



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:09 PM GMT

PDB ID : 1J1J
Title : Crystal Structure of human Translin
Authors : Sugiura, I.; Sasaki, C.; Hasegawa, T.; Kohno, T.; Sugio, S.; Moriyama, H.; Kasai, M.; Matsuzaki, T.
Deposited on : 2002-12-06
Resolution : 2.20 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

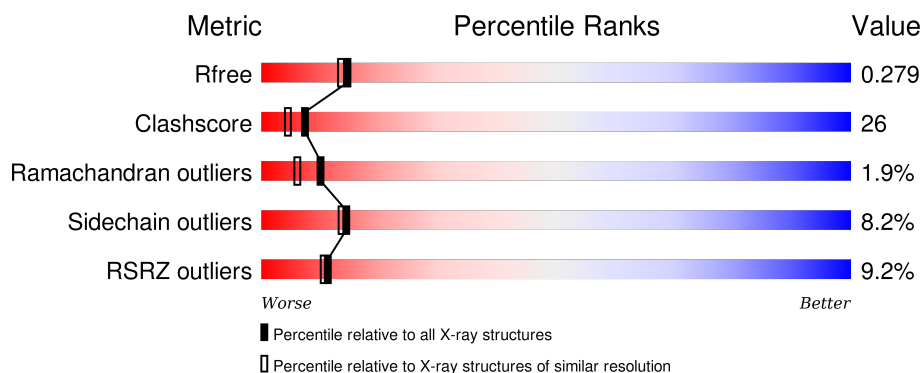
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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	240	<div> <div>7%</div> <div> <div></div> <div>59%</div> <div>27%</div> <div>•</div> <div>10%</div> </div> </div>
1	B	240	<div> <div>10%</div> <div> <div></div> <div>53%</div> <div>33%</div> <div>5%</div> <div>10%</div> </div> </div>
1	C	240	<div> <div>11%</div> <div> <div></div> <div>50%</div> <div>36%</div> <div>•</div> <div>10%</div> </div> </div>
1	D	240	<div> <div>5%</div> <div> <div></div> <div>54%</div> <div>32%</div> <div>•</div> <div>10%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7494 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 Translin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	217	Total	C	N	O	S	0	0	0
			1770	1135	305	328	2			
1	B	217	Total	C	N	O	S	0	0	0
			1770	1135	305	328	2			
1	C	217	Total	C	N	O	S	0	0	0
			1770	1135	305	328	2			
1	D	217	Total	C	N	O	S	0	0	0
			1770	1135	305	328	2			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	EXPRESSION TAG	UNP Q15631
A	-10	ARG	-	EXPRESSION TAG	UNP Q15631
A	-9	GLY	-	EXPRESSION TAG	UNP Q15631
A	-8	SER	-	EXPRESSION TAG	UNP Q15631
A	-7	HIS	-	EXPRESSION TAG	UNP Q15631
A	-6	HIS	-	EXPRESSION TAG	UNP Q15631
A	-5	HIS	-	EXPRESSION TAG	UNP Q15631
A	-4	HIS	-	EXPRESSION TAG	UNP Q15631
A	-3	HIS	-	EXPRESSION TAG	UNP Q15631
A	-2	HIS	-	EXPRESSION TAG	UNP Q15631
A	-1	GLY	-	EXPRESSION TAG	UNP Q15631
A	0	SER	-	EXPRESSION TAG	UNP Q15631
B	-11	MET	-	EXPRESSION TAG	UNP Q15631
B	-10	ARG	-	EXPRESSION TAG	UNP Q15631
B	-9	GLY	-	EXPRESSION TAG	UNP Q15631
B	-8	SER	-	EXPRESSION TAG	UNP Q15631
B	-7	HIS	-	EXPRESSION TAG	UNP Q15631
B	-6	HIS	-	EXPRESSION TAG	UNP Q15631
B	-5	HIS	-	EXPRESSION TAG	UNP Q15631
B	-4	HIS	-	EXPRESSION TAG	UNP Q15631
B	-3	HIS	-	EXPRESSION TAG	UNP Q15631

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	HIS	-	EXPRESSION TAG	UNP Q15631
B	-1	GLY	-	EXPRESSION TAG	UNP Q15631
B	0	SER	-	EXPRESSION TAG	UNP Q15631
C	-11	MET	-	EXPRESSION TAG	UNP Q15631
C	-10	ARG	-	EXPRESSION TAG	UNP Q15631
C	-9	GLY	-	EXPRESSION TAG	UNP Q15631
C	-8	SER	-	EXPRESSION TAG	UNP Q15631
C	-7	HIS	-	EXPRESSION TAG	UNP Q15631
C	-6	HIS	-	EXPRESSION TAG	UNP Q15631
C	-5	HIS	-	EXPRESSION TAG	UNP Q15631
C	-4	HIS	-	EXPRESSION TAG	UNP Q15631
C	-3	HIS	-	EXPRESSION TAG	UNP Q15631
C	-2	HIS	-	EXPRESSION TAG	UNP Q15631
C	-1	GLY	-	EXPRESSION TAG	UNP Q15631
C	0	SER	-	EXPRESSION TAG	UNP Q15631
D	-11	MET	-	EXPRESSION TAG	UNP Q15631
D	-10	ARG	-	EXPRESSION TAG	UNP Q15631
D	-9	GLY	-	EXPRESSION TAG	UNP Q15631
D	-8	SER	-	EXPRESSION TAG	UNP Q15631
D	-7	HIS	-	EXPRESSION TAG	UNP Q15631
D	-6	HIS	-	EXPRESSION TAG	UNP Q15631
D	-5	HIS	-	EXPRESSION TAG	UNP Q15631
D	-4	HIS	-	EXPRESSION TAG	UNP Q15631
D	-3	HIS	-	EXPRESSION TAG	UNP Q15631
D	-2	HIS	-	EXPRESSION TAG	UNP Q15631
D	-1	GLY	-	EXPRESSION TAG	UNP Q15631
D	0	SER	-	EXPRESSION TAG	UNP Q15631

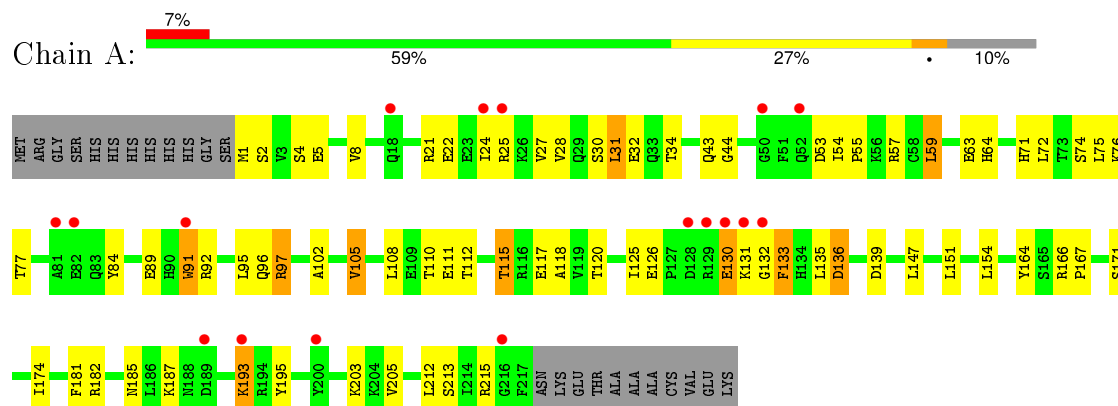
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	126	Total O 126 126	0	0
2	B	86	Total O 86 86	0	0
2	C	91	Total O 91 91	0	0
2	D	111	Total O 111 111	0	0

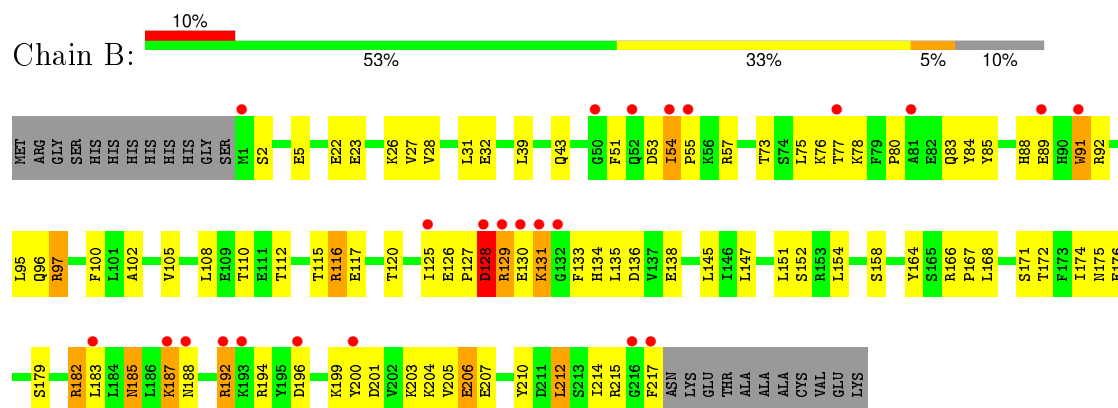
3 Residue-property plots [i](#)

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

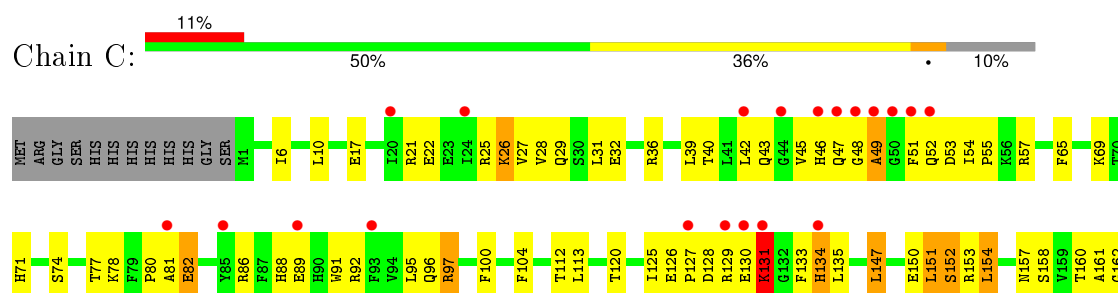
• Molecule 1: Translin

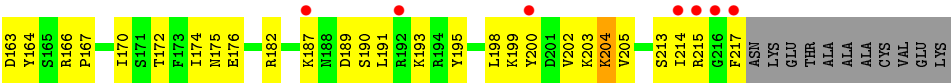


• Molecule 1: Translin

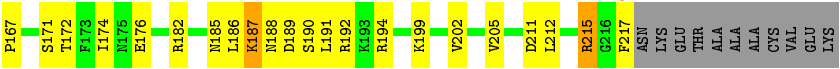
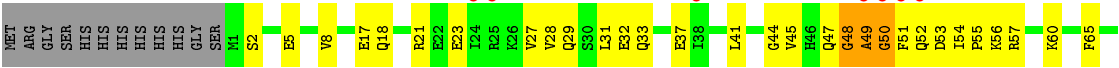


• Molecule 1: Translin





• Molecule 1: Translin



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	129.42Å 135.27Å 134.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.20 15.04 – 2.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) (15.00-2.20) 96.2 (15.04-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.04 (at 2.20Å)	Xtriage
Refinement program	CNX	Depositor
R, R_{free}	0.229 , 0.265 0.246 , 0.279	Depositor DCC
R_{free} test set	2907 reflections (5.06%)	DCC
Wilson B-factor (Å ²)	43.3	Xtriage
Anisotropy	0.289	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 57.9	EDS
Estimated twinning fraction	0.017 for -k,-h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	3 of 57472 reflections (0.005%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7494	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.74% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.40	0/1803	0.54	0/2433
1	B	0.36	0/1803	0.57	2/2433 (0.1%)
1	C	0.36	0/1803	0.55	0/2433
1	D	0.37	0/1803	0.57	0/2433
All	All	0.37	0/7212	0.56	2/9732 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	54	ILE	N-CA-C	-5.68	95.65	111.00
1	B	54	ILE	C-N-CD	-5.64	108.19	120.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	1770	0	1787	72	0
1	B	1770	0	1787	102	0
1	C	1770	0	1787	123	0
1	D	1770	0	1787	95	0
2	A	126	0	0	12	0
2	B	86	0	0	8	1
2	C	91	0	0	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	111	0	0	14	0
All	All	7494	0	7148	366	1

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 26.

All (366) 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:C:97:ARG:HB3	1:C:97:ARG:HH11	1.12	1.09
1:D:187:LYS:HE3	1:D:187:LYS:H	1.10	1.08
1:B:54:ILE:HA	2:B:229:HOH:O	1.55	1.05
1:B:97:ARG:HH11	1:B:97:ARG:HB3	1.21	1.04
1:A:97:ARG:HH11	1:A:97:ARG:HB3	1.18	1.03
1:D:187:LYS:CE	1:D:187:LYS:H	1.79	0.96
1:D:187:LYS:HE3	1:D:187:LYS:N	1.81	0.95
1:C:131:LYS:HA	1:C:131:LYS:HE3	1.52	0.91
1:B:136:ASP:OD2	1:B:138:GLU:HG2	1.71	0.90
1:B:128:ASP:HA	1:B:134:HIS:HD2	1.37	0.88
1:D:103:ALA:HA	1:D:114:VAL:HG21	1.55	0.88
1:D:136:ASP:HB2	2:D:230:HOH:O	1.73	0.88
1:B:110:THR:OG1	1:B:112:THR:HG22	1.76	0.86
1:D:125:ILE:HG12	1:D:126:GLU:H	1.41	0.85
1:C:199:LYS:HG2	2:C:243:HOH:O	1.74	0.85
1:C:45:VAL:HB	1:C:57:ARG:HD3	1.58	0.84
1:A:110:THR:OG1	1:A:112:THR:HG22	1.75	0.84
1:B:97:ARG:HH11	1:B:97:ARG:CB	1.92	0.83
1:D:129:ARG:HA	1:D:129:ARG:CZ	2.09	0.83
1:D:129:ARG:NH1	1:D:129:ARG:HA	1.95	0.82
1:D:103:ALA:HA	1:D:114:VAL:CG2	2.09	0.81
1:D:115:THR:HG22	1:D:118:ALA:H	1.45	0.81
1:D:106:VAL:HB	1:D:114:VAL:HG22	1.62	0.79
1:B:89:GLU:HG2	1:B:92:ARG:HH22	1.46	0.79
1:A:28:VAL:O	1:A:32:GLU:HG3	1.83	0.78
1:D:51:PHE:O	1:D:54:ILE:HG12	1.85	0.77
1:C:97:ARG:CB	1:C:97:ARG:HH11	1.94	0.77
1:B:53:ASP:HB2	1:B:57:ARG:HH11	1.49	0.77
1:D:125:ILE:HG12	1:D:126:GLU:N	2.01	0.76
1:A:72:LEU:O	1:A:76:LYS:HG3	1.86	0.75
1:C:28:VAL:O	1:C:32:GLU:HG3	1.87	0.75
1:C:213:SER:HA	1:C:217:PHE:HB2	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:147:LEU:CD1	1:D:151:LEU:HD22	2.17	0.74
1:A:92:ARG:O	1:A:96:GLN:HG3	1.87	0.74
1:C:54:ILE:HB	1:C:55:PRO:HD3	1.68	0.74
1:B:171:SER:HA	1:B:205:VAL:HG11	1.71	0.72
1:B:89:GLU:HG2	1:B:92:ARG:HH12	1.52	0.72
1:C:42:LEU:O	1:C:45:VAL:HG12	1.89	0.72
1:D:56:LYS:HE2	1:D:60:LYS:NZ	2.03	0.72
1:B:53:ASP:HB2	1:B:57:ARG:NH1	2.04	0.72
1:C:157:ASN:O	1:C:160:THR:HG22	1.89	0.72
1:C:45:VAL:HG21	1:C:54:ILE:HD13	1.72	0.71
1:B:39:LEU:HD11	1:B:43:GLN:HE21	1.56	0.71
1:B:27:VAL:HG11	1:B:75:LEU:HB2	1.73	0.70
1:A:97:ARG:HH11	1:A:97:ARG:CB	2.01	0.70
1:B:89:GLU:HG2	1:B:92:ARG:NH2	2.07	0.70
1:C:153:ARG:HG3	2:C:311:HOH:O	1.90	0.70
1:D:147:LEU:HD11	1:D:151:LEU:HD22	1.73	0.70
1:D:110:THR:OG1	1:D:112:THR:HG22	1.93	0.69
1:C:97:ARG:HD3	2:C:308:HOH:O	1.91	0.68
1:C:74:SER:O	1:C:77:THR:HB	1.93	0.68
1:C:31:LEU:HD11	1:C:71:HIS:HB3	1.74	0.68
1:D:188:ASN:HD22	1:D:191:LEU:H	1.39	0.68
1:B:172:THR:O	1:B:176:GLU:HG3	1.93	0.67
1:B:185:ASN:HD21	1:C:36:ARG:NH1	1.92	0.67
1:C:27:VAL:O	1:C:31:LEU:HD13	1.95	0.67
1:B:128:ASP:HA	1:B:134:HIS:CD2	2.27	0.67
1:C:52:GLN:O	1:C:55:PRO:HD2	1.95	0.67
1:D:44:GLY:HA3	1:D:57:ARG:NH2	2.09	0.67
1:A:136:ASP:HB2	2:A:244:HOH:O	1.96	0.66
1:D:54:ILE:HB	1:D:55:PRO:HD3	1.76	0.65
1:B:89:GLU:HG2	1:B:92:ARG:NH1	2.11	0.65
1:A:59:LEU:O	1:A:63:GLU:HG3	1.97	0.65
1:A:27:VAL:HG11	1:A:75:LEU:HB2	1.79	0.65
1:C:89:GLU:HG2	1:C:92:ARG:NH2	2.11	0.64
1:D:130:GLU:O	1:D:131:LYS:HB2	1.98	0.64
1:A:125:ILE:HG22	1:A:126:GLU:N	2.12	0.64
1:B:92:ARG:O	1:B:96:GLN:HG3	1.98	0.64
1:B:187:LYS:HD3	1:B:187:LYS:H	1.63	0.64
1:C:88:HIS:CE1	1:C:92:ARG:HE	2.15	0.64
1:B:185:ASN:HD21	1:C:36:ARG:HD3	1.63	0.64
1:B:125:ILE:HG12	1:B:133:PHE:O	1.98	0.64
1:C:204:LYS:C	1:C:204:LYS:HD3	2.18	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:2:SER:OG	1:D:5:GLU:HG3	1.98	0.63
1:A:174:ILE:HD12	1:A:205:VAL:HG21	1.81	0.63
1:D:31:LEU:CD2	1:D:71:HIS:HB3	2.28	0.63
1:B:120:THR:HA	1:B:125:ILE:CG2	2.29	0.62
1:C:45:VAL:CG2	1:C:54:ILE:HD13	2.30	0.62
1:D:53:ASP:O	1:D:57:ARG:HG3	1.99	0.62
1:C:157:ASN:HA	1:C:160:THR:HG22	1.81	0.62
1:A:126:GLU:HG3	1:A:130:GLU:CD	2.20	0.62
1:A:125:ILE:HG23	1:A:133:PHE:O	1.99	0.62
1:B:55:PRO:HA	2:B:229:HOH:O	1.98	0.62
1:A:215:ARG:HH12	1:B:215:ARG:HH22	1.48	0.62
1:C:167:PRO:HD3	2:C:248:HOH:O	2.00	0.61
1:C:126:GLU:HB2	1:C:130:GLU:HB3	1.82	0.61
1:C:182:ARG:HG2	1:C:182:ARG:HH11	1.65	0.61
1:C:89:GLU:HG2	1:C:92:ARG:HH22	1.64	0.61
1:D:41:LEU:HD11	1:D:60:LYS:HB3	1.83	0.60
1:B:89:GLU:CG	1:B:92:ARG:HH12	2.14	0.60
1:C:51:PHE:C	1:C:53:ASP:H	2.05	0.60
1:C:213:SER:CA	1:C:217:PHE:HB2	2.32	0.60
1:D:97:ARG:NH1	2:D:237:HOH:O	2.29	0.60
1:C:47:GLN:HB2	1:C:161:ALA:HB2	1.84	0.60
1:D:147:LEU:C	1:D:147:LEU:HD13	2.21	0.59
1:A:21:ARG:O	1:A:25:ARG:HG3	2.01	0.59
1:A:95:LEU:HD21	1:A:135:LEU:HD13	1.84	0.59
1:C:213:SER:C	1:C:215:ARG:H	2.04	0.59
1:A:126:GLU:HB2	1:A:132:GLY:O	2.02	0.59
1:D:106:VAL:CB	1:D:114:VAL:HG22	2.31	0.59
1:D:8:VAL:HG11	2:D:302:HOH:O	2.02	0.59
1:D:78:LYS:HD2	1:D:78:LYS:N	2.16	0.59
1:C:97:ARG:NH1	1:C:97:ARG:HB3	1.98	0.59
1:D:97:ARG:HG3	1:D:97:ARG:HH11	1.68	0.59
1:A:97:ARG:HB3	1:A:97:ARG:NH1	2.02	0.59
1:C:31:LEU:CD1	1:C:71:HIS:HB3	2.32	0.58
1:A:95:LEU:HD21	1:A:135:LEU:CD1	2.33	0.58
1:C:46:HIS:ND1	1:C:154:LEU:HA	2.18	0.58
1:C:80:PRO:C	1:C:82:GLU:H	2.06	0.58
1:D:21:ARG:HD3	2:D:257:HOH:O	2.03	0.58
1:C:133:PHE:N	2:C:262:HOH:O	2.35	0.58
1:C:166:ARG:HB3	2:C:248:HOH:O	2.02	0.58
1:C:151:LEU:HD23	1:C:174:ILE:HD11	1.85	0.58
1:D:188:ASN:ND2	1:D:191:LEU:H	2.01	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:95:LEU:HD22	1:A:139:ASP:HB3	1.85	0.57
1:A:24:ILE:HG23	1:A:75:LEU:HD11	1.87	0.57
1:B:145:LEU:HD13	1:B:194:ARG:HB3	1.87	0.57
1:D:188:ASN:HD21	1:D:190:SER:HB2	1.69	0.57
1:D:130:GLU:O	1:D:131:LYS:CB	2.53	0.57
1:C:214:ILE:HG21	1:D:215:ARG:HH11	1.70	0.57
1:C:39:LEU:HD22	2:C:299:HOH:O	2.04	0.57
1:A:215:ARG:HH12	1:B:215:ARG:NH2	2.03	0.57
1:D:56:LYS:HE2	1:D:60:LYS:HZ1	1.67	0.57
1:D:31:LEU:HD22	1:D:71:HIS:HB3	1.84	0.57
1:A:74:SER:O	1:A:77:THR:HB	2.05	0.57
1:C:205:VAL:HG13	2:C:240:HOH:O	2.05	0.57
1:D:186:LEU:HA	1:D:187:LYS:HE3	1.87	0.56
1:B:120:THR:HA	1:B:125:ILE:HG22	1.86	0.56
1:C:166:ARG:HB3	1:C:167:PRO:HD3	1.87	0.56
1:A:193:LYS:NZ	1:A:193:LYS:HB2	2.20	0.56
1:C:112:THR:HG23	2:C:236:HOH:O	2.05	0.56
1:C:45:VAL:HB	1:C:57:ARG:CD	2.33	0.56
1:D:147:LEU:HD13	1:D:151:LEU:HD22	1.87	0.56
1:A:215:ARG:CZ	2:A:235:HOH:O	2.54	0.56
1:D:93:PHE:O	1:D:97:ARG:HG2	2.05	0.56
1:A:115:THR:HG22	1:A:117:GLU:N	2.20	0.56
1:A:89:GLU:HB2	2:A:297:HOH:O	2.06	0.56
1:B:182:ARG:HG2	2:B:266:HOH:O	2.06	0.56
1:B:125:ILE:HG13	1:B:133:PHE:HB3	1.88	0.56
1:B:145:LEU:CD1	1:B:194:ARG:HB3	2.36	0.56
1:B:194:ARG:HD2	2:B:264:HOH:O	2.06	0.56
1:C:170:ILE:O	1:C:174:ILE:HG12	2.06	0.55
1:D:120:THR:HG23	1:D:125:ILE:HG23	1.88	0.55
1:A:171:SER:HB2	1:A:205:VAL:HG12	1.88	0.55
1:B:183:LEU:HB2	2:B:258:HOH:O	2.06	0.55
1:B:125:ILE:HG12	1:B:126:GLU:H	1.72	0.55
1:A:120:THR:HG22	2:A:282:HOH:O	2.07	0.55
1:B:102:ALA:O	1:B:105:VAL:HG12	2.07	0.54
1:C:214:ILE:HG21	1:D:215:ARG:NH1	2.21	0.54
1:C:131:LYS:CA	1:C:131:LYS:HE3	2.31	0.54
1:C:215:ARG:HH22	1:C:217:PHE:HE1	1.54	0.54
1:B:115:THR:HG22	1:B:117:GLU:H	1.73	0.54
1:D:171:SER:HB2	1:D:205:VAL:HG12	1.88	0.54
1:A:44:GLY:HA3	1:A:57:ARG:NH2	2.23	0.54
1:C:86:ARG:HH11	1:C:86:ARG:HG3	1.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:97:ARG:NH1	1:B:97:ARG:HB3	2.06	0.54
1:A:215:ARG:NE	2:A:235:HOH:O	2.41	0.53
1:C:65:PHE:O	1:C:69:LYS:HG3	2.08	0.53
1:B:174:ILE:HD12	1:B:205:VAL:HG21	1.90	0.53
1:A:125:ILE:CG2	1:A:126:GLU:N	2.71	0.53
1:C:172:THR:O	1:C:176:GLU:HG3	2.08	0.53
1:B:77:THR:HG22	1:B:77:THR:O	2.08	0.53
1:C:161:ALA:O	1:C:163:ASP:N	2.42	0.53
1:D:115:THR:HG23	2:D:248:HOH:O	2.08	0.53
1:B:89:GLU:HG2	1:B:92:ARG:CZ	2.39	0.53
1:B:185:ASN:ND2	1:C:36:ARG:HD3	2.23	0.52
1:B:185:ASN:ND2	1:C:36:ARG:NH1	2.56	0.52
1:C:120:THR:HG22	2:C:288:HOH:O	2.08	0.52
1:B:152:SER:OG	1:B:201:ASP:HB3	2.09	0.52
1:B:168:LEU:HD22	1:B:168:LEU:N	2.25	0.52
1:B:89:GLU:CG	1:B:92:ARG:HH22	2.19	0.52
1:D:199:LYS:HG2	2:D:308:HOH:O	2.09	0.52
1:A:111:GLU:HG2	2:A:317:HOH:O	2.08	0.52
1:C:39:LEU:O	1:C:43:GLN:HG3	2.09	0.52
1:C:127:PRO:C	1:C:129:ARG:H	2.13	0.52
1:C:46:HIS:HB2	2:C:289:HOH:O	2.10	0.52
1:C:204:LYS:HD3	1:C:204:LYS:O	2.10	0.52
1:C:198:LEU:O	1:C:202:VAL:HG23	2.09	0.52
1:C:214:ILE:HG23	1:C:214:ILE:O	2.09	0.52
1:A:182:ARG:NH1	1:B:43:GLN:HG3	2.25	0.52
1:B:28:VAL:O	1:B:32:GLU:HG3	2.10	0.52
1:D:125:ILE:HG12	1:D:133:PHE:O	2.11	0.51
1:A:1:MET:N	2:A:309:HOH:O	2.42	0.51
1:C:215:ARG:NH1	1:C:215:ARG:HB2	2.25	0.51
1:B:182:ARG:HD2	1:C:153:ARG:NH2	2.25	0.51
1:D:28:VAL:O	1:D:32:GLU:HG3	2.11	0.51
1:D:44:GLY:HA3	1:D:57:ARG:CZ	2.40	0.51
1:C:48:GLY:O	1:C:49:ALA:HB2	2.11	0.51
1:D:174:ILE:HD12	1:D:205:VAL:HG21	1.93	0.51
1:B:206:GLU:HG3	1:B:207:GLU:N	2.26	0.51
1:D:93:PHE:CE1	1:D:97:ARG:HD3	2.46	0.51
1:C:151:LEU:HD23	1:C:174:ILE:CD1	2.40	0.51
1:B:2:SER:OG	1:B:5:GLU:HG3	2.09	0.51
1:D:189:ASP:HA	1:D:192:ARG:HH11	1.75	0.51
1:A:31:LEU:HD13	1:A:71:HIS:HB2	1.92	0.51
1:D:76:LYS:HD3	2:D:286:HOH:O	2.09	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:115:THR:HG22	1:D:117:GLU:N	2.27	0.50
1:B:185:ASN:HD21	1:C:36:ARG:HH11	1.59	0.50
1:B:183:LEU:HD11	2:C:234:HOH:O	2.11	0.50
1:A:115:THR:HG22	1:A:117:GLU:H	1.77	0.50
1:B:210:TYR:HE1	1:C:164:TYR:CZ	2.29	0.50
1:C:77:THR:HG22	1:C:78:LYS:HD3	1.93	0.50
1:C:22:GLU:HB3	2:C:241:HOH:O	2.12	0.50
1:B:89:GLU:CB	1:B:92:ARG:HH12	2.25	0.49
1:C:203:LYS:NZ	1:D:153:ARG:HB2	2.27	0.49
1:D:103:ALA:HA	1:D:114:VAL:HG23	1.94	0.49
1:C:46:HIS:HB3	1:C:157:ASN:CB	2.42	0.49
1:B:188:ASN:O	1:B:192:ARG:HD3	2.12	0.49
1:B:76:LYS:HD3	1:B:133:PHE:HB2	1.94	0.49
1:C:158:SER:OG	1:C:166:ARG:HG2	2.12	0.49
1:A:4:SER:O	1:A:8:VAL:HG23	2.12	0.49
1:D:114:VAL:HG23	2:D:231:HOH:O	2.12	0.49
1:C:17:GLU:OE2	1:C:21:ARG:NH2	2.45	0.49
1:C:134:HIS:H	1:C:134:HIS:CD2	2.30	0.49
1:C:213:SER:C	1:C:215:ARG:N	2.66	0.49
1:B:23:GLU:HB3	1:B:78:LYS:HD2	1.94	0.49
1:A:215:ARG:HH11	1:A:215:ARG:HG2	1.78	0.49
1:B:53:ASP:OD2	1:B:57:ARG:NH1	2.46	0.48
1:D:147:LEU:HD11	1:D:151:LEU:CD2	2.41	0.48
1:B:127:PRO:C	1:B:129:ARG:H	2.17	0.48
1:D:65:PHE:O	1:D:69:LYS:HG3	2.13	0.48
1:B:182:ARG:NH1	1:C:39:LEU:HD21	2.28	0.48
1:C:80:PRO:O	1:C:82:GLU:N	2.47	0.48
1:C:147:LEU:HD22	1:C:151:LEU:HD13	1.95	0.48
1:D:125:ILE:CD1	1:D:133:PHE:HD2	2.26	0.48
1:C:47:GLN:CB	1:C:161:ALA:HB2	2.43	0.48
1:D:211:ASP:O	1:D:215:ARG:HB2	2.14	0.48
1:A:53:ASP:O	1:A:57:ARG:HG3	2.14	0.48
1:A:115:THR:HG22	1:A:118:ALA:H	1.77	0.48
1:B:88:HIS:HA	1:B:91:TRP:CZ2	2.49	0.47
1:A:117:GLU:O	1:A:120:THR:HB	2.14	0.47
1:A:126:GLU:HB3	1:A:130:GLU:HB3	1.95	0.47
1:C:200:TYR:N	2:C:235:HOH:O	2.39	0.47
1:C:152:SER:HA	1:C:205:VAL:HG22	1.96	0.47
1:B:206:GLU:HA	2:C:237:HOH:O	2.14	0.47
1:A:30:SER:HB3	1:A:71:HIS:CE1	2.49	0.47
1:A:181:PHE:HB3	1:A:195:TYR:CE1	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:168:LEU:HD21	1:B:212:LEU:HD23	1.97	0.47
1:D:166:ARG:HG3	2:D:232:HOH:O	2.15	0.47
1:D:48:GLY:O	1:D:50:GLY:N	2.45	0.47
1:C:214:ILE:CG2	1:D:215:ARG:HH11	2.28	0.47
1:A:34:THR:HG23	1:A:64:HIS:CE1	2.49	0.47
1:B:97:ARG:HH11	1:B:97:ARG:CG	2.28	0.47
1:A:115:THR:HG23	1:A:117:GLU:OE1	2.15	0.47
1:C:6:ILE:O	1:C:10:LEU:HG	2.14	0.47
1:D:106:VAL:HB	1:D:114:VAL:CG2	2.39	0.46
1:B:210:TYR:OH	1:C:215:ARG:NE	2.45	0.46
1:B:125:ILE:HG12	1:B:126:GLU:N	2.30	0.46
1:A:213:SER:HB2	2:A:305:HOH:O	2.14	0.46
1:B:130:GLU:HG2	1:B:130:GLU:O	2.13	0.46
1:A:215:ARG:NH1	1:B:215:ARG:NH2	2.63	0.46
1:B:120:THR:O	1:B:125:ILE:HG22	2.16	0.46
1:A:84:TYR:CZ	1:A:91:TRP:CZ3	3.04	0.46
1:C:51:PHE:C	1:C:53:ASP:N	2.68	0.46
1:C:190:SER:O	1:C:193:LYS:HB2	2.15	0.46
1:D:33:GLN:O	1:D:37:GLU:HG3	2.14	0.46
1:A:125:ILE:CG2	1:A:126:GLU:H	2.29	0.46
1:C:112:THR:HG22	1:C:113:LEU:N	2.30	0.46
1:C:215:ARG:NH2	1:C:217:PHE:CE1	2.83	0.46
1:B:120:THR:HG22	2:B:270:HOH:O	2.15	0.46
1:D:31:LEU:HD21	1:D:71:HIS:HB3	1.97	0.46
1:B:127:PRO:O	1:B:129:ARG:N	2.48	0.46
1:D:166:ARG:HB3	1:D:167:PRO:HD3	1.98	0.46
1:A:31:LEU:HD13	1:A:71:HIS:CB	2.45	0.46
1:A:97:ARG:CD	2:A:229:HOH:O	2.63	0.46
1:C:112:THR:CG2	1:C:113:LEU:N	2.79	0.46
1:D:76:LYS:HE3	1:D:81:ALA:HB2	1.98	0.46
1:A:203:LYS:HE2	1:B:200:TYR:HE2	1.81	0.46
1:B:175:ASN:CG	1:C:47:GLN:HE22	2.19	0.45
1:C:187:LYS:HE2	2:D:272:HOH:O	2.16	0.45
1:C:29:GLN:HB2	2:C:304:HOH:O	2.16	0.45
1:C:46:HIS:NE2	1:C:150:GLU:OE1	2.47	0.45
1:A:102:ALA:O	1:A:105:VAL:HG12	2.16	0.45
1:B:80:PRO:HB2	1:B:83:GLN:HG3	1.99	0.45
1:C:126:GLU:CD	1:C:126:GLU:N	2.71	0.45
1:D:27:VAL:HG12	1:D:31:LEU:HD23	1.98	0.45
1:D:97:ARG:CG	1:D:97:ARG:HH11	2.29	0.45
1:C:134:HIS:HB2	2:C:244:HOH:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:129:ARG:HA	1:B:129:ARG:CZ	2.46	0.44
1:D:187:LYS:NZ	1:D:188:ASN:H	2.15	0.44
1:B:212:LEU:O	1:B:217:PHE:N	2.44	0.44
1:D:92:ARG:NH2	2:D:273:HOH:O	2.50	0.44
1:D:136:ASP:OD1	1:D:138:GLU:OE2	2.34	0.44
1:C:45:VAL:CB	1:C:57:ARG:HD3	2.38	0.44
1:B:53:ASP:CB	1:B:57:ARG:NH1	2.77	0.44
1:B:120:THR:HG23	1:B:125:ILE:HG23	1.98	0.44
1:D:50:GLY:O	1:D:51:PHE:HB2	2.16	0.44
1:D:130:GLU:C	1:D:134:HIS:CE1	2.90	0.44
1:B:73:THR:HA	1:B:76:LYS:HE2	1.99	0.44
1:A:2:SER:OG	1:A:5:GLU:HG3	2.17	0.44
1:D:47:GLN:O	1:D:49:ALA:N	2.49	0.44
1:B:164:TYR:N	1:B:164:TYR:CD1	2.85	0.44
1:D:120:THR:HA	1:D:125:ILE:CG2	2.47	0.44
1:D:23:GLU:HB3	1:D:78:LYS:CG	2.47	0.44
1:D:188:ASN:O	1:D:192:ARG:HG3	2.17	0.44
1:C:157:ASN:CA	1:C:160:THR:HG22	2.48	0.43
1:C:43:GLN:HB2	1:C:153:ARG:HH22	1.83	0.43
1:A:25:ARG:HG2	1:A:25:ARG:HH11	1.83	0.43
1:C:174:ILE:HG22	1:C:202:VAL:HG22	1.99	0.43
1:A:95:LEU:HD23	1:A:95:LEU:C	2.38	0.43
1:B:196:ASP:O	1:B:199:LYS:HG2	2.19	0.43
1:C:199:LYS:HB2	2:C:235:HOH:O	2.18	0.43
1:D:45:VAL:CG2	1:D:57:ARG:HD3	2.49	0.43
1:D:23:GLU:HB3	1:D:78:LYS:HG3	2.00	0.43
1:D:172:THR:O	1:D:176:GLU:HG3	2.18	0.43
1:B:88:HIS:HA	1:B:91:TRP:CH2	2.53	0.43
1:B:51:PHE:HZ	1:B:158:SER:HA	1.83	0.43
1:A:115:THR:CG2	1:A:117:GLU:H	2.32	0.43
1:B:115:THR:HG22	1:B:116:ARG:N	2.34	0.43
1:B:84:TYR:CZ	1:B:91:TRP:CZ3	3.07	0.43
1:A:164:TYR:N	1:A:164:TYR:CD1	2.87	0.43
1:D:120:THR:O	1:D:125:ILE:HG22	2.19	0.43
1:A:92:ARG:NH1	2:A:297:HOH:O	2.51	0.43
1:A:54:ILE:HB	1:A:55:PRO:HD3	1.99	0.43
1:C:126:GLU:HB2	1:C:130:GLU:CB	2.47	0.43
1:D:48:GLY:HA2	2:D:291:HOH:O	2.18	0.42
1:C:127:PRO:HD2	1:C:130:GLU:HB2	2.01	0.42
1:B:182:ARG:HD2	1:C:153:ARG:HH21	1.83	0.42
1:D:136:ASP:OD1	1:D:138:GLU:HG2	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:125:ILE:HG22	1:A:126:GLU:H	1.84	0.42
1:B:187:LYS:HA	1:B:192:ARG:HE	1.83	0.42
1:A:193:LYS:HZ3	1:A:193:LYS:HB2	1.84	0.42
1:D:187:LYS:HG2	1:D:188:ASN:N	2.35	0.42
1:C:25:ARG:O	1:C:25:ARG:HD2	2.19	0.42
1:B:166:ARG:HB3	1:B:167:PRO:HD3	2.01	0.42
1:A:125:ILE:CG2	1:A:133:PHE:O	2.65	0.42
1:B:130:GLU:O	1:B:131:LYS:O	2.38	0.42
1:B:51:PHE:CZ	1:B:158:SER:HA	2.54	0.42
1:C:25:ARG:NH2	2:C:241:HOH:O	2.53	0.42
1:C:195:TYR:O	2:C:243:HOH:O	2.22	0.41
1:D:48:GLY:HA3	2:D:229:HOH:O	2.19	0.41
1:B:203:LYS:HE3	1:C:204:LYS:NZ	2.35	0.41
1:B:179:SER:O	1:B:183:LEU:HG	2.20	0.41
1:C:175:ASN:HB3	1:D:47:GLN:NE2	2.35	0.41
1:D:41:LEU:O	1:D:41:LEU:HD23	2.20	0.41
1:A:130:GLU:O	1:A:130:GLU:HG2	2.20	0.41
1:D:174:ILE:HG22	1:D:202:VAL:HG22	2.02	0.41
1:B:22:GLU:O	1:B:26:LYS:HG3	2.20	0.41
1:D:17:GLU:OE2	1:D:21:ARG:NH1	2.43	0.41
1:C:22:GLU:O	1:C:26:LYS:HE3	2.19	0.41
1:A:166:ARG:NH1	2:A:295:HOH:O	2.45	0.41
1:C:53:ASP:OD2	1:C:57:ARG:HG3	2.20	0.41
1:C:189:ASP:C	1:C:191:LEU:H	2.23	0.41
1:B:204:LYS:HG3	2:B:272:HOH:O	2.20	0.41
1:B:80:PRO:O	1:B:83:GLN:HB2	2.19	0.41
1:C:42:LEU:HB3	1:C:104:PHE:CE2	2.55	0.41
1:C:182:ARG:HG2	1:C:182:ARG:NH1	2.34	0.41
1:A:133:PHE:N	2:A:243:HOH:O	2.53	0.41
1:D:52:GLN:HA	2:D:281:HOH:O	2.20	0.41
1:C:88:HIS:HE1	1:C:92:ARG:HE	1.61	0.41
1:C:161:ALA:C	1:C:163:ASP:H	2.24	0.41
1:C:47:GLN:HB2	1:C:48:GLY:H	1.72	0.41
1:B:85:TYR:HD1	2:B:268:HOH:O	2.04	0.41
1:A:187:LYS:HD3	1:A:187:LYS:HA	1.91	0.40
1:B:185:ASN:HD21	1:C:36:ARG:CZ	2.34	0.40
1:B:183:LEU:HD22	1:C:40:THR:OG1	2.21	0.40
1:A:43:GLN:OE1	1:D:182:ARG:NH2	2.53	0.40
1:B:215:ARG:HH11	1:B:215:ARG:HG2	1.86	0.40
1:A:44:GLY:HA3	1:A:57:ARG:CZ	2.50	0.40
1:B:210:TYR:HE1	1:C:164:TYR:CE1	2.39	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:120:THR:HG23	1:C:125:ILE:HG13	2.02	0.40
1:A:166:ARG:N	1:A:167:PRO:CD	2.85	0.40
1:C:51:PHE:CD2	1:C:52:GLN:HG2	2.55	0.40
1:C:92:ARG:O	1:C:96:GLN:HG3	2.22	0.40
1:B:2:SER:N	1:B:5:GLU:OE2	2.42	0.40
1:D:145:LEU:HD12	1:D:194:ARG:HD2	2.02	0.40

All (1) 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:268:HOH:O	2:B:268:HOH:O[4_555]	1.74	0.46

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	215/240 (90%)	205 (95%)	7 (3%)	3 (1%)	14	10
1	B	215/240 (90%)	205 (95%)	8 (4%)	2 (1%)	21	19
1	C	215/240 (90%)	191 (89%)	19 (9%)	5 (2%)	8	4
1	D	215/240 (90%)	204 (95%)	5 (2%)	6 (3%)	6	3
All	All	860/960 (90%)	805 (94%)	39 (4%)	16 (2%)	10	6

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	130	GLU
1	A	131	LYS
1	B	128	ASP
1	B	131	LYS

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Mol	Chain	Res	Type
1	C	49	ALA
1	D	131	LYS
1	A	133	PHE
1	C	81	ALA
1	C	162	GLY
1	C	131	LYS
1	D	49	ALA
1	D	127	PRO
1	C	128	ASP
1	D	48	GLY
1	D	129	ARG
1	D	50	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	194/212 (92%)	179 (92%)	15 (8%)	16	16
1	B	194/212 (92%)	174 (90%)	20 (10%)	9	8
1	C	194/212 (92%)	180 (93%)	14 (7%)	18	18
1	D	194/212 (92%)	179 (92%)	15 (8%)	16	16
All	All	776/848 (92%)	712 (92%)	64 (8%)	14	13

All (64) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	GLU
1	A	31	LEU
1	A	59	LEU
1	A	91	TRP
1	A	97	ARG
1	A	105	VAL
1	A	108	LEU
1	A	115	THR
1	A	136	ASP

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Mol	Chain	Res	Type
1	A	147	LEU
1	A	151	LEU
1	A	154	LEU
1	A	185	ASN
1	A	193	LYS
1	A	212	LEU
1	B	31	LEU
1	B	91	TRP
1	B	95	LEU
1	B	97	ARG
1	B	100	PHE
1	B	108	LEU
1	B	116	ARG
1	B	128	ASP
1	B	129	ARG
1	B	135	LEU
1	B	147	LEU
1	B	151	LEU
1	B	154	LEU
1	B	182	ARG
1	B	185	ASN
1	B	187	LYS
1	B	192	ARG
1	B	206	GLU
1	B	212	LEU
1	B	214	ILE
1	C	26	LYS
1	C	82	GLU
1	C	91	TRP
1	C	95	LEU
1	C	97	ARG
1	C	100	PHE
1	C	131	LYS
1	C	134	HIS
1	C	135	LEU
1	C	147	LEU
1	C	151	LEU
1	C	152	SER
1	C	154	LEU
1	C	204	LYS
1	D	18	GLN
1	D	29	GLN

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Mol	Chain	Res	Type
1	D	78	LYS
1	D	95	LEU
1	D	108	LEU
1	D	115	THR
1	D	117	GLU
1	D	129	ARG
1	D	151	LEU
1	D	154	LEU
1	D	185	ASN
1	D	187	LYS
1	D	212	LEU
1	D	215	ARG
1	D	217	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	71	HIS
1	A	83	GLN
1	A	185	ASN
1	B	71	HIS
1	B	134	HIS
1	B	169	HIS
1	B	175	ASN
1	B	185	ASN
1	B	188	ASN
1	C	47	GLN
1	C	64	HIS
1	C	83	GLN
1	C	157	ASN
1	D	29	GLN
1	D	47	GLN
1	D	71	HIS
1	D	185	ASN
1	D	188	ASN

5.3.3 RNA ⓘ

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](#)

There are no ligands in this entry.

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	217/240 (90%)	0.57	17 (7%) 16 15	29, 47, 67, 96	0
1	B	217/240 (90%)	0.53	24 (11%) 7 7	31, 51, 78, 93	0
1	C	217/240 (90%)	1.05	27 (12%) 5 5	30, 51, 91, 106	0
1	D	217/240 (90%)	0.38	12 (5%) 29 28	31, 46, 73, 99	0
All	All	868/960 (90%)	0.63	80 (9%) 11 10	29, 49, 81, 106	0

All (80) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	49	ALA	15.4
1	C	48	GLY	11.6
1	C	50	GLY	10.4
1	C	47	GLN	9.0
1	C	51	PHE	8.5
1	C	215	ARG	7.8
1	A	129	ARG	7.1
1	D	51	PHE	6.7
1	C	129	ARG	6.7
1	D	50	GLY	6.4
1	C	216	GLY	6.4
1	D	130	GLU	6.3
1	A	131	LYS	6.3
1	C	200	TYR	5.9
1	A	130	GLU	5.9
1	C	46	HIS	5.6
1	D	49	ALA	5.4
1	D	217	PHE	5.4
1	C	217	PHE	5.4
1	B	129	ARG	4.9
1	D	131	LYS	4.4

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Mol	Chain	Res	Type	RSRZ
1	C	214	ILE	4.4
1	C	85	TYR	4.0
1	B	196	ASP	3.9
1	B	131	LYS	3.9
1	D	129	ARG	3.8
1	C	130	GLU	3.8
1	B	217	PHE	3.8
1	D	52	GLN	3.6
1	D	128	ASP	3.6
1	C	187	LYS	3.5
1	A	189	ASP	3.4
1	B	192	ARG	3.4
1	B	200	TYR	3.3
1	C	131	LYS	3.2
1	B	183	LEU	3.2
1	A	24	ILE	3.1
1	B	132	GLY	3.1
1	A	193	LYS	3.1
1	C	89	GLU	3.0
1	B	193	LYS	2.9
1	C	52	GLN	2.9
1	B	187	LYS	2.8
1	C	81	ALA	2.8
1	A	216	GLY	2.8
1	A	25	ARG	2.8
1	A	128	ASP	2.8
1	B	54	ILE	2.7
1	B	91	TRP	2.7
1	A	18	GLN	2.7
1	B	55	PRO	2.7
1	B	128	ASP	2.7
1	A	50	GLY	2.6
1	A	82	GLU	2.5
1	A	132	GLY	2.5
1	C	93	PHE	2.5
1	B	188	ASN	2.4
1	B	89	GLU	2.4
1	C	20	ILE	2.4
1	C	192	ARG	2.4
1	A	52	GLN	2.4
1	A	91	TRP	2.3
1	B	216	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	38	ILE	2.3
1	C	44	GLY	2.2
1	A	81	ALA	2.2
1	D	24	ILE	2.2
1	B	52	GLN	2.2
1	A	200	TYR	2.2
1	B	81	ALA	2.2
1	C	134	HIS	2.1
1	B	50	GLY	2.1
1	C	42	LEU	2.1
1	B	125	ILE	2.1
1	C	24	ILE	2.1
1	C	127	PRO	2.1
1	B	77	THR	2.1
1	B	1	MET	2.0
1	B	130	GLU	2.0
1	D	25	ARG	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.