:187:ILE:HA	1:A:212:HIS:O	2.21	0.40
1:A:122:VAL:HA	1:A:123:PRO:HD3	1.84	0.40
1:A:41:HIS:HB3	5:A:1320:HOH:O	2.20	0.40
1:C:39:LEU:HD13	1:C:304:LEU:HD12	2.02	0.40
1:C:76:SER:O	1:C:76:SER:OG	2.29	0.40
1:C:251:ALA:HB2	1:C:276:ASP:OD2	2.22	0.40
1:C:42:LYS:HD3	1:C:42:LYS:HA	1.90	0.40
1:C:176:LEU:HD23	1:C:176:LEU:HA	1.76	0.40
1:A:187:ILE:HD13	1:A:214:SER:C	2.41	0.40
1:A:10:ILE:N	1:A:10:ILE:HD13	2.36	0.40
2:B:69:ASP:OD1	2:B:69:ASP:N	2.54	0.40

All (5) 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)
2:B:112:SER:OG	5:C:1441:HOH:O[2_655]	1.16	1.04
2:B:144:GLU:O	5:C:1425:HOH:O[2_655]	1.47	0.73
2:B:112:SER:N	5:C:1441:HOH:O[2_655]	1.92	0.28
2:B:112:SER:CB	5:C:1441:HOH:O[2_655]	1.95	0.25
2:B:112:SER:CA	5:C:1441:HOH:O[2_655]	2.18	0.02

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	308/310 (99%)	274 (89%)	31 (10%)	3 (1%)	19	33
1	C	308/310 (99%)	276 (90%)	24 (8%)	8 (3%)	7	9
2	B	151/153 (99%)	130 (86%)	15 (10%)	6 (4%)	4	4
2	D	151/153 (99%)	128 (85%)	19 (13%)	4 (3%)	7	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	918/926 (99%)	808 (88%)	89 (10%)	21 (2%)	8	11

All (21) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	79	THR
2	B	6	LYS
2	B	13	LYS
1	C	75	ASP
1	C	270	VAL
2	D	8	GLN
2	D	12	ILE
2	B	105	ASN
1	C	231	GLN
1	C	258	LYS
1	A	219	MET
2	B	12	ILE
1	C	132	ASN
2	D	132	ASN
1	A	244	LYS
1	C	244	LYS
2	B	51	GLY
1	C	84	LYS
1	C	309	VAL
2	D	29	LEU
2	B	9	VAL

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	260/260 (100%)	204 (78%)	56 (22%)	1	2
1	C	260/260 (100%)	206 (79%)	54 (21%)	1	2
2	B	137/137 (100%)	97 (71%)	40 (29%)	0	0
2	D	137/137 (100%)	101 (74%)	36 (26%)	0	1

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	794/794 (100%)	608 (77%)	186 (23%)	1 1

All (186) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	ASN
1	A	11	SER
1	A	16	SER
1	A	17	ARG
1	A	37	GLU
1	A	40	LYS
1	A	54	ARG
1	A	59	PHE
1	A	69	SER
1	A	83	LYS
1	A	84	LYS
1	A	86	GLU
1	A	92	ILE
1	A	94	VAL
1	A	108	GLN
1	A	109	GLU
1	A	113	ARG
1	A	121	ASN
1	A	126	ASN
1	A	146	GLN
1	A	149	GLN
1	A	151	ARG
1	A	152	LEU
1	A	157	VAL
1	A	160	VAL
1	A	164	LYS
1	A	169	VAL
1	A	171	SER
1	A	174	GLN
1	A	183	ARG
1	A	199	LEU
1	A	201	MET
1	A	205	LYS
1	A	212	HIS
1	A	213	SER
1	A	216	GLU
1	A	229	ARG

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Mol	Chain	Res	Type
1	A	231	GLN
1	A	232	LYS
1	A	233	GLU
1	A	238	SER
1	A	243	VAL
1	A	246	GLN
1	A	252	SER
1	A	254	LEU
1	A	256	ASN
1	A	261	MET
1	A	264	LEU
1	A	269	ARG
1	A	275	THR
1	A	279	LYS
1	A	285	TYR
1	A	297	GLN
1	A	299	LEU
1	A	308	LEU
1	A	310	LEU
2	B	1	MET
2	B	2	THR
2	B	5	ASN
2	B	6	LYS
2	B	7	LEU
2	B	10	GLU
2	B	12	ILE
2	B	14	ARG
2	B	16	THR
2	B	31	SER
2	B	32	LEU
2	B	34	LYS
2	B	35	LEU
2	B	36	THR
2	B	40	GLN
2	B	41	ARG
2	B	50	SER
2	B	52	GLU
2	B	53	MET
2	B	55	ARG
2	B	56	LYS
2	B	58	LEU
2	B	63	ASN

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Mol	Chain	Res	Type
2	B	66	LEU
2	B	69	ASP
2	B	70	GLN
2	B	74	LEU
2	B	85	ARG
2	B	91	VAL
2	B	92	VAL
2	B	94	LYS
2	B	96	ARG
2	B	103	ILE
2	B	121	VAL
2	B	130	ARG
2	B	136	LEU
2	B	137	LYS
2	B	139	LYS
2	B	146	SER
2	B	151	LEU
1	C	2	ASN
1	C	6	GLN
1	C	7	LYS
1	C	9	ILE
1	C	44	ILE
1	C	53	THR
1	C	59	PHE
1	C	69	SER
1	C	74	SER
1	C	75	ASP
1	C	76	SER
1	C	80	SER
1	C	83	LYS
1	C	84	LYS
1	C	87	THR
1	C	92	ILE
1	C	98	TYR
1	C	108	GLN
1	C	121	ASN
1	C	134	HIS
1	C	147	GLU
1	C	149	GLN
1	C	159	MET
1	C	171	SER
1	C	180	ASP

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Mol	Chain	Res	Type
1	C	183	ARG
1	C	190	ASP
1	C	194	MET
1	C	201	MET
1	C	205	LYS
1	C	211	LEU
1	C	214	SER
1	C	216	GLU
1	C	228	THR
1	C	231	GLN
1	C	232	LYS
1	C	234	ARG
1	C	235	LEU
1	C	239	GLU
1	C	243	VAL
1	C	244	LYS
1	C	256	ASN
1	C	262	LYS
1	C	264	LEU
1	C	267	LEU
1	C	271	ASP
1	C	276	ASP
1	C	280	THR
1	C	284	TRP
1	C	285	TYR
1	C	306	ARG
1	C	307	ASP
1	C	308	LEU
1	C	310	LEU
2	D	2	THR
2	D	6	LYS
2	D	9	VAL
2	D	10	GLU
2	D	12	ILE
2	D	14	ARG
2	D	30	LEU
2	D	31	SER
2	D	34	LYS
2	D	36	THR
2	D	40	GLN
2	D	48	LEU
2	D	52	GLU

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Mol	Chain	Res	Type
2	D	55	ARG
2	D	56	LYS
2	D	60	LYS
2	D	62	GLU
2	D	64	THR
2	D	67	SER
2	D	68	GLU
2	D	69	ASP
2	D	70	GLN
2	D	74	LEU
2	D	76	LEU
2	D	80	GLN
2	D	91	VAL
2	D	92	VAL
2	D	95	SER
2	D	98	SER
2	D	101	GLU
2	D	102	ARG
2	D	107	LEU
2	D	122	SER
2	D	128	ARG
2	D	134	ILE
2	D	150	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	35	GLN
1	A	64	HIS
1	A	126	ASN
1	A	132	ASN
1	A	134	HIS
1	A	149	GLN
1	A	154	ASN
1	A	212	HIS
1	A	288	GLN
1	A	305	ASN
2	B	40	GLN
2	B	63	ASN
2	B	70	GLN
2	B	84	ASN
2	B	111	ASN

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Mol	Chain	Res	Type
2	B	132	ASN
2	B	147	HIS
1	C	21	ASN
1	C	64	HIS
1	C	108	GLN
1	C	154	ASN
1	C	156	HIS
1	C	246	GLN
1	C	291	ASN
2	D	20	HIS
2	D	40	GLN
2	D	63	ASN
2	D	80	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	$\# Z > 2$
4	PCT	A	1311	-	7,7,7	2.96	4 (57%)	9,10,10	1.50	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	PCT	C	1312	-	7,7,7	2.98	4 (57%)	9,10,10	1.44	1 (11%)

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	PCT	A	1311	-	-	0/4/5/5	0/0/0/0
4	PCT	C	1312	-	-	0/4/5/5	0/0/0/0

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	1312	PCT	P-O2P	2.37	1.60	1.54
4	A	1311	PCT	P-O2P	2.38	1.60	1.54
4	A	1311	PCT	P-O3P	3.20	1.62	1.54
4	C	1312	PCT	P-O3P	3.21	1.62	1.54
4	A	1311	PCT	P-O1P	4.69	1.60	1.50
4	C	1312	PCT	P-O1P	4.73	1.61	1.50
4	A	1311	PCT	P-C1P	4.74	1.86	1.79
4	C	1312	PCT	P-C1P	4.78	1.86	1.79

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	1312	PCT	O1-C1-C1P	2.61	122.92	119.90

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1311	PCT	1	0
4	C	1312	PCT	6	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	310/310 (100%)	-0.22	13 (4%)	40 46	3, 27, 104, 158	0
1	C	310/310 (100%)	-0.38	11 (3%)	48 54	2, 20, 95, 158	0
2	B	153/153 (100%)	0.28	13 (8%)	13 15	11, 49, 158, 158	1 (0%)
2	D	153/153 (100%)	0.49	13 (8%)	13 15	10, 55, 158, 158	3 (1%)
All	All	926/926 (100%)	-0.07	50 (5%)	29 34	2, 35, 141, 158	4 (0%)

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	2	THR	9.0
2	B	1	MET	8.0
2	B	9	VAL	7.7
2	D	5	ASN	7.4
1	A	79	THR	7.2
2	D	3	HIS	6.9
1	A	81	LEU	6.2
2	D	153	ASN	5.7
1	C	83	LYS	5.6
2	D	6	LYS	5.5
1	A	82	GLY	5.4
2	D	1	MET	5.3
1	C	77	ALA	5.1
2	D	8	GLN	5.0
1	C	84	LYS	4.8
2	B	10	GLU	4.5
2	D	7	LEU	4.4
2	B	3	HIS	4.2
2	B	2	THR	4.2
2	B	7	LEU	3.9
1	A	215	ILE	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	77	ALA	3.8
2	D	53	MET	3.8
2	B	8	GLN	3.7
2	B	153	ASN	3.6
1	C	80	SER	3.5
1	C	81	LEU	3.5
2	D	134	ILE	3.4
2	D	4	ASP	3.3
1	C	82	GLY	3.2
2	D	9	VAL	3.2
1	A	80	SER	3.2
1	C	78	ASN	3.1
1	A	83	LYS	3.1
1	A	84	LYS	3.1
2	B	12	ILE	3.0
1	C	76	SER	3.0
2	B	4	ASP	2.9
2	B	5	ASN	2.8
1	C	85	GLY	2.8
1	C	75	ASP	2.6
1	A	75	ASP	2.5
1	A	218	VAL	2.4
1	C	79	THR	2.4
2	B	6	LYS	2.4
1	A	310	LEU	2.2
1	A	74	SER	2.1
2	D	10	GLU	2.1
1	A	76	SER	2.1
2	B	129	LYS	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 [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	PCT	C	1312	8/8	0.89	0.20	0.67	54,64,75,87	0
4	PCT	A	1311	8/8	0.90	0.25	0.65	24,54,73,78	0
3	ZN	D	155	1/1	0.99	0.05	-2.14	18,18,18,18	0
3	ZN	B	154	1/1	0.99	0.04	-2.25	19,19,19,19	0

6.5 Other polymers [i](#)

There are no such residues in this entry.