



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2014 – 11:47 AM GMT

PDB ID : 1KBU
Title : CRE RECOMBINASE BOUND TO A LOXP HOLLIDAY JUNCTION
Authors : Martin, S.S.; Pulido, E.; Chu, V.C.; Lechner, T.; Baldwin, E.P.
Deposited on : 2001-11-06
Resolution : 2.20 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

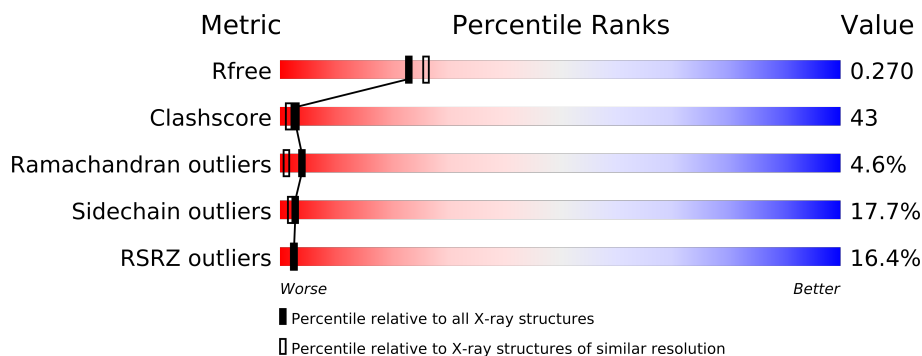
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

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}	66092	2938 (2.20-2.20)
Clashscore	79885	3751 (2.20-2.20)
Ramachandran outliers	78287	3681 (2.20-2.20)
Sidechain outliers	78261	3682 (2.20-2.20)
RSRZ outliers	66119	2939 (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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	C	34	
2	D	34	
3	A	349	
3	B	349	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6837 atoms, of which 0 are hydrogen and 0 are deuterium.

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 DNA chain called LOXP.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	34	Total	C	N	O	P	0	4	0
			740	357	132	216	35			

- Molecule 2 is a DNA chain called LOXP.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	34	Total	C	N	O	P	0	4	0
			771	373	137	224	37			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	30	DC	G	see remark 999	GB 215626

- Molecule 3 is a protein called CRE RECOMBINASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	324	Total	C	N	O	S	54	0	0
			2562	1591	488	468	15			
3	B	319	Total	C	N	O	S	12	0	0
			2527	1572	483	457	15			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	HIS	-	EXPRESSION TAG	UNP P06956
A	-3	HIS	-	EXPRESSION TAG	UNP P06956
A	-2	HIS	-	EXPRESSION TAG	UNP P06956
A	-1	HIS	-	EXPRESSION TAG	UNP P06956
A	0	HIS	-	EXPRESSION TAG	UNP P06956
A	1	HIS	-	EXPRESSION TAG	UNP P06956
B	-4	HIS	-	EXPRESSION TAG	UNP P06956

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	HIS	-	EXPRESSION TAG	UNP P06956
B	-2	HIS	-	EXPRESSION TAG	UNP P06956
B	-1	HIS	-	EXPRESSION TAG	UNP P06956
B	0	HIS	-	EXPRESSION TAG	UNP P06956
B	1	HIS	-	EXPRESSION TAG	UNP P06956

- Molecule 4 is water.

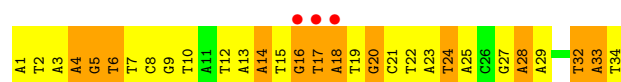
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	59	Total	O	0	0
			59	59		
4	B	124	Total	O	0	0
			124	124		
4	C	20	Total	O	0	0
			20	20		
4	D	34	Total	O	0	0
			34	34		

3 Residue-property plots

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

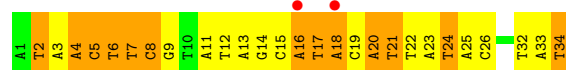
• Molecule 1: LOXP

Chain C: 



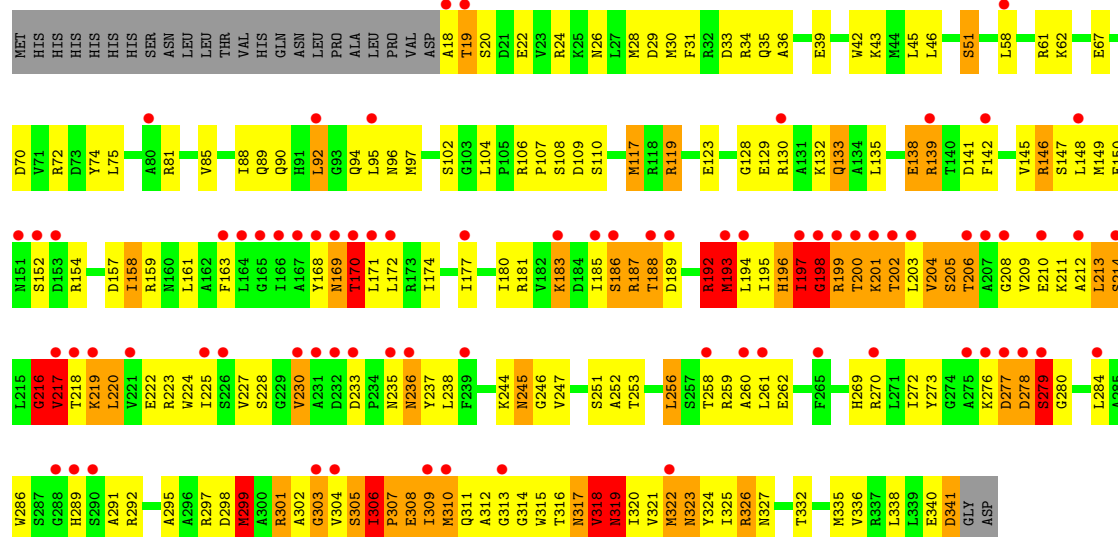
• Molecule 2: LOXP

Chain D: 



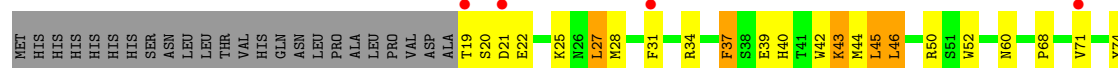
• Molecule 3: CRE RECOMBINASE

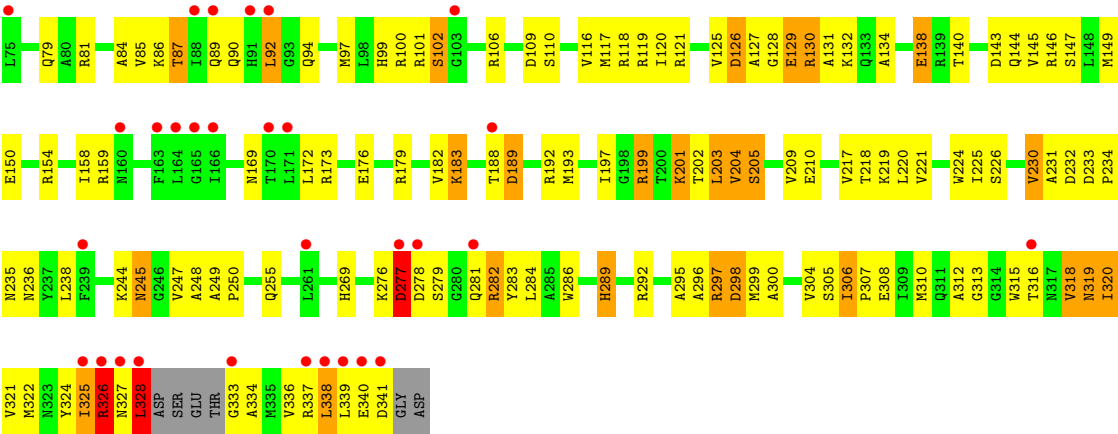
Chain A: 



• Molecule 3: CRE RECOMBINASE

Chain B: 





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	107.17Å 121.60Å 179.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	5.00 – 2.20 24.52 – 2.20	Depositor EDS
% Data completeness (in resolution range)	89.0 (5.00-2.20) 89.3 (24.52-2.20)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.47 (at 2.19Å)	Xtriage
Refinement program	TNT	Depositor
R, R_{free}	0.231 , 0.279 0.241 , 0.270	Depositor DCC
R_{free} test set	2682 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	48.0	Xtriage
Anisotropy	0.289	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 83.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 53233 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6837	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.07% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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	C	0.95	3/830 (0.4%)	2.60	27/1281 (2.1%)
2	D	0.54	0/864	1.67	24/1330 (1.8%)
3	A	0.42	0/2603	1.05	16/3510 (0.5%)
3	B	0.42	0/2567	0.89	5/3459 (0.1%)
All	All	0.53	3/6864 (0.0%)	1.41	72/9580 (0.8%)

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
3	A	1	0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	16[A]	DG	O3'-P	13.54	1.77	1.61
1	C	16[B]	DG	O3'-P	13.54	1.77	1.61
1	C	18[B]	DA	O3'-P	9.57	1.72	1.61

All (72) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	16[A]	DG	P-O3'-C3'	40.18	167.91	119.70
1	C	16[B]	DG	P-O3'-C3'	40.18	167.91	119.70
1	C	18[B]	DA	OP1-P-O3'	-36.31	25.32	105.20
3	A	301	ARG	NE-CZ-NH2	-21.76	109.42	120.30
1	C	18[B]	DA	OP2-P-O3'	16.78	142.12	105.20
2	D	24	DT	C6-C5-C7	-11.66	115.91	122.90
2	D	24	DT	C4-C5-C7	11.26	125.75	119.00
1	C	16[A]	DG	OP2-P-O3'	11.12	129.67	105.20
1	C	16[B]	DG	OP2-P-O3'	11.12	129.67	105.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	18[B]	DA	P-O3'-C3'	10.88	132.75	119.70
3	A	301	ARG	NE-CZ-NH1	9.81	125.20	120.30
2	D	21	DT	C1'-O4'-C4'	-9.72	100.38	110.10
3	A	279	SER	N-CA-C	9.56	136.80	111.00
1	C	20	DG	C4-N9-C1'	-9.53	114.11	126.50
1	C	4	DA	O4'-C1'-N9	8.77	114.14	108.00
1	C	20	DG	C8-N9-C1'	8.39	137.91	127.00
3	A	299	MET	CG-SD-CE	-8.29	86.94	100.20
2	D	4	DA	O4'-C1'-N9	7.85	113.50	108.00
3	A	306	ILE	C-N-CD	-7.82	103.40	120.60
3	B	326	ARG	N-CA-C	7.44	131.08	111.00
3	A	318	VAL	N-CA-C	7.29	130.68	111.00
2	D	21	DT	N3-C4-O4	-7.24	115.56	119.90
1	C	18[B]	DA	O4'-C1'-N9	7.21	113.05	108.00
3	B	328	LEU	CB-CG-CD1	7.19	123.22	111.00
2	D	18[A]	DA	O4'-C4'-C3'	-7.09	101.66	104.50
2	D	18[B]	DA	O4'-C4'-C3'	-7.09	101.66	104.50
2	D	8	DC	P-O5'-C5'	-7.07	109.58	120.90
1	C	32	DT	P-O5'-C5'	-6.97	109.75	120.90
1	C	16[A]	DG	O3'-P-O5'	-6.84	91.00	104.00
1	C	16[B]	DG	O3'-P-O5'	-6.84	91.00	104.00
2	D	8	DC	O4'-C1'-N1	-6.77	103.26	108.00
1	C	3	DA	O4'-C1'-N9	-6.60	103.38	108.00
2	D	21	DT	P-O5'-C5'	-6.55	110.42	120.90
2	D	25	DA	O4'-C1'-N9	-6.52	103.44	108.00
3	A	217	VAL	N-CA-C	6.49	128.53	111.00
1	C	8	DC	O4'-C1'-N1	6.40	112.48	108.00
2	D	24	DT	P-O3'-C3'	6.28	127.23	119.70
1	C	17[B]	DT	O4'-C1'-N1	6.12	112.29	108.00
1	C	28	DA	O4'-C1'-N9	6.07	112.25	108.00
1	C	5	DG	P-O3'-C3'	-6.06	112.43	119.70
2	D	17[A]	DT	O4'-C1'-N1	6.04	112.22	108.00
2	D	17[B]	DT	O4'-C1'-N1	6.04	112.22	108.00
2	D	16[A]	DA	P-O3'-C3'	5.96	126.85	119.70
2	D	16[B]	DA	P-O3'-C3'	5.96	126.85	119.70
2	D	5	DC	O4'-C1'-N1	-5.86	103.90	108.00
3	A	216	GLY	N-CA-C	-5.82	98.55	113.10
3	A	280	GLY	N-CA-C	-5.77	98.68	113.10
2	D	20	DA	P-O3'-C3'	-5.76	112.78	119.70
3	B	318	VAL	N-CA-C	5.71	126.42	111.00
1	C	3	DA	N1-C2-N3	5.64	132.12	129.30
3	B	338	LEU	N-CA-C	-5.59	95.90	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	309	ILE	CB-CA-C	5.55	122.70	111.60
2	D	2	DT	P-O3'-C3'	5.51	126.31	119.70
2	D	6	DT	C6-C5-C7	-5.39	119.67	122.90
1	C	14	DA	C3'-C2'-C1'	-5.33	96.10	102.50
1	C	33	DA	O4'-C1'-N9	-5.32	104.28	108.00
1	C	7	DT	P-O3'-C3'	5.31	126.07	119.70
3	B	282	ARG	NE-CZ-NH1	5.25	122.93	120.30
2	D	34	DT	C6-C5-C7	-5.22	119.77	122.90
3	A	301	ARG	NH1-CZ-NH2	5.21	125.13	119.40
2	D	18[A]	DA	P-O5'-C5'	-5.16	112.65	120.90
2	D	18[B]	DA	P-O5'-C5'	-5.16	112.65	120.90
3	A	198	GLY	N-CA-C	-5.15	100.23	113.10
1	C	17[B]	DT	P-O3'-C3'	-5.14	113.53	119.70
1	C	6	DT	O4'-C1'-N1	-5.14	104.40	108.00
3	A	319	ASN	N-CA-CB	5.12	119.81	110.60
3	A	170	THR	N-CA-C	5.11	124.80	111.00
3	A	200	THR	CA-CB-CG2	-5.04	105.35	112.40
1	C	24	DT	P-O3'-C3'	5.03	125.74	119.70
2	D	7	DT	O4'-C1'-N1	-5.03	104.48	108.00
3	A	319	ASN	N-CA-C	-5.01	97.48	111.00
1	C	3	DA	C5-C6-N6	-5.00	119.70	123.70

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	217	VAL	CA

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	740	0	413	45	0
2	D	771	0	433	69	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	2562	0	2583	270	0
3	B	2527	0	2555	212	0
4	A	59	0	0	5	0
4	B	124	0	0	11	0
4	C	20	0	0	3	0
4	D	34	0	0	0	0
All	All	6837	0	5984	533	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 43.

All (533) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:18[B]:DA:H1'	1:C:19[B]:DT:H5''	1.19	1.16
2:D:16[B]:DA:H1'	2:D:17[B]:DT:H5''	1.23	1.15
3:A:188:THR:HG21	3:A:194:LEU:HG	1.22	1.07
2:D:33:DA:H2''	2:D:34:DT:H5''	1.33	1.06
3:A:309:ILE:HG22	3:A:321:VAL:HG11	1.35	1.04
3:B:173:ARG:HG2	3:B:289:HIS:HE1	1.24	0.99
1:C:4:DA:H2''	1:C:5:DG:H5''	1.47	0.97
2:D:18[A]:DA:H5''	2:D:18[A]:DA:C8	2.03	0.94
2:D:18[A]:DA:H5''	2:D:18[A]:DA:H8	1.30	0.93
3:B:320:ILE:H	3:B:320:ILE:HD13	1.34	0.91
3:B:328:LEU:H	3:B:328:LEU:HD12	1.36	0.90
1:C:28:DA:H2''	1:C:29:DA:C8	2.07	0.90
3:A:206:THR:HB	3:B:328:LEU:HD23	1.54	0.90
2:D:16[A]:DA:H2''	2:D:17[A]:DT:C7	2.03	0.89
3:A:200:THR:HG21	3:A:206:THR:HG23	1.52	0.89
3:A:195:ILE:HG22	3:A:197:ILE:HG22	1.56	0.88
3:A:62:LYS:HE2	3:A:62:LYS:HA	1.54	0.87
3:A:188:THR:HG21	3:A:194:LEU:CG	2.05	0.87
3:A:159:ARG:HB2	3:A:224:TRP:CZ3	2.10	0.86
3:B:320:ILE:HG12	3:B:321:VAL:H	1.40	0.86
3:A:194:LEU:HD13	3:A:210:GLU:HG2	1.56	0.86
3:A:158:ILE:HD11	3:A:224:TRP:HA	1.55	0.85
3:A:163:PHE:CE1	3:A:261:LEU:HD22	2.11	0.85
3:B:313:GLY:HA3	3:B:315:TRP:CZ3	2.12	0.85
3:A:213:LEU:HB3	3:A:217:VAL:CG2	2.08	0.84
3:B:173:ARG:HG2	3:B:289:HIS:CE1	2.12	0.84
3:A:200:THR:HG21	3:A:206:THR:CG2	2.08	0.83
3:A:310:MET:HA	3:A:321:VAL:HG21	1.59	0.83
1:C:16[B]:DG:H2''	1:C:17[B]:DT:H5''	1.59	0.83

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:A:213:LEU:HB3	3:A:217:VAL:HG22	1.60	0.83
3:B:315:TRP:NE1	3:B:320:ILE:HG13	1.93	0.83
3:A:236:ASN:HA	3:A:252:ALA:HA	1.61	0.83
1:C:18[B]:DA:H1'	1:C:19[B]:DT:C5'	2.07	0.82
1:C:28:DA:H2''	1:C:29:DA:H8	1.45	0.82
3:A:158:ILE:CD1	3:A:224:TRP:HA	2.10	0.81
3:B:279:SER:HB2	3:B:281:GLN:HG3	1.62	0.81
3:A:203:LEU:HA	3:B:130:ARG:HD2	1.63	0.80
3:A:90:GLN:NE2	3:A:94:GLN:HE21	1.79	0.80
2:D:33:DA:C2'	2:D:34:DT:H5''	2.12	0.80
1:C:18[B]:DA:C1'	1:C:19[B]:DT:H5''	2.08	0.79
3:A:177:ILE:HA	3:A:180:ILE:CD1	2.11	0.79
3:B:84:ALA:HB3	3:B:87:THR:CG2	2.12	0.78
1:C:9:DG:N7	3:B:43:LYS:NZ	2.29	0.78
3:B:277:ASP:HB2	3:B:284:LEU:HD13	1.65	0.78
1:C:12:DT:OP2	3:B:87:THR:HG21	1.83	0.78
3:B:217:VAL:O	3:B:221:VAL:HG23	1.84	0.78
3:A:172:LEU:HD21	3:A:197:ILE:HD13	1.64	0.76
2:D:5:DC:H2'	2:D:6:DT:C6	2.20	0.76
3:A:209:VAL:HG22	3:A:210:GLU:H	1.51	0.75
3:A:194:LEU:HD22	3:A:210:GLU:HG2	1.69	0.75
3:A:258:THR:O	3:A:262:GLU:HG3	1.85	0.75
1:C:16[B]:DG:H2''	1:C:17[B]:DT:C5'	2.17	0.74
3:A:206:THR:CB	3:B:328:LEU:HD23	2.17	0.74
3:B:233:ASP:O	3:B:236:ASN:HB2	1.87	0.74
3:B:125:VAL:HG21	4:B:407:HOH:O	1.87	0.74
3:B:193:MET:CE	3:B:221:VAL:HG11	2.17	0.73
3:A:245:ASN:ND2	3:A:247:VAL:H	1.86	0.73
3:B:85:VAL:O	3:B:89:GLN:HG3	1.88	0.73
2:D:17[A]:DT:H3'	3:B:121:ARG:NE	2.04	0.72
3:B:193:MET:HE3	3:B:221:VAL:HG11	1.71	0.72
3:A:139:ARG:HH12	3:B:339:LEU:HA	1.55	0.72
3:A:309:ILE:HG22	3:A:321:VAL:CG1	2.15	0.72
3:A:318:VAL:HG12	3:A:319:ASN:H	1.55	0.72
3:A:212:ALA:O	3:A:213:LEU:HD23	1.89	0.72
2:D:17[A]:DT:OP2	3:A:202:THR:HA	1.89	0.72
3:A:194:LEU:CD1	3:A:210:GLU:HG2	2.19	0.72
3:B:289:HIS:ND1	4:B:363:HOH:O	2.23	0.72
3:A:177:ILE:HA	3:A:180:ILE:HD12	1.71	0.72
2:D:12:DT:H2''	2:D:13:DA:C8	2.25	0.71
3:A:185:ILE:HG23	3:A:193:MET:HG2	1.72	0.71
3:A:197:ILE:HD11	3:A:199:ARG:CB	2.21	0.71

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:A:301:ARG:NH2	4:A:388:HOH:O	2.15	0.71
3:B:310:MET:SD	3:B:318:VAL:HG12	2.31	0.71
1:C:5:DG:H2'	1:C:6:DT:H72	1.73	0.71
2:D:18[B]:DA:C2'	2:D:19[B]:DC:H5''	2.21	0.70
3:A:197:ILE:HD12	3:A:198:GLY:H	1.55	0.70
3:A:197:ILE:CG1	3:A:198:GLY:H	2.05	0.70
3:B:125:VAL:HG23	3:B:126:ASP:N	2.07	0.69
3:A:194:LEU:HD22	3:A:210:GLU:CG	2.22	0.69
3:A:310:MET:HA	3:A:321:VAL:CG2	2.20	0.69
2:D:23:DA:H5'	3:B:201:LYS:CG	2.22	0.69
3:A:195:ILE:HG22	3:A:197:ILE:CG2	2.23	0.68
3:B:315:TRP:CD1	3:B:320:ILE:HG13	2.28	0.68
3:A:159:ARG:HB2	3:A:224:TRP:CE3	2.28	0.68
3:A:141:ASP:O	3:A:145:VAL:HG23	1.93	0.68
3:A:169:ASN:HA	3:B:339:LEU:HD11	1.76	0.68
2:D:16[A]:DA:H2''	2:D:17[A]:DT:H71	1.76	0.68
3:A:310:MET:CA	3:A:321:VAL:HG21	2.24	0.68
3:B:320:ILE:HG12	3:B:321:VAL:N	2.08	0.68
3:A:158:ILE:HD11	3:A:227:VAL:HG22	1.75	0.68
3:B:90:GLN:HE21	3:B:94:GLN:HE21	1.42	0.68
3:A:309:ILE:C	3:A:321:VAL:HG21	2.15	0.68
3:A:194:LEU:HD13	3:A:210:GLU:CG	2.24	0.67
3:A:326:ARG:HG3	3:A:327:ASN:N	2.10	0.67
3:B:19:THR:O	3:B:21:ASP:N	2.27	0.67
3:A:199:ARG:HH21	3:A:313:GLY:HA2	1.59	0.67
3:A:158:ILE:HD11	3:A:227:VAL:CG2	2.25	0.67
3:A:202:THR:O	3:B:130:ARG:NE	2.28	0.67
2:D:32:DT:H2''	2:D:33:DA:C8	2.30	0.67
3:A:197:ILE:CD1	3:A:198:GLY:H	2.08	0.67
1:C:15:DT:H4'	3:B:202:THR:CG2	2.25	0.67
2:D:21:DT:OP2	3:B:100:ARG:NH2	2.28	0.66
3:B:276:LYS:NZ	4:B:434:HOH:O	2.28	0.66
3:A:310:MET:HB2	3:A:318:VAL:HG22	1.77	0.66
3:A:18:ALA:HB3	3:A:104:LEU:CD2	2.25	0.66
3:A:307:PRO:O	3:A:309:ILE:N	2.26	0.65
3:A:142:PHE:O	3:A:146:ARG:HB2	1.96	0.65
3:B:146:ARG:O	3:B:150:GLU:HB2	1.96	0.65
1:C:27:DG:N3	4:C:53:HOH:O	2.28	0.65
3:A:24:ARG:O	3:A:28:MET:HG3	1.95	0.65
3:A:199:ARG:CB	3:A:199:ARG:HH11	2.08	0.65
3:A:194:LEU:CD2	3:A:210:GLU:HG2	2.27	0.65
3:B:319:ASN:OD1	3:B:319:ASN:N	2.30	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:A:197:ILE:HD11	3:A:199:ARG:HB3	1.79	0.65
3:A:197:ILE:HD11	3:A:199:ARG:HD2	1.79	0.65
3:A:172:LEU:CD2	3:A:197:ILE:HD13	2.26	0.65
3:A:199:ARG:HH22	3:A:292:ARG:NH1	1.95	0.65
1:C:19[A]:DT:H2''	1:C:20:DG:C8	2.32	0.65
3:A:197:ILE:HD11	3:A:199:ARG:CG	2.27	0.65
3:A:277:ASP:N	3:A:277:ASP:OD1	2.29	0.64
3:B:203:LEU:CD1	3:B:205:SER:HB3	2.27	0.64
3:A:340:GLU:O	3:A:341:ASP:HB2	1.96	0.64
3:B:193:MET:HG3	3:B:218:THR:HG23	1.80	0.64
2:D:23:DA:H5'	3:B:201:LYS:HG3	1.77	0.64
1:C:14:DA:N7	3:B:86:LYS:NZ	2.41	0.64
3:A:318:VAL:HG12	3:A:319:ASN:N	2.12	0.64
3:B:320:ILE:N	3:B:320:ILE:HD13	2.09	0.64
1:C:16[B]:DG:C2'	1:C:17[B]:DT:H5''	2.24	0.64
1:C:10:DT:OP2	3:B:50:ARG:NH1	2.30	0.64
3:A:203:LEU:O	3:B:130:ARG:HD2	1.97	0.64
2:D:16[A]:DA:H4'	2:D:17[A]:DT:OP1	1.97	0.64
1:C:5:DG:H2'	1:C:6:DT:C7	2.28	0.64
3:A:214:SER:HB2	3:A:216:GLY:H	1.62	0.64
2:D:33:DA:H2''	2:D:34:DT:C5'	2.21	0.64
3:B:231:ALA:HB3	4:B:415:HOH:O	1.98	0.64
3:A:202:THR:OG1	3:A:205:SER:HB2	1.97	0.63
2:D:14:DG:H2''	2:D:15:DC:H6	1.62	0.63
2:D:16[B]:DA:H2''	2:D:17[B]:DT:OP2	1.98	0.63
3:A:199:ARG:HH22	3:A:292:ARG:HH12	1.45	0.63
3:A:321:VAL:O	3:A:325:ILE:HG12	1.97	0.63
3:A:256:LEU:HD22	3:A:260:ALA:CB	2.27	0.63
2:D:18[B]:DA:H2''	2:D:19[B]:DC:C4'	2.29	0.63
3:A:154:ARG:HB2	3:A:157:ASP:HB2	1.79	0.63
3:B:203:LEU:HD12	3:B:205:SER:HB3	1.80	0.63
3:A:204:VAL:HG13	3:B:131:ALA:HB3	1.79	0.63
1:C:21:DC:H2''	1:C:22:DT:O5'	1.97	0.63
1:C:16[B]:DG:H5'	3:B:202:THR:HB	1.81	0.63
3:B:42:TRP:O	3:B:46:LEU:HD22	1.98	0.63
3:A:90:GLN:NE2	3:A:94:GLN:NE2	2.46	0.63
3:B:238:LEU:O	3:B:238:LEU:HD12	1.99	0.63
3:A:206:THR:O	3:B:130:ARG:HG2	1.98	0.63
3:B:320:ILE:H	3:B:320:ILE:CD1	2.11	0.63
2:D:18[B]:DA:H2''	2:D:19[B]:DC:O4'	1.99	0.63
3:A:192:ARG:NH2	3:B:340:GLU:OE2	2.31	0.62
3:B:326:ARG:HH11	3:B:326:ARG:HG3	1.64	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:A:139:ARG:NH1	3:B:339:LEU:HA	2.14	0.62
1:C:14:DA:N3	3:B:201:LYS:NZ	2.44	0.62
3:B:90:GLN:NE2	3:B:94:GLN:HE21	1.98	0.62
2:D:18[A]:DA:H2''	2:D:19[A]:DC:H5''	1.81	0.62
3:B:209:VAL:HG12	3:B:210:GLU:N	2.14	0.62
3:A:225:ILE:HG12	3:A:230:VAL:HG12	1.81	0.62
3:A:228:SER:OG	3:A:230:VAL:HB	1.98	0.62
3:A:133:GLN:NE2	3:A:323:ASN:O	2.31	0.62
3:A:297:ARG:NH1	3:A:327:ASN:OD1	2.31	0.62
3:B:172:LEU:HD11	3:B:197:ILE:HD11	1.82	0.62
3:B:183:LYS:HG3	3:B:234:PRO:O	2.00	0.62
3:A:199:ARG:HB3	3:A:199:ARG:HH11	1.65	0.61
3:B:328:LEU:N	3:B:328:LEU:HD12	2.10	0.61
3:A:212:ALA:C	3:A:213:LEU:HD23	2.20	0.61
3:A:206:THR:HB	3:B:328:LEU:CD2	2.28	0.61
3:B:129:GLU:O	3:B:130:ARG:HD3	2.01	0.61
3:B:79:GLN:HG3	3:B:120:ILE:HG23	1.81	0.61
3:A:219:LYS:O	3:A:222:GLU:N	2.29	0.61
3:A:146:ARG:O	3:A:150:GLU:HG2	2.01	0.61
3:A:139:ARG:NH2	3:B:339:LEU:HD23	2.15	0.61
3:A:181:ARG:HA	3:A:237:TYR:HA	1.83	0.61
3:B:326:ARG:CB	3:B:328:LEU:HD13	2.31	0.61
3:A:139:ARG:CZ	3:B:339:LEU:HD23	2.30	0.61
3:A:203:LEU:CA	3:B:130:ARG:HD2	2.30	0.61
2:D:16[A]:DA:H2''	2:D:17[A]:DT:H73	1.82	0.60
3:B:305:SER:O	3:B:308:GLU:N	2.32	0.60
3:A:203:LEU:CD1	3:B:129:GLU:HG2	2.31	0.60
3:A:88:ILE:HG22	3:A:117:MET:CE	2.32	0.60
3:B:84:ALA:HB3	3:B:87:THR:HG22	1.83	0.59
2:D:2:DT:O2	3:A:244:LYS:NZ	2.34	0.59
3:A:225:ILE:HD11	3:A:238:LEU:CD1	2.32	0.59
3:A:209:VAL:HG23	3:B:328:LEU:N	2.17	0.59
2:D:4:DA:H2''	2:D:5:DC:H5''	1.84	0.59
3:A:192:ARG:HD2	3:A:213:LEU:O	2.03	0.59
3:A:315:TRP:O	3:A:317:ASN:N	2.34	0.59
3:B:128:GLY:O	3:B:130:ARG:NH1	2.35	0.59
3:A:169:ASN:HD22	3:A:170:THR:HG22	1.66	0.59
3:A:26:ASN:ND2	3:A:102:SER:O	2.29	0.59
3:B:183:LYS:N	3:B:234:PRO:O	2.30	0.58
3:B:81:ARG:NH1	4:B:426:HOH:O	2.35	0.58
1:C:15:DT:H4'	3:B:202:THR:HG21	1.85	0.58
3:A:236:ASN:HA	3:A:252:ALA:CA	2.30	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:A:197:ILE:HD11	3:A:199:ARG:CD	2.33	0.58
3:B:193:MET:CG	3:B:218:THR:HG23	2.34	0.58
3:A:171:LEU:HD11	3:A:295:ALA:HB1	1.85	0.58
1:C:27:DG:H1'	4:C:53:HOH:O	2.04	0.58
3:B:188:THR:O	3:B:189:ASP:HB2	2.03	0.58
3:A:194:LEU:CG	3:A:210:GLU:HG2	2.33	0.58
3:A:224:TRP:CE2	3:A:228:SER:HB3	2.39	0.58
3:A:299:MET:C	3:A:309:ILE:HD11	2.24	0.57
3:A:185:ILE:CG2	3:A:193:MET:HG2	2.34	0.57
2:D:18[A]:DA:H2''	2:D:19[A]:DC:C5'	2.33	0.57
3:B:322:MET:O	3:B:326:ARG:HD2	2.05	0.57
3:A:213:LEU:HB3	3:A:217:VAL:HG23	1.86	0.57
3:B:19:THR:O	3:B:22:GLU:N	2.37	0.57
3:A:39:GLU:O	3:A:43:LYS:HG2	2.04	0.57
3:A:214:SER:O	3:A:218:THR:HG22	2.05	0.57
3:B:179:ARG:HG2	3:B:255:GLN:NE2	2.20	0.57
3:B:318:VAL:O	3:B:322:MET:HG2	2.04	0.57
3:B:326:ARG:HB2	3:B:328:LEU:HD13	1.85	0.57
3:A:195:ILE:O	3:A:197:ILE:HG23	2.04	0.57
3:A:245:ASN:N	3:A:245:ASN:HD22	2.03	0.57
3:A:318:VAL:CG1	3:A:319:ASN:H	2.17	0.56
3:B:313:GLY:HA3	3:B:315:TRP:CE3	2.40	0.56
3:A:199:ARG:HH21	3:A:313:GLY:CA	2.18	0.56
3:A:158:ILE:HG12	3:A:227:VAL:HG21	1.87	0.56
3:A:318:VAL:HG11	3:A:322:MET:CE	2.35	0.56
3:B:84:ALA:O	3:B:87:THR:HG23	2.04	0.56
1:C:9:DG:H2''	1:C:10:DT:C6	2.41	0.56
2:D:23:DA:H5'	3:B:201:LYS:CB	2.35	0.56
3:A:269:HIS:HB2	3:A:286:TRP:CE3	2.40	0.56
3:A:209:VAL:HG13	3:A:210:GLU:N	2.19	0.56
1:C:32:DT:H2''	1:C:33:DA:C8	2.41	0.56
3:B:138:GLU:HG3	4:B:377:HOH:O	2.05	0.56
3:B:106:ARG:O	3:B:109:ASP:HB2	2.06	0.56
3:A:181:ARG:HG2	3:A:236:ASN:O	2.06	0.56
3:B:203:LEU:HD23	4:B:445:HOH:O	2.05	0.56
3:B:140:THR:O	3:B:144:GLN:HG3	2.05	0.56
2:D:19[B]:DC:H2''	2:D:20:DA:O5'	2.06	0.55
3:A:172:LEU:HD21	3:A:197:ILE:CD1	2.33	0.55
3:A:119:ARG:O	3:A:123:GLU:HG3	2.06	0.55
3:A:194:LEU:HB3	3:A:210:GLU:CG	2.36	0.55
3:A:92:LEU:HD12	3:A:117:MET:HG2	1.87	0.55
3:A:245:ASN:HD22	3:A:246:GLY:N	2.04	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:A:18:ALA:HB3	3:A:104:LEU:HD23	1.88	0.55
3:A:315:TRP:HE1	3:A:320:ILE:HG21	1.69	0.55
3:A:315:TRP:HZ2	3:A:324:TYR:HE1	1.53	0.55
1:C:10:DT:H73	3:B:43:LYS:HD3	1.89	0.55
3:A:256:LEU:HD22	3:A:260:ALA:HB3	1.88	0.55
3:A:196:HIS:HA	3:A:209:VAL:O	2.06	0.55
3:A:315:TRP:CZ2	3:A:324:TYR:HE1	2.25	0.55
3:A:291:ALA:HB3	4:A:356:HOH:O	2.07	0.55
3:B:279:SER:OG	3:B:281:GLN:NE2	2.33	0.55
2:D:23:DA:H2'	2:D:24:DT:C6	2.41	0.55
3:A:299:MET:O	3:A:309:ILE:HD11	2.07	0.54
3:A:306:ILE:HA	3:A:309:ILE:HB	1.87	0.54
2:D:21:DT:OP2	3:B:97:MET:HG3	2.08	0.54
3:B:52:TRP:HZ3	3:B:74:TYR:HB2	1.72	0.54
3:A:213:LEU:HD13	3:A:217:VAL:HG23	1.89	0.54
3:B:125:VAL:HG23	3:B:126:ASP:H	1.73	0.54
3:B:97:MET:HG2	3:B:101:ARG:HG3	1.89	0.54
3:A:96:ASN:OD1	3:A:107:PRO:HD2	2.08	0.54
3:B:337:ARG:O	3:B:341:ASP:N	2.37	0.54
3:B:279:SER:HB2	3:B:281:GLN:CG	2.35	0.54
3:A:72:ARG:HH11	3:A:72:ARG:HG2	1.73	0.54
3:A:192:ARG:O	3:A:193:MET:HB2	2.07	0.54
3:A:186:SER:O	3:A:187:ARG:HD3	2.08	0.53
3:A:211:LYS:HE3	4:A:360:HOH:O	2.08	0.53
3:A:276:LYS:HE3	3:A:284:LEU:HB2	1.90	0.53
3:B:336:VAL:O	3:B:340:GLU:HB2	2.08	0.53
3:B:128:GLY:O	3:B:129:GLU:C	2.47	0.53
3:B:326:ARG:HH11	3:B:326:ARG:CG	2.22	0.53
3:B:276:LYS:HE2	4:B:398:HOH:O	2.09	0.53
3:B:305:SER:OG	3:B:308:GLU:HB2	2.09	0.53
3:A:235:ASN:H	3:A:235:ASN:HD22	1.54	0.53
3:A:159:ARG:HG3	3:A:224:TRP:CE2	2.44	0.53
3:B:306:ILE:HG22	3:B:307:PRO:N	2.24	0.52
3:A:35:GLN:HG3	4:A:382:HOH:O	2.09	0.52
2:D:15:DC:OP2	3:A:315:TRP:NE1	2.41	0.52
3:A:177:ILE:HA	3:A:180:ILE:HD11	1.88	0.52
3:A:138:GLU:O	3:A:141:ASP:HB2	2.10	0.52
3:B:225:ILE:CG2	3:B:231:ALA:HB2	2.39	0.52
2:D:7:DT:H2''	2:D:8:DC:H5'	1.90	0.52
3:A:307:PRO:C	3:A:309:ILE:H	2.11	0.52
3:B:326:ARG:HB3	3:B:328:LEU:CD1	2.40	0.52
3:A:197:ILE:HD12	3:A:198:GLY:C	2.30	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:D:7:DT:O4	3:A:259:ARG:HG2	2.10	0.52
2:D:7:DT:H2''	2:D:8:DC:C5'	2.39	0.52
3:B:68:PRO:HB3	3:B:110:SER:OG	2.09	0.52
3:A:181:ARG:NH1	3:A:235:ASN:O	2.38	0.52
3:A:185:ILE:HG21	3:A:193:MET:SD	2.50	0.52
3:A:194:LEU:HD21	3:A:212:ALA:HB2	1.92	0.52
2:D:2:DT:H2''	2:D:3:DA:C8	2.44	0.52
3:B:306:ILE:N	3:B:307:PRO:HD2	2.25	0.52
3:B:278:ASP:OD1	3:B:278:ASP:N	2.43	0.52
1:C:13:DA:H5''	3:B:132:LYS:O	2.09	0.52
3:B:173:ARG:HB2	3:B:176:GLU:OE2	2.11	0.51
3:A:96:ASN:ND2	3:A:108:SER:OG	2.29	0.51
3:B:25:LYS:O	3:B:25:LYS:HG2	2.09	0.51
3:B:143:ASP:O	3:B:147:SER:HB3	2.10	0.51
3:A:306:ILE:HG22	3:A:306:ILE:O	2.09	0.51
3:A:309:ILE:O	3:A:321:VAL:HG21	2.10	0.51
3:B:340:GLU:O	3:B:341:ASP:HB2	2.09	0.51
2:D:11:DA:OP1	3:A:81:ARG:NH2	2.29	0.51
2:D:12:DT:H2''	2:D:13:DA:H8	1.73	0.51
3:A:128:GLY:O	3:A:130:ARG:HG2	2.09	0.51
3:A:310:MET:N	3:A:321:VAL:HG21	2.25	0.51
2:D:18[B]:DA:O5'	2:D:18[B]:DA:H8	1.93	0.51
2:D:32:DT:H2''	2:D:33:DA:N7	2.26	0.51
3:A:306:ILE:HG22	3:A:310:MET:CG	2.41	0.51
3:A:319:ASN:HD22	3:A:319:ASN:C	2.09	0.51
3:A:201:LYS:NZ	3:B:130:ARG:HH22	2.09	0.51
3:B:320:ILE:HG12	3:B:321:VAL:HG23	1.93	0.51
3:A:158:ILE:CG1	3:A:227:VAL:HG21	2.41	0.51
3:A:194:LEU:HD13	3:A:210:GLU:CD	2.31	0.51
3:B:328:LEU:N	3:B:328:LEU:CD1	2.73	0.51
1:C:4:DA:C2'	1:C:5:DG:H5''	2.29	0.51
2:D:18[B]:DA:H2''	2:D:19[B]:DC:C5'	2.41	0.51
3:B:128:GLY:O	3:B:129:GLU:O	2.29	0.50
3:A:299:MET:HG3	3:B:338:LEU:HD12	1.92	0.50
2:D:15:DC:H2'	2:D:16[B]:DA:N7	2.26	0.50
2:D:18[B]:DA:H2''	2:D:19[B]:DC:H5''	1.91	0.50
3:A:170:THR:O	3:A:171:LEU:HB2	2.11	0.50
3:B:179:ARG:HG2	3:B:255:GLN:HE22	1.76	0.50
3:A:217:VAL:HA	3:A:220:LEU:HD12	1.93	0.50
3:B:183:LYS:NZ	3:B:235:ASN:OD1	2.29	0.50
2:D:23:DA:H2'	2:D:24:DT:C7	2.42	0.50
3:B:39:GLU:HG3	3:B:40:HIS:N	2.26	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:A:168:TYR:CE2	3:B:339:LEU:HD21	2.47	0.50
3:A:51:SER:HG	3:A:74:TYR:HH	1.55	0.50
2:D:14:DG:C4	2:D:15:DC:C6	3.00	0.50
3:B:179:ARG:NH2	3:B:199:ARG:O	2.41	0.49
3:A:306:ILE:O	3:A:310:MET:HG3	2.11	0.49
3:B:209:VAL:HG12	3:B:210:GLU:H	1.75	0.49
3:A:75:LEU:HD11	3:A:92:LEU:HG	1.94	0.49
3:B:154:ARG:O	3:B:158:ILE:HG13	2.12	0.49
2:D:21:DT:H2'	2:D:22:DT:H71	1.94	0.49
1:C:1:DA:H8	1:C:1:DA:O5'	1.94	0.49
3:A:309:ILE:C	3:A:311:GLN:H	2.15	0.49
3:A:315:TRP:CD1	3:A:320:ILE:HB	2.46	0.49
2:D:17[B]:DT:H6	2:D:17[B]:DT:H5'	1.76	0.49
1:C:16[A]:DG:O5'	3:B:316:THR:OG1	2.31	0.49
3:A:201:LYS:CE	3:A:201:LYS:HA	2.43	0.49
3:A:319:ASN:O	3:A:323:ASN:N	2.39	0.49
3:A:171:LEU:O	3:A:292:ARG:HD2	2.12	0.49
3:B:276:LYS:O	3:B:277:ASP:O	2.30	0.49
2:D:15:DC:H2''	2:D:16[B]:DA:C8	2.47	0.49
3:A:62:LYS:CE	3:A:62:LYS:HA	2.31	0.49
3:A:203:LEU:HA	3:B:130:ARG:CD	2.40	0.49
3:A:205:SER:HB3	3:A:206:THR:HG23	1.94	0.49
3:A:306:ILE:HG22	3:A:310:MET:HG2	1.93	0.49
3:B:277:ASP:CB	3:B:284:LEU:HD13	2.37	0.49
3:B:92:LEU:HD12	3:B:117:MET:HG2	1.95	0.49
2:D:17[A]:DT:H2''	2:D:18[A]:DA:N7	2.28	0.48
3:A:197:ILE:HG13	3:A:198:GLY:H	1.78	0.48
3:A:158:ILE:HD12	3:A:224:TRP:HA	1.93	0.48
3:A:277:ASP:HB2	3:A:278:ASP:H	1.31	0.48
3:A:311:GLN:O	3:A:314:GLY:N	2.46	0.48
3:B:322:MET:HE2	3:B:326:ARG:HH22	1.78	0.48
3:A:200:THR:HG21	3:A:206:THR:HG21	1.93	0.48
3:A:158:ILE:HG13	3:A:159:ARG:N	2.29	0.48
3:B:306:ILE:HG22	3:B:307:PRO:HD3	1.95	0.48
3:B:297:ARG:O	3:B:300:ALA:N	2.47	0.48
3:A:318:VAL:HG11	3:A:322:MET:HE2	1.94	0.48
1:C:1:DA:H2''	1:C:2:DT:O5'	2.13	0.48
3:A:193:MET:HB2	3:A:218:THR:OG1	2.14	0.48
3:A:200:THR:CG2	3:A:206:THR:HG23	2.33	0.48
3:A:138:GLU:OE2	3:A:301:ARG:NH2	2.47	0.48
3:A:139:ARG:NH2	3:A:146:ARG:HH21	2.11	0.47
3:A:192:ARG:O	3:A:218:THR:OG1	2.33	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:B:338:LEU:O	3:B:341:ASP:OD1	2.33	0.47
3:A:310:MET:CB	3:A:318:VAL:HG22	2.43	0.47
3:A:299:MET:HA	3:B:338:LEU:HD11	1.96	0.47
2:D:15:DC:C2'	2:D:16[B]:DA:C8	2.97	0.47
3:B:320:ILE:CG1	3:B:321:VAL:H	2.19	0.47
3:B:276:LYS:HD2	3:B:284:LEU:HB2	1.95	0.47
3:B:304:VAL:CG1	3:B:308:GLU:HB3	2.45	0.47
1:C:33:DA:H2''	1:C:34:DT:OP2	2.14	0.47
3:A:203:LEU:C	3:B:130:ARG:HD2	2.34	0.47
3:A:197:ILE:CG1	3:A:198:GLY:N	2.77	0.47
3:B:134:ALA:HA	3:B:283:TYR:CD2	2.50	0.47
3:A:208:GLY:O	3:B:328:LEU:HA	2.15	0.47
1:C:15:DT:H4'	3:B:202:THR:HG22	1.96	0.47
3:A:177:ILE:CA	3:A:180:ILE:HD12	2.43	0.47
3:A:235:ASN:N	3:A:235:ASN:HD22	2.13	0.47
3:B:230:VAL:C	3:B:232:ASP:H	2.18	0.47
3:B:199:ARG:HB2	3:B:204:VAL:HG12	1.96	0.47
3:A:269:HIS:HA	3:A:286:TRP:CZ3	2.50	0.47
2:D:19[A]:DC:H2''	2:D:20:DA:O5'	2.14	0.47
3:B:326:ARG:NH1	3:B:326:ARG:CG	2.78	0.46
2:D:23:DA:C4'	3:B:201:LYS:HG3	2.45	0.46
3:A:219:LYS:O	3:A:220:LEU:C	2.51	0.46
3:B:333:GLY:N	3:B:336:VAL:HG23	2.31	0.46
1:C:15:DT:H2''	1:C:16[A]:DG:N7	2.31	0.46
1:C:16[A]:DG:H5'	3:B:202:THR:HB	1.95	0.46
3:A:245:ASN:N	3:A:245:ASN:ND2	2.62	0.46
3:B:297:ARG:O	3:B:298:ASP:C	2.53	0.46
3:B:319:ASN:O	3:B:322:MET:HB2	2.16	0.46
3:B:84:ALA:HB3	3:B:87:THR:HG23	1.95	0.46
3:B:282:ARG:O	3:B:283:TYR:HB2	2.14	0.46
3:A:319:ASN:ND2	3:A:319:ASN:O	2.31	0.46
3:A:299:MET:HB3	3:A:299:MET:HE3	1.37	0.46
3:A:318:VAL:HG11	3:A:322:MET:HE1	1.97	0.46
3:A:85:VAL:HG23	3:A:129:GLU:OE2	2.15	0.46
3:B:247:VAL:HG12	3:B:248:ALA:O	2.16	0.46
2:D:17[A]:DT:H3'	3:B:121:ARG:CD	2.45	0.46
3:A:197:ILE:HD12	3:A:198:GLY:N	2.28	0.46
3:B:279:SER:CB	3:B:281:GLN:HG3	2.40	0.46
3:A:245:ASN:H	3:A:245:ASN:ND2	2.14	0.46
1:C:25:DA:H5'	1:C:25:DA:H8	1.81	0.46
3:A:315:TRP:NE1	3:A:320:ILE:CG2	2.79	0.46
3:A:223:ARG:O	3:A:227:VAL:HG13	2.15	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:B:125:VAL:C	3:B:127:ALA:H	2.18	0.46
3:A:92:LEU:HD22	3:A:96:ASN:ND2	2.31	0.46
1:C:16[B]:DG:P	3:B:316:THR:HG1	2.39	0.45
3:B:279:SER:CB	3:B:281:GLN:NE2	2.79	0.45
3:B:326:ARG:HB3	3:B:328:LEU:HD13	1.98	0.45
3:A:201:LYS:HA	3:B:130:ARG:NH2	2.31	0.45
2:D:11:DA:H2''	2:D:12:DT:O5'	2.15	0.45
3:A:299:MET:HG3	3:B:338:LEU:CD1	2.46	0.45
3:A:209:VAL:HG22	3:A:210:GLU:N	2.26	0.45
3:B:193:MET:HE1	3:B:221:VAL:HG11	1.95	0.45
3:B:306:ILE:HG22	3:B:307:PRO:CD	2.46	0.45
3:B:269:HIS:HB2	3:B:286:TRP:CE3	2.52	0.45
3:A:206:THR:CG2	3:B:328:LEU:HD23	2.47	0.45
3:A:158:ILE:CD1	3:A:227:VAL:HG21	2.47	0.45
3:B:27:LEU:HD12	3:B:27:LEU:HA	1.70	0.45
3:A:201:LYS:HE3	3:A:201:LYS:HA	1.99	0.45
3:A:139:ARG:NH2	3:A:146:ARG:NH2	2.65	0.45
3:A:34:ARG:C	3:A:36:ALA:H	2.19	0.45
3:A:158:ILE:HD11	3:A:227:VAL:HG21	1.98	0.45
3:B:217:VAL:O	3:B:220:LEU:HB2	2.16	0.45
3:B:295:ALA:O	3:B:296:ALA:C	2.55	0.45
3:A:42:TRP:CE3	3:A:45:LEU:HD23	2.52	0.45
3:A:218:THR:CG2	3:A:219:LYS:N	2.81	0.44
3:B:333:GLY:N	3:B:336:VAL:CG2	2.79	0.44
2:D:23:DA:C5'	3:B:201:LYS:HG3	2.44	0.44
3:B:322:MET:HE2	3:B:326:ARG:NH2	2.32	0.44
3:B:297:ARG:O	3:B:299:MET:N	2.50	0.44
3:A:139:ARG:NH2	3:B:339:LEU:CD2	2.80	0.44
3:B:277:ASP:HB2	3:B:284:LEU:CD1	2.42	0.44
3:A:194:LEU:CD2	3:A:212:ALA:HB2	2.47	0.44
3:A:174:ILE:HD12	3:A:258:THR:HB	1.98	0.44
3:B:306:ILE:N	3:B:307:PRO:CD	2.80	0.44
3:B:249:ALA:N	3:B:250:PRO:HD3	2.32	0.44
2:D:22:DT:OP2	3:B:37:PHE:HB3	2.17	0.44
1:C:19[B]:DT:H2''	1:C:20:DG:C8	2.53	0.44
1:C:25:DA:H5'	1:C:25:DA:C8	2.53	0.44
3:A:299:MET:HB2	3:A:299:MET:HE2	1.63	0.43
2:D:16[B]:DA:O5'	2:D:16[B]:DA:H2'	2.18	0.43
3:A:161:LEU:HD23	3:A:161:LEU:HA	1.64	0.43
3:A:26:ASN:HB3	3:A:102:SER:HA	2.00	0.43
3:B:322:MET:CE	3:B:326:ARG:NH2	2.82	0.43
3:A:88:ILE:HG22	3:A:117:MET:HE1	2.01	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:B:299:MET:CE	3:B:312:ALA:HB2	2.48	0.43
3:A:310:MET:O	3:A:315:TRP:O	2.36	0.43
3:B:150:GLU:HG3	4:B:419:HOH:O	2.18	0.43
3:B:299:MET:HE1	3:B:312:ALA:HB2	2.01	0.43
3:A:31:PHE:O	3:A:34:ARG:HD3	2.18	0.43
3:B:145:VAL:HG13	3:B:149:MET:SD	2.58	0.43
3:B:159:ARG:HB2	3:B:224:TRP:CZ3	2.53	0.43
3:A:106:ARG:NH1	3:A:109:ASP:OD1	2.51	0.43
3:A:256:LEU:HD23	3:A:256:LEU:HA	1.72	0.43
2:D:16[A]:DA:H2''	2:D:17[A]:DT:C5	2.54	0.43
3:B:31:PHE:O	3:B:34:ARG:HG3	2.19	0.43
1:C:23:DA:H2'	1:C:24:DT:C6	2.54	0.43
3:B:289:HIS:CE1	4:B:363:HOH:O	2.69	0.43
1:C:5:DG:H2''	1:C:6:DT:O5'	2.18	0.43
3:B:279:SER:CB	3:B:281:GLN:HE21	2.31	0.43
3:A:33:ASP:OD1	3:B:119:ARG:NH1	2.43	0.43
3:B:333:GLY:O	3:B:337:ARG:HD3	2.19	0.43
3:A:225:ILE:HD11	3:A:238:LEU:HD11	2.01	0.43
3:B:125:VAL:CG2	3:B:126:ASP:N	2.77	0.43
3:A:332:THR:HG21	3:A:336:VAL:HG11	2.00	0.43
3:B:172:LEU:HD21	3:B:197:ILE:HG13	2.01	0.42
3:A:183:LYS:O	3:A:183:LYS:HD2	2.18	0.42
1:C:4:DA:H8	4:C:42:HOH:O	2.00	0.42
3:A:181:ARG:HG2	3:A:235:ASN:O	2.20	0.42
3:A:308:GLU:HG3	3:B:334:ALA:HB2	2.01	0.42
3:A:199:ARG:NH1	3:A:199:ARG:HB2	2.34	0.42
3:B:297:ARG:NE	3:B:324:TYR:O	2.51	0.42
3:B:337:ARG:HA	3:B:340:GLU:HB2	2.01	0.42
3:B:116:VAL:O	3:B:120:ILE:HG13	2.20	0.42
2:D:15:DC:H2'	2:D:16[A]:DA:N7	2.33	0.42
3:A:75:LEU:HD22	3:A:88:ILE:HG23	2.01	0.42
3:A:36:ALA:O	3:B:118:ARG:NH1	2.52	0.42
3:A:149:MET:O	3:A:152:SER:N	2.46	0.42
2:D:14:DG:C2'	2:D:15:DC:H6	2.28	0.42
3:B:297:ARG:HA	3:B:325:ILE:HG22	2.02	0.42
2:D:5:DC:H2'	2:D:6:DT:C5	2.53	0.42
2:D:5:DC:H2''	2:D:6:DT:H5'	2.00	0.42
3:A:24:ARG:HH11	3:A:24:ARG:HG3	1.84	0.42
3:A:302:ALA:O	3:A:303:GLY:O	2.36	0.42
3:A:26:ASN:O	3:A:29:ASP:HB2	2.20	0.42
3:B:188:THR:OG1	3:B:192:ARG:HB2	2.20	0.42
2:D:8:DC:H2''	2:D:9:DG:C8	2.55	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:B:245:ASN:OD1	3:B:247:VAL:HB	2.20	0.42
3:A:194:LEU:HB3	3:A:210:GLU:CD	2.39	0.41
3:A:168:TYR:OH	3:A:298:ASP:OD2	2.30	0.41
2:D:23:DA:H5'	4:B:388:HOH:O	2.20	0.41
3:B:85:VAL:HG11	3:B:121:ARG:HG3	2.01	0.41
1:C:9:DG:H2'	1:C:10:DT:H71	2.02	0.41
3:B:99:HIS:O	3:B:102:SER:HB2	2.20	0.41
3:B:71:VAL:O	3:B:74:TYR:HB3	2.19	0.41
3:A:272:ILE:CG2	3:A:273:TYR:CE1	3.03	0.41
3:A:186:SER:O	3:A:193:MET:HG3	2.20	0.41
3:A:209:VAL:HG21	3:B:327:ASN:CG	2.40	0.41
3:A:315:TRP:CZ2	3:A:324:TYR:CE1	3.07	0.41
1:C:17[B]:DT:H2'	1:C:17[B]:DT:H6	1.72	0.41
3:B:209:VAL:CG1	3:B:210:GLU:N	2.82	0.41
3:A:315:TRP:NE1	3:A:320:ILE:HG21	2.34	0.41
3:A:258:THR:HA	3:A:261:LEU:HD12	2.03	0.41
3:A:61:ARG:NH1	3:A:70:ASP:OD1	2.53	0.41
3:A:194:LEU:HB3	3:A:210:GLU:OE2	2.20	0.41
3:A:194:LEU:HA	3:A:194:LEU:HD23	1.94	0.41
3:B:193:MET:HE2	3:B:193:MET:HB3	1.86	0.41
3:A:217:VAL:CA	3:A:220:LEU:HD12	2.51	0.41
3:A:320:ILE:O	3:A:321:VAL:C	2.57	0.41
3:A:206:THR:CG2	3:B:328:LEU:CD2	2.99	0.41
2:D:14:DG:C4	2:D:15:DC:C5	3.09	0.41
3:A:107:PRO:O	3:A:110:SER:OG	2.37	0.41
3:B:39:GLU:CG	3:B:40:HIS:N	2.83	0.41
3:A:42:TRP:CZ3	3:A:45:LEU:CD2	3.04	0.41
3:B:182:VAL:HG23	3:B:236:ASN:O	2.20	0.41
2:D:17[A]:DT:H2'	2:D:18[A]:DA:C8	2.56	0.41
3:B:320:ILE:HG12	3:B:321:VAL:CG2	2.50	0.41
3:A:304:VAL:O	3:A:305:SER:C	2.58	0.41
3:A:58:LEU:HD23	4:A:374:HOH:O	2.21	0.41
3:B:44:MET:O	3:B:45:LEU:C	2.59	0.41
3:A:310:MET:O	3:A:310:MET:SD	2.79	0.41
3:A:199:ARG:HB2	3:A:199:ARG:HH11	1.82	0.40
2:D:23:DA:H2'	2:D:24:DT:H72	2.04	0.40
3:A:42:TRP:CZ3	3:A:45:LEU:HD23	2.56	0.40
3:A:310:MET:SD	3:A:318:VAL:CG2	3.10	0.40
2:D:26:DC:H5'	3:B:282:ARG:HG2	2.03	0.40
3:A:95:LEU:HA	3:A:95:LEU:HD23	1.87	0.40
2:D:17[B]:DT:H5'	2:D:17[B]:DT:H2'	1.88	0.40
1:C:23:DA:C8	1:C:24:DT:H72	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	A	322/349 (92%)	269 (84%)	32 (10%)	21 (6%)	2	0
3	B	315/349 (90%)	288 (91%)	19 (6%)	8 (2%)	9	4
All	All	637/698 (91%)	557 (87%)	51 (8%)	29 (5%)	4	1

All (29) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	188	THR
3	A	189	ASP
3	A	192	ARG
3	A	193	MET
3	A	236	ASN
3	A	278	ASP
3	A	279	SER
3	A	305	SER
3	A	306	ILE
3	A	308	GLU
3	A	317	ASN
3	B	20	SER
3	B	129	GLU
3	B	277	ASP
3	A	19	THR
3	A	197	ILE
3	A	303	GLY
3	A	307	PRO
3	A	318	VAL
3	A	319	ASN
3	B	189	ASP
3	B	326	ARG
3	B	298	ASP
3	A	198	GLY

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Mol	Chain	Res	Type
3	A	216	GLY
3	A	312	ALA
3	B	126	ASP
3	B	297	ARG
3	A	217	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	
3	A	270/293 (92%)	208 (77%)	62 (23%)	1	1
3	B	266/293 (91%)	233 (88%)	33 (12%)	7	5
All	All	536/586 (92%)	441 (82%)	95 (18%)	3	2

All (95) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	19	THR
3	A	20	SER
3	A	22	GLU
3	A	30	MET
3	A	46	LEU
3	A	51	SER
3	A	67	GLU
3	A	89	GLN
3	A	92	LEU
3	A	97	MET
3	A	117	MET
3	A	119	ARG
3	A	132	LYS
3	A	133	GLN
3	A	135	LEU
3	A	138	GLU
3	A	139	ARG
3	A	146	ARG
3	A	147	SER
3	A	148	LEU

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Mol	Chain	Res	Type
3	A	158	ILE
3	A	169	ASN
3	A	170	THR
3	A	183	LYS
3	A	186	SER
3	A	187	ARG
3	A	192	ARG
3	A	193	MET
3	A	196	HIS
3	A	197	ILE
3	A	199	ARG
3	A	201	LYS
3	A	202	THR
3	A	204	VAL
3	A	205	SER
3	A	206	THR
3	A	213	LEU
3	A	214	SER
3	A	219	LYS
3	A	220	LEU
3	A	230	VAL
3	A	233	ASP
3	A	245	ASN
3	A	251	SER
3	A	253	THR
3	A	256	LEU
3	A	270	ARG
3	A	277	ASP
3	A	279	SER
3	A	289	HIS
3	A	299	MET
3	A	306	ILE
3	A	310	MET
3	A	316	THR
3	A	318	VAL
3	A	319	ASN
3	A	322	MET
3	A	323	ASN
3	A	326	ARG
3	A	335	MET
3	A	338	LEU
3	A	341	ASP

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Mol	Chain	Res	Type
3	B	27	LEU
3	B	28	MET
3	B	37	PHE
3	B	43	LYS
3	B	45	LEU
3	B	46	LEU
3	B	60	ASN
3	B	87	THR
3	B	92	LEU
3	B	102	SER
3	B	130	ARG
3	B	138	GLU
3	B	169	ASN
3	B	183	LYS
3	B	199	ARG
3	B	201	LYS
3	B	203	LEU
3	B	204	VAL
3	B	205	SER
3	B	219	LYS
3	B	226	SER
3	B	230	VAL
3	B	244	LYS
3	B	245	ASN
3	B	277	ASP
3	B	289	HIS
3	B	292	ARG
3	B	306	ILE
3	B	319	ASN
3	B	320	ILE
3	B	325	ILE
3	B	326	ARG
3	B	328	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	90	GLN
3	A	133	GLN
3	A	144	GLN
3	A	196	HIS
3	A	235	ASN

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Mol	Chain	Res	Type
3	A	245	ASN
3	A	269	HIS
3	B	26	ASN
3	B	35	GLN
3	B	90	GLN
3	B	255	GLN
3	B	281	GLN
3	B	289	HIS

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

There are no ligands in this entry.

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	C	34/34 (100%)	0.52	3 (8%) 10 9	32, 50, 86, 90	2 (5%)
2	D	34/34 (100%)	0.02	2 (5%) 22 21	33, 51, 80, 82	0
3	A	320/349 (91%)	1.33	77 (24%) 1 1	30, 65, 96, 99	9 (2%)
3	B	319/349 (91%)	0.56	34 (10%) 6 6	27, 46, 84, 98	3 (0%)
All	All	707/766 (92%)	0.88	116 (16%) 2 2	27, 55, 94, 99	14 (1%)

All (116) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	A	304	VAL	15.6
1	C	17[B]	DT	12.5
3	A	207	ALA	10.5
3	A	18	ALA	9.6
3	B	328	LEU	9.5
3	A	19	THR	7.7
3	A	200	THR	7.3
3	A	202	THR	6.7
3	B	325	ILE	6.7
3	A	206	THR	6.4
3	A	276	LYS	6.3
3	B	327	ASN	5.8
3	A	232	ASP	5.8
3	A	194	LEU	5.7
3	A	163	PHE	5.6
3	A	278	ASP	5.6
3	A	219	LYS	5.4
3	B	338	LEU	5.4
3	A	177	ILE	5.3
3	A	167	ALA	5.2
3	A	168	TYR	5.0

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Mol	Chain	Res	Type	RSRZ
3	A	303	GLY	5.0
3	A	218	THR	5.0
3	A	310	MET	5.0
3	A	261	LEU	4.8
1	C	18[B]	DA	4.8
3	A	185	ILE	4.8
3	A	231	ALA	4.8
3	A	164	LEU	4.6
3	A	198	GLY	4.6
3	A	197	ILE	4.5
3	B	339	LEU	4.5
3	A	235	ASN	4.4
3	B	341	ASP	4.4
3	A	217	VAL	4.4
3	A	92	LEU	4.1
3	A	183	LYS	4.1
3	B	188	THR	4.0
3	A	201	LYS	4.0
3	B	326	ARG	4.0
3	B	166	ILE	4.0
3	A	148	LEU	3.9
3	A	284	LEU	3.9
3	A	166	ILE	3.9
3	A	279	SER	3.9
3	B	337	ARG	3.8
3	A	165	GLY	3.7
3	A	313	GLY	3.7
3	A	210	GLU	3.7
3	A	309	ILE	3.6
3	A	186	SER	3.6
3	A	152	SER	3.6
3	A	189	ASP	3.5
3	A	170	THR	3.5
3	B	340	GLU	3.5
3	B	71	VAL	3.5
3	A	153	ASP	3.5
3	A	270	ARG	3.4
3	A	169	ASN	3.3
3	A	199	ARG	3.3
3	B	164	LEU	3.3
3	A	151	ASN	3.3
3	A	322	MET	3.2

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Mol	Chain	Res	Type	RSRZ
3	B	92	LEU	3.2
3	A	171	LEU	3.1
3	B	88	ILE	3.1
3	A	212	ALA	3.1
3	A	203	LEU	3.1
3	A	230	VAL	3.0
3	A	236	ASN	3.0
3	A	221	VAL	2.9
3	B	316	THR	2.9
3	A	233	ASP	2.8
3	B	91	HIS	2.8
1	C	16[A]	DG	2.7
3	B	281	GLN	2.7
3	A	226	SER	2.6
3	A	239	PHE	2.6
3	A	277	ASP	2.6
3	B	278	ASP	2.6
3	B	170	THR	2.6
3	A	58	LEU	2.6
3	A	142	PHE	2.5
3	B	31	PHE	2.5
3	B	89	GLN	2.5
3	A	265	PHE	2.5
3	B	19	THR	2.5
3	A	172	LEU	2.5
3	A	290	SER	2.5
3	B	103	GLY	2.5
2	D	18[A]	DA	2.5
3	B	165	GLY	2.4
3	A	130	ARG	2.4
3	A	275	ALA	2.3
3	A	208	GLY	2.3
3	A	193	MET	2.3
2	D	16[A]	DA	2.3
3	A	260	ALA	2.3
3	A	80	ALA	2.2
3	B	75	LEU	2.2
3	B	160	ASN	2.2
3	B	333	GLY	2.2
3	B	239	PHE	2.2
3	B	261	LEU	2.2
3	A	214	SER	2.2

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Mol	Chain	Res	Type	RSRZ
3	A	188	THR	2.2
3	B	171	LEU	2.2
3	A	258	THR	2.1
3	A	289	HIS	2.1
3	B	163	PHE	2.1
3	A	95	LEU	2.1
3	A	139	ARG	2.1
3	A	288	GLY	2.1
3	B	21	ASP	2.1
3	A	225	ILE	2.1
3	B	277	ASP	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 ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.