



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 12:50 pm GMT

PDB ID : 1VH1
Title : Crystal structure of CMP-KDO synthetase
Authors : Structural GenomiX
Deposited on : 2003-12-01
Resolution : 2.60 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
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	recalc28949

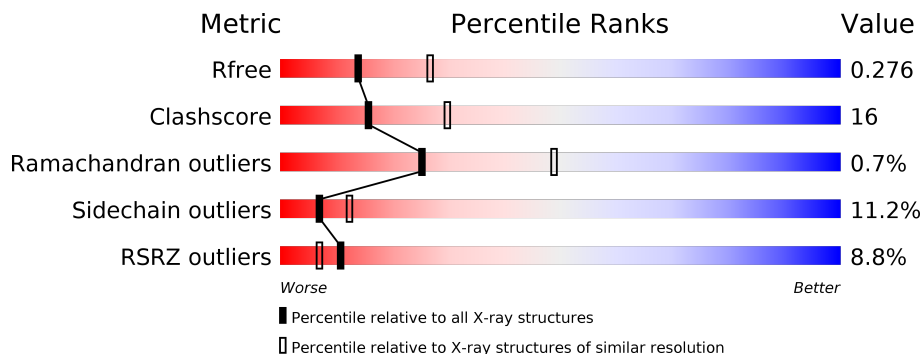
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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}	100719	2542 (2.60-2.60)
Clashscore	112137	2895 (2.60-2.60)
Ramachandran outliers	110173	2848 (2.60-2.60)
Sidechain outliers	110143	2848 (2.60-2.60)
RSRZ outliers	101464	2550 (2.60-2.60)

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	256	<div> <div>8%</div> <div>64%</div> <div>24%</div> <div>5%</div> <div>7%</div> </div>
1	B	256	<div> <div>11%</div> <div>51%</div> <div>27%</div> <div>8%</div> <div>13%</div> </div>
1	C	256	<div> <div>5%</div> <div>64%</div> <div>22%</div> <div>5%</div> <div>9%</div> </div>
1	D	256	<div> <div>7%</div> <div>60%</div> <div>29%</div> <div>5%</div> <div>6%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7321 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 3-deoxy-manno-octulosonate cytidyltransferase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	239	Total	C	N	O	S	Se	0	0	0
			1826	1157	324	337	2	6			
1	B	224	Total	C	N	O	S	Se	0	0	0
			1729	1096	310	315	2	6			
1	C	233	Total	C	N	O	S	Se	0	0	0
			1782	1133	313	328	2	6			
1	D	241	Total	C	N	O	S	Se	0	0	0
			1828	1161	321	338	2	6			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	cloning artifact	UNP P04951
A	29	MSE	MET	modified residue	UNP P04951
A	67	MSE	MET	modified residue	UNP P04951
A	103	MSE	MET	modified residue	UNP P04951
A	123	MSE	MET	modified residue	UNP P04951
A	208	MSE	MET	modified residue	UNP P04951
A	247	MSE	MET	modified residue	UNP P04951
A	249	GLY	-	cloning artifact	UNP P04951
A	250	SER	-	cloning artifact	UNP P04951
A	251	HIS	-	cloning artifact	UNP P04951
A	252	HIS	-	cloning artifact	UNP P04951
A	253	HIS	-	cloning artifact	UNP P04951
A	254	HIS	-	cloning artifact	UNP P04951
A	255	HIS	-	cloning artifact	UNP P04951
A	256	HIS	-	cloning artifact	UNP P04951
B	1	MSE	-	cloning artifact	UNP P04951
B	29	MSE	MET	modified residue	UNP P04951
B	67	MSE	MET	modified residue	UNP P04951
B	103	MSE	MET	modified residue	UNP P04951
B	123	MSE	MET	modified residue	UNP P04951
B	208	MSE	MET	modified residue	UNP P04951

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Chain	Residue	Modelled	Actual	Comment	Reference
B	247	MSE	MET	modified residue	UNP P04951
B	249	GLY	-	cloning artifact	UNP P04951
B	250	SER	-	cloning artifact	UNP P04951
B	251	HIS	-	cloning artifact	UNP P04951
B	252	HIS	-	cloning artifact	UNP P04951
B	253	HIS	-	cloning artifact	UNP P04951
B	254	HIS	-	cloning artifact	UNP P04951
B	255	HIS	-	cloning artifact	UNP P04951
B	256	HIS	-	cloning artifact	UNP P04951
C	1	MSE	-	cloning artifact	UNP P04951
C	29	MSE	MET	modified residue	UNP P04951
C	67	MSE	MET	modified residue	UNP P04951
C	103	MSE	MET	modified residue	UNP P04951
C	123	MSE	MET	modified residue	UNP P04951
C	208	MSE	MET	modified residue	UNP P04951
C	247	MSE	MET	modified residue	UNP P04951
C	249	GLY	-	cloning artifact	UNP P04951
C	250	SER	-	cloning artifact	UNP P04951
C	251	HIS	-	cloning artifact	UNP P04951
C	252	HIS	-	cloning artifact	UNP P04951
C	253	HIS	-	cloning artifact	UNP P04951
C	254	HIS	-	cloning artifact	UNP P04951
C	255	HIS	-	cloning artifact	UNP P04951
C	256	HIS	-	cloning artifact	UNP P04951
D	1	MSE	-	cloning artifact	UNP P04951
D	29	MSE	MET	modified residue	UNP P04951
D	67	MSE	MET	modified residue	UNP P04951
D	103	MSE	MET	modified residue	UNP P04951
D	123	MSE	MET	modified residue	UNP P04951
D	208	MSE	MET	modified residue	UNP P04951
D	247	MSE	MET	modified residue	UNP P04951
D	249	GLY	-	cloning artifact	UNP P04951
D	250	SER	-	cloning artifact	UNP P04951
D	251	HIS	-	cloning artifact	UNP P04951
D	252	HIS	-	cloning artifact	UNP P04951
D	253	HIS	-	cloning artifact	UNP P04951
D	254	HIS	-	cloning artifact	UNP P04951
D	255	HIS	-	cloning artifact	UNP P04951
D	256	HIS	-	cloning artifact	UNP P04951

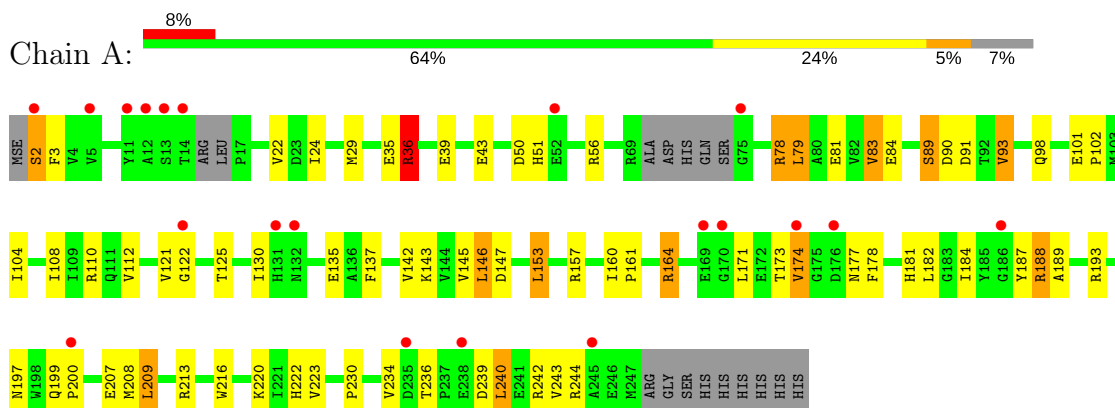
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	45	Total 45	O 45	0	0
2	B	34	Total 34	O 34	0	0
2	C	42	Total 42	O 42	0	0
2	D	35	Total 35	O 35	0	0

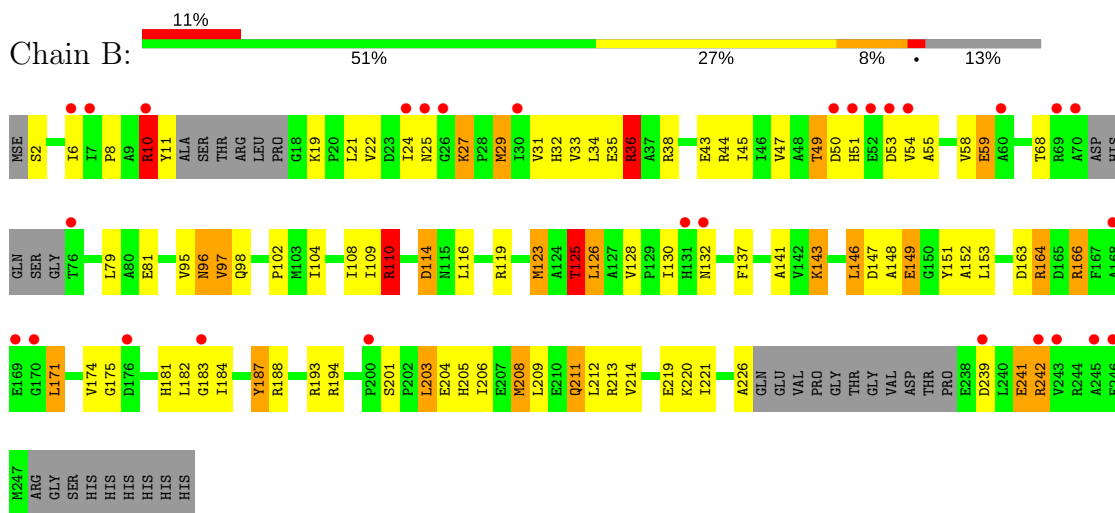
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

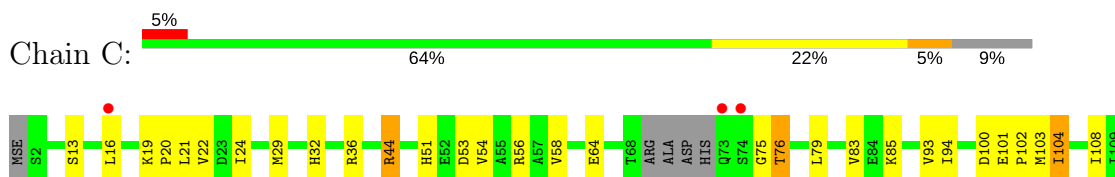
• Molecule 1: 3-deoxy-manno-octulosonate cytidyltransferase

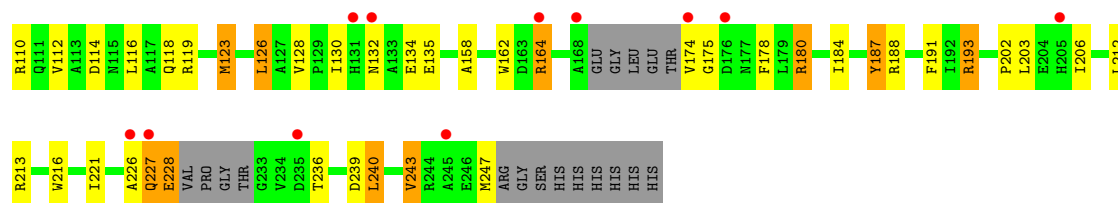


• Molecule 1: 3-deoxy-manno-octulosonate cytidyltransferase

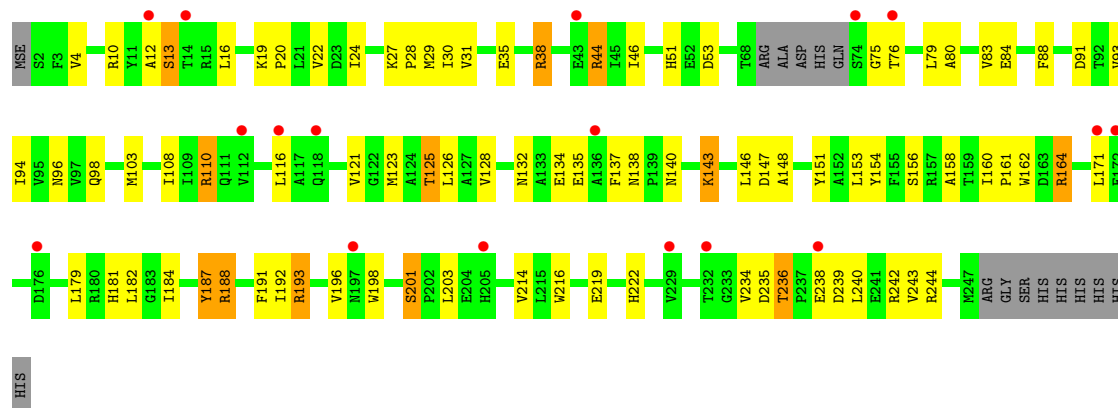


• Molecule 1: 3-deoxy-manno-octulosonate cytidyltransferase





- Molecule 1: 3-deoxy-manno-octulosonate cytidylyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	51.59Å 130.81Å 159.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.92 – 2.60 19.92 – 2.60	Depositor EDS
% Data completeness (in resolution range)	(Not available) (19.92-2.60) 100.0 (19.92-2.60)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.88 (at 2.59Å)	Xtriage
Refinement program	REFMAC 4	Depositor
R, R_{free}	0.240 , 0.302 0.220 , 0.276	Depositor DCC
R_{free} test set	1718 reflections (5.34%)	DCC
Wilson B-factor (Å ²)	42.7	Xtriage
Anisotropy	0.304	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 64.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7321	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.36% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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	A	0.61	0/1856	1.11	13/2517 (0.5%)
1	B	0.60	0/1755	1.15	14/2374 (0.6%)
1	C	0.62	0/1810	1.12	9/2453 (0.4%)
1	D	0.61	0/1859	1.15	12/2525 (0.5%)
All	All	0.61	0/7280	1.13	48/9869 (0.5%)

There are no bond length outliers.

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	38	ARG	CD-NE-CZ	12.28	140.79	123.60
1	C	193	ARG	CD-NE-CZ	10.70	138.58	123.60
1	D	38	ARG	NE-CZ-NH1	10.33	125.46	120.30
1	A	78	ARG	CD-NE-CZ	10.05	137.67	123.60
1	D	188	ARG	NE-CZ-NH1	-9.77	115.42	120.30
1	D	38	ARG	NE-CZ-NH2	-9.39	115.61	120.30
1	B	110	ARG	NE-CZ-NH1	8.11	124.35	120.30
1	C	44	ARG	NE-CZ-NH1	8.11	124.36	120.30
1	B	10	ARG	NE-CZ-NH1	-8.02	116.29	120.30
1	C	36	ARG	NE-CZ-NH2	-7.83	116.39	120.30
1	A	78	ARG	NE-CZ-NH1	7.81	124.20	120.30
1	B	36	ARG	CD-NE-CZ	7.50	134.10	123.60
1	B	193	ARG	NE-CZ-NH2	-7.47	116.56	120.30
1	A	213	ARG	NE-CZ-NH1	-7.28	116.66	120.30
1	C	188	ARG	NE-CZ-NH1	-7.01	116.79	120.30
1	C	187	TYR	CA-CB-CG	6.89	126.49	113.40
1	C	110	ARG	CD-NE-CZ	6.72	133.00	123.60
1	C	213	ARG	NE-CZ-NH1	-6.58	117.01	120.30
1	B	188	ARG	NE-CZ-NH2	-6.52	117.04	120.30
1	D	244	ARG	CD-NE-CZ	6.46	132.64	123.60
1	B	114	ASP	CB-CG-OD1	6.33	124.00	118.30
1	B	119	ARG	NE-CZ-NH1	6.23	123.42	120.30
1	C	180	ARG	NE-CZ-NH2	-6.08	117.26	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	188	ARG	NE-CZ-NH1	6.06	123.33	120.30
1	A	242	ARG	NE-CZ-NH1	5.99	123.30	120.30
1	D	110	ARG	NE-CZ-NH1	5.98	123.29	120.30
1	D	242	ARG	NE-CZ-NH1	5.97	123.28	120.30
1	A	36	ARG	NE-CZ-NH1	-5.86	117.37	120.30
1	D	110	ARG	CA-CB-CG	5.77	126.09	113.40
1	B	193	ARG	NE-CZ-NH1	5.72	123.16	120.30
1	A	56	ARG	NE-CZ-NH1	5.64	123.12	120.30
1	A	36	ARG	CB-CG-CD	5.64	126.26	111.60
1	B	10	ARG	NE-CZ-NH2	5.59	123.09	120.30
1	A	164	ARG	NE-CZ-NH1	5.57	123.09	120.30
1	B	110	ARG	CD-NE-CZ	5.54	131.36	123.60
1	A	36	ARG	CD-NE-CZ	-5.33	116.14	123.60
1	B	110	ARG	NE-CZ-NH2	-5.31	117.64	120.30
1	D	147	ASP	CB-CG-OD1	5.26	123.04	118.30
1	C	193	ARG	NE-CZ-NH1	5.23	122.92	120.30
1	A	56	ARG	NE-CZ-NH2	-5.19	117.71	120.30
1	B	188	ARG	NE-CZ-NH1	5.17	122.88	120.30
1	D	193	ARG	CA-CB-CG	5.14	124.70	113.40
1	A	164	ARG	CD-NE-CZ	5.13	130.78	123.60
1	B	147	ASP	CB-CG-OD1	5.11	122.90	118.30
1	D	164	ARG	CA-CB-CG	5.04	124.50	113.40
1	D	35	GLU	OE1-CD-OE2	-5.04	117.25	123.30
1	B	125	THR	N-CA-CB	5.01	119.83	110.30
1	A	36	ARG	CA-CB-CG	5.00	124.41	113.40

There are no chirality outliers.

There are no planarity outliers.

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	1826	0	1785	45	0
1	B	1729	0	1693	80	0
1	C	1782	0	1741	54	0
1	D	1828	0	1786	61	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	45	0	0	2	0
2	B	34	0	0	4	0
2	C	42	0	0	3	0
2	D	35	0	0	5	0
All	All	7321	0	7005	232	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 16.

All (232) 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:103:MSE:HG3	1:C:247:MSE:HE2	1.46	0.97
1:B:49:THR:HG21	1:B:54:VAL:HB	1.54	0.89
1:D:236:THR:HG22	1:D:239:ASP:H	1.37	0.88
1:B:125:THR:HG21	1:B:181:HIS:HE1	1.40	0.87
1:A:29:MSE:HG3	1:A:102:PRO:HG3	1.57	0.86
1:B:209:LEU:HD22	1:B:211:GLN:HE21	1.36	0.86
1:C:102:PRO:HG2	1:C:247:MSE:HE1	1.55	0.84
1:D:125:THR:HG21	1:D:181:HIS:HE1	1.44	0.83
1:C:243:VAL:HG13	1:C:247:MSE:HE3	1.61	0.82
1:B:123:MSE:HE3	1:B:221:ILE:HG12	1.61	0.80
1:B:108:ILE:HD12	1:B:126:LEU:HD22	1.61	0.80
1:B:36:ARG:HG2	1:B:36:ARG:HH11	1.50	0.77
1:B:209:LEU:HD22	1:B:211:GLN:NE2	1.99	0.76
1:C:93:VAL:HG13	1:C:116:LEU:HD23	1.66	0.76
1:B:110:ARG:HB3	1:B:110:ARG:HH11	1.50	0.74
1:B:8:PRO:HG3	1:B:96:ASN:HD21	1.52	0.73
1:D:236:THR:CG2	1:D:239:ASP:H	2.01	0.73
1:B:125:THR:HG21	1:B:181:HIS:CE1	2.25	0.72
1:B:123:MSE:HE2	1:B:214:VAL:HG21	1.71	0.72
1:D:79:LEU:HD22	1:D:96:ASN:HD22	1.55	0.71
1:A:220:LYS:HD3	2:A:257:HOH:O	1.92	0.70
1:D:236:THR:HG22	1:D:239:ASP:N	2.07	0.69
1:B:126:LEU:HD11	1:B:226:ALA:HB2	1.75	0.68
1:A:36:ARG:HG3	1:A:104:ILE:O	1.92	0.68
1:B:35:GLU:HB2	1:B:36:ARG:NH1	2.08	0.67
1:B:109:ILE:HA	1:B:184:ILE:HD11	1.76	0.67
1:D:132:ASN:OD1	1:D:135:GLU:HB2	1.94	0.67
1:C:19:LYS:HB2	1:C:20:PRO:CD	2.25	0.67
1:D:79:LEU:HD22	1:D:96:ASN:ND2	2.10	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:203:LEU:HD13	1:B:212:LEU:HD13	1.77	0.66
1:B:205:HIS:HA	1:B:208:MSE:HE3	1.78	0.66
1:B:125:THR:HG22	1:B:184:ILE:O	1.95	0.65
1:D:236:THR:HG23	1:D:238:GLU:H	1.62	0.65
1:A:24:ILE:HD13	1:A:243:VAL:HG11	1.78	0.65
1:C:19:LYS:HB2	1:C:20:PRO:HD3	1.79	0.65
1:A:240:LEU:HD13	1:A:244:ARG:NH2	2.12	0.65
1:B:104:ILE:HD11	1:B:108:ILE:HD11	1.78	0.65
1:B:208:MSE:CE	1:B:208:MSE:HA	2.26	0.65
1:B:114:ASP:HB3	2:B:268:HOH:O	1.97	0.64
1:C:174:VAL:HG22	1:C:175:GLY:H	1.60	0.64
1:A:208:MSE:HG3	1:B:164:ARG:NH2	2.13	0.64
1:A:240:LEU:HD13	1:A:244:ARG:HH21	1.62	0.64
1:A:137:PHE:CD1	1:A:171:LEU:HD13	2.33	0.64
1:A:147:ASP:HB3	1:A:153:LEU:HD13	1.80	0.63
1:B:55:ALA:O	1:B:59:GLU:HB2	1.99	0.63
1:C:13:SER:HB3	1:C:16:LEU:O	1.99	0.62
1:A:50:ASP:OD1	1:A:51:HIS:ND1	2.33	0.62
1:C:21:LEU:HD11	1:C:53:ASP:HB2	1.80	0.62
1:D:125:THR:HG21	1:D:181:HIS:CE1	2.31	0.61
1:B:49:THR:HG21	1:B:54:VAL:CB	2.30	0.61
1:B:96:ASN:O	1:B:97:VAL:HB	2.00	0.61
1:B:32:HIS:O	1:B:36:ARG:NH1	2.34	0.60
1:C:132:ASN:HD21	1:C:134:GLU:HB3	1.66	0.60
1:A:121:VAL:HG22	1:A:122:GLY:H	1.67	0.60
1:B:242:ARG:HB3	1:B:242:ARG:HH11	1.65	0.60
1:C:103:MSE:CG	1:C:247:MSE:HE2	2.27	0.60
1:A:35:GLU:O	1:A:39:GLU:HG3	2.02	0.60
1:B:24:ILE:HB	1:B:32:HIS:HE1	1.66	0.59
1:A:182:LEU:HD13	1:A:230:PRO:HG2	1.84	0.59
1:D:187:TYR:CD2	1:D:192:ILE:HD11	2.38	0.59
1:B:31:VAL:O	1:B:35:GLU:HG3	2.03	0.58
1:B:19:LYS:HA	1:B:22:VAL:HG23	1.86	0.58
1:B:95:VAL:HG12	1:B:97:VAL:HG23	1.84	0.58
1:C:44:ARG:NH2	1:C:64:GLU:OE2	2.28	0.58
1:D:137:PHE:CE2	1:D:171:LEU:HD23	2.38	0.58
1:A:208:MSE:HG3	1:B:164:ARG:HH21	1.67	0.58
1:B:10:ARG:O	1:B:11:TYR:HB2	2.04	0.58
1:D:154:TYR:CE1	1:D:156:SER:HB2	2.38	0.58
1:D:188:ARG:NH1	2:D:259:HOH:O	2.36	0.58
1:C:128:VAL:HG12	1:C:226:ALA:O	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:128:VAL:HG23	1:D:182:LEU:HD11	1.86	0.58
1:D:192:ILE:O	1:D:196:VAL:HG13	2.03	0.58
1:A:234:VAL:CG2	1:A:243:VAL:HG21	2.34	0.57
1:B:24:ILE:HB	1:B:32:HIS:CE1	2.39	0.57
1:D:29:MSE:HE1	1:D:234:VAL:HG11	1.87	0.57
1:C:112:VAL:HG22	1:C:126:LEU:HD23	1.87	0.56
1:B:35:GLU:HB2	1:B:36:ARG:HH12	1.68	0.56
1:B:38:ARG:HA	1:B:45:ILE:HD11	1.87	0.56
1:A:234:VAL:HG22	1:A:243:VAL:HG21	1.87	0.56
1:C:21:LEU:CD1	1:C:53:ASP:HB2	2.35	0.56
1:B:125:THR:CG2	1:B:181:HIS:HE1	2.17	0.56
1:B:239:ASP:O	1:B:241:GLU:HG3	2.06	0.56
1:B:34:LEU:HD21	1:B:38:ARG:HH21	1.71	0.56
1:A:193:ARG:O	1:A:197:ASN:HB2	2.06	0.56
1:D:46:ILE:HD12	1:D:88:PHE:HZ	1.70	0.55
1:B:137:PHE:CE2	1:B:171:LEU:HG	2.41	0.55
1:B:201:SER:O	1:B:204:GLU:HG2	2.07	0.55
1:C:93:VAL:HG13	1:C:116:LEU:CD2	2.36	0.54
1:A:108:ILE:HD13	1:A:230:PRO:HG3	1.89	0.54
1:B:10:ARG:O	1:B:11:TYR:CB	2.55	0.54
1:C:51:HIS:HB3	1:C:53:ASP:OD1	2.07	0.54
1:D:236:THR:HG23	1:D:238:GLU:N	2.22	0.54
1:D:121:VAL:HG21	1:D:151:TYR:HE2	1.72	0.54
1:A:130:ILE:HG23	1:A:135:GLU:OE2	2.08	0.53
1:B:194:ARG:NH2	1:B:219:GLU:OE2	2.42	0.53
1:C:54:VAL:O	1:C:58:VAL:HG23	2.08	0.53
1:D:91:ASP:HB2	2:D:259:HOH:O	2.09	0.53
1:C:226:ALA:O	1:C:228:GLU:HG2	2.08	0.53
1:B:33:VAL:HG22	1:B:102:PRO:HA	1.91	0.53
1:C:132:ASN:ND2	1:C:134:GLU:HB3	2.24	0.53
1:D:13:SER:HB3	1:D:16:LEU:O	2.09	0.53
1:B:123:MSE:HG3	1:B:187:TYR:CD1	2.44	0.52
1:A:98:GLN:HB2	1:A:101:GLU:OE2	2.09	0.52
1:B:203:LEU:HD13	1:B:212:LEU:HB3	1.92	0.52
1:C:76:THR:HG22	2:C:263:HOH:O	2.10	0.52
1:C:22:VAL:CG1	1:C:240:LEU:HD11	2.41	0.51
1:D:108:ILE:HB	1:D:126:LEU:CD1	2.41	0.51
1:C:162:TRP:HB2	1:D:158:ALA:HB2	1.93	0.51
1:B:34:LEU:HD21	1:B:38:ARG:NH2	2.26	0.51
1:C:101:GLU:O	1:C:104:ILE:HG22	2.10	0.51
1:B:98:GLN:NE2	1:B:183:GLY:HA3	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:130:ILE:HG22	1:B:132:ASN:H	1.74	0.50
1:B:141:ALA:O	1:B:143:LYS:HE2	2.11	0.50
1:C:130:ILE:HG23	1:C:135:GLU:OE2	2.10	0.50
1:B:208:MSE:HE3	1:B:208:MSE:HA	1.92	0.50
1:B:34:LEU:HD12	1:B:45:ILE:HG21	1.94	0.50
1:B:123:MSE:CE	1:B:214:VAL:HG21	2.40	0.50
1:D:214:VAL:HG13	1:D:219:GLU:HB2	1.94	0.50
1:B:47:VAL:HG11	1:B:58:VAL:HG21	1.94	0.50
1:A:89:SER:HB3	1:A:91:ASP:OD2	2.12	0.50
1:B:19:LYS:HB2	1:B:29:MSE:CE	2.42	0.50
1:C:79:LEU:O	1:C:83:VAL:HG23	2.12	0.50
1:B:146:LEU:HD12	1:B:152:ALA:HA	1.93	0.50
1:B:123:MSE:HE3	1:B:221:ILE:CG1	2.38	0.49
1:B:242:ARG:HB3	1:B:242:ARG:NH1	2.26	0.49
1:C:51:HIS:HA	2:C:272:HOH:O	2.12	0.49
1:C:112:VAL:CG2	1:C:126:LEU:HD23	2.43	0.49
1:D:80:ALA:HB2	1:D:196:VAL:HG11	1.94	0.49
1:D:98:GLN:HG2	2:D:276:HOH:O	2.12	0.49
1:B:2:SER:HA	1:B:43:GLU:OE2	2.12	0.49
1:D:198:TRP:HH2	1:D:219:GLU:HG3	1.77	0.49
1:B:104:ILE:CD1	1:B:108:ILE:HD11	2.43	0.49
1:A:177:ASN:ND2	1:B:206:ILE:HD13	2.28	0.48
1:C:203:LEU:HG	1:C:212:LEU:HD13	1.95	0.48
1:A:89:SER:O	1:A:189:ALA:HB3	2.13	0.48
1:D:22:VAL:HG11	1:D:240:LEU:CD1	2.44	0.48
1:D:28:PRO:HG2	1:D:31:VAL:CG2	2.43	0.48
1:D:201:SER:HB2	1:D:216:TRP:CE3	2.50	0.47
1:B:203:LEU:CD1	1:B:212:LEU:HD13	2.42	0.47
1:C:130:ILE:HD12	1:C:178:PHE:HB3	1.95	0.47
1:C:236:THR:O	1:C:239:ASP:HB2	2.15	0.47
1:D:143:LYS:HE2	1:D:143:LYS:N	2.30	0.47
1:A:81:GLU:O	1:A:84:GLU:HB3	2.15	0.47
1:C:103:MSE:HG3	1:C:247:MSE:CE	2.32	0.47
1:C:114:ASP:O	1:C:118:GLN:HG3	2.15	0.47
1:D:125:THR:HG22	1:D:184:ILE:O	2.14	0.47
1:B:110:ARG:CB	1:B:110:ARG:HH11	2.22	0.47
1:D:4:VAL:HG22	1:D:44:ARG:HB3	1.97	0.47
1:A:36:ARG:HH11	1:A:36:ARG:HD2	1.54	0.46
1:C:202:PRO:O	1:C:206:ILE:HD12	2.15	0.46
1:D:28:PRO:HG2	1:D:31:VAL:HG23	1.97	0.46
1:A:145:VAL:HG22	1:A:161:PRO:HD3	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:146:LEU:HD11	1:A:223:VAL:HB	1.98	0.46
1:B:36:ARG:HG2	1:B:36:ARG:NH1	2.19	0.46
1:A:216:TRP:CE2	1:B:148:ALA:HB2	2.50	0.46
1:C:226:ALA:HB1	1:C:228:GLU:OE1	2.15	0.46
1:D:19:LYS:NZ	1:D:235:ASP:HB3	2.30	0.45
1:C:19:LYS:N	1:C:20:PRO:HD2	2.31	0.45
1:C:164:ARG:NH2	1:D:140:ASN:OD1	2.43	0.45
1:A:90:ASP:O	1:A:188:ARG:HB3	2.17	0.45
1:B:104:ILE:CG1	1:B:108:ILE:HD11	2.47	0.45
1:D:160:ILE:HA	1:D:161:PRO:C	2.36	0.45
1:A:157:ARG:HH11	1:A:157:ARG:HD2	1.59	0.44
1:A:207:GLU:O	1:A:208:MSE:HB2	2.17	0.44
1:C:24:ILE:O	1:C:32:HIS:HE1	2.00	0.44
1:D:123:MSE:HG2	1:D:187:TYR:HD1	1.82	0.44
1:C:24:ILE:O	1:C:32:HIS:CE1	2.71	0.44
1:D:236:THR:HG22	1:D:239:ASP:CB	2.47	0.44
1:C:22:VAL:HG11	1:C:240:LEU:HD11	1.99	0.44
1:C:102:PRO:CG	1:C:247:MSE:HE1	2.37	0.44
1:B:36:ARG:HD3	1:B:36:ARG:HA	1.77	0.44
1:A:24:ILE:HD13	1:A:243:VAL:CG1	2.45	0.44
1:D:29:MSE:HE1	1:D:234:VAL:CG1	2.47	0.44
1:D:132:ASN:OD1	1:D:135:GLU:N	2.43	0.44
1:A:160:ILE:HA	1:A:161:PRO:C	2.38	0.44
1:A:3:PHE:HB2	1:A:93:VAL:HG22	2.00	0.44
1:B:126:LEU:HD23	1:B:182:LEU:HD12	2.00	0.43
1:B:49:THR:HG22	1:B:50:ASP:H	1.82	0.43
1:C:103:MSE:SE	1:C:243:VAL:HG22	2.68	0.43
1:B:24:ILE:HD12	1:B:29:MSE:HA	1.99	0.43
1:C:19:LYS:NZ	1:C:100:ASP:OD1	2.51	0.43
1:C:19:LYS:CB	1:C:20:PRO:CD	2.92	0.43
1:B:204:GLU:OE1	1:B:213:ARG:HB2	2.18	0.43
1:D:51:HIS:HB3	1:D:53:ASP:OD1	2.19	0.43
1:A:236:THR:O	1:A:239:ASP:N	2.49	0.43
1:C:130:ILE:HG12	1:C:180:ARG:HB2	2.00	0.43
1:A:125:THR:OG1	1:A:181:HIS:HE1	2.02	0.43
1:D:143:LYS:HA	1:D:179:LEU:O	2.19	0.43
1:C:158:ALA:HB2	1:D:162:TRP:HB2	2.00	0.43
1:D:134:GLU:O	1:D:138:ASN:HB2	2.18	0.43
1:D:83:VAL:HG21	1:D:192:ILE:HG21	2.01	0.43
1:B:164:ARG:HG2	2:B:284:HOH:O	2.19	0.42
1:B:6:ILE:HG21	1:B:79:LEU:HG	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2:SER:HB3	1:A:43:GLU:OE2	2.20	0.42
1:B:149:GLU:HB3	1:B:151:TYR:HD1	1.84	0.42
1:D:12:ALA:O	1:D:13:SER:HB2	2.19	0.42
1:D:154:TYR:HE2	1:D:203:LEU:HD21	1.84	0.42
1:A:145:VAL:HG23	1:A:160:ILE:HG13	2.01	0.42
1:B:27:LYS:HB2	1:B:32:HIS:CE1	2.55	0.42
1:D:123:MSE:HE2	1:D:187:TYR:CD1	2.55	0.42
1:D:93:VAL:HG22	1:D:116:LEU:HD12	2.02	0.42
1:D:103:MSE:HE2	1:D:243:VAL:HG22	2.01	0.42
1:C:216:TRP:CE2	1:D:148:ALA:HB2	2.54	0.42
1:B:242:ARG:HD2	1:B:242:ARG:H	1.85	0.42
1:D:10:ARG:O	1:D:20:PRO:HD3	2.20	0.42
1:B:203:LEU:HD13	1:B:212:LEU:CD1	2.47	0.42
1:D:191:PHE:HZ	1:D:214:VAL:HG22	1.85	0.42
1:C:123:MSE:HE2	1:C:221:ILE:CD1	2.50	0.42
1:A:199:GLN:HG2	1:A:200:PRO:HD2	2.02	0.41
1:D:19:LYS:HZ1	1:D:235:ASP:HB3	1.86	0.41
1:A:121:VAL:HG22	1:A:122:GLY:N	2.33	0.41
1:D:19:LYS:N	1:D:20:PRO:HD2	2.35	0.41
1:D:24:ILE:HD11	1:D:29:MSE:HE2	2.02	0.41
1:D:30:ILE:HA	1:D:30:ILE:HD12	1.86	0.41
1:A:104:ILE:HD11	1:A:184:ILE:HD12	2.03	0.41
1:B:68:THR:HA	1:B:81:GLU:OE2	2.21	0.41
1:B:143:LYS:NZ	2:B:257:HOH:O	2.48	0.41
1:B:220:LYS:NZ	2:B:289:HOH:O	2.53	0.41
1:C:243:VAL:HG13	1:C:247:MSE:CE	2.40	0.41
1:A:174:VAL:HG22	1:A:178:PHE:CE1	2.56	0.41
1:A:79:LEU:O	1:A:83:VAL:HG13	2.20	0.40
1:C:116:LEU:O	1:C:119:ARG:O	2.38	0.40
1:A:222:HIS:HD2	2:A:283:HOH:O	2.05	0.40
1:D:123:MSE:HE2	1:D:187:TYR:CE1	2.56	0.40
1:C:108:ILE:HG21	1:C:108:ILE:HD13	1.90	0.40
1:C:19:LYS:HB3	1:C:29:MSE:CE	2.51	0.40
1:C:75:GLY:HA2	2:C:279:HOH:O	2.22	0.40
1:D:222:HIS:HD2	2:D:267:HOH:O	2.04	0.40
1:A:142:VAL:HG21	1:A:209:LEU:HD11	2.03	0.40
1:B:163:ASP:OD2	1:B:166:ARG:HD2	2.22	0.40
1:C:123:MSE:HG3	1:C:191:PHE:CE2	2.56	0.40
1:D:80:ALA:HB3	2:D:278:HOH:O	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	233/256 (91%)	225 (97%)	8 (3%)	0	100	100
1	B	216/256 (84%)	202 (94%)	11 (5%)	3 (1%)	13	26
1	C	225/256 (88%)	215 (96%)	9 (4%)	1 (0%)	38	63
1	D	237/256 (93%)	230 (97%)	5 (2%)	2 (1%)	22	44
All	All	911/1024 (89%)	872 (96%)	33 (4%)	6 (1%)	25	49

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	227	GLN
1	D	13	SER
1	B	96	ASN
1	B	97	VAL
1	D	75	GLY
1	B	175	GLY

5.3.2 Protein sidechains [i](#)

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	185/203 (91%)	166 (90%)	19 (10%)	8	15
1	B	174/203 (86%)	143 (82%)	31 (18%)	2	3
1	C	180/203 (89%)	165 (92%)	15 (8%)	13	25
1	D	185/203 (91%)	169 (91%)	16 (9%)	12	23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	724/812 (89%)	643 (89%)	81 (11%)	7 12

All (81) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	SER
1	A	22	VAL
1	A	36	ARG
1	A	78	ARG
1	A	79	LEU
1	A	83	VAL
1	A	89	SER
1	A	93	VAL
1	A	110	ARG
1	A	112	VAL
1	A	143	LYS
1	A	146	LEU
1	A	153	LEU
1	A	164	ARG
1	A	173	THR
1	A	174	VAL
1	A	187	TYR
1	A	209	LEU
1	A	240	LEU
1	B	10	ARG
1	B	21	LEU
1	B	25	ASN
1	B	27	LYS
1	B	29	MSE
1	B	36	ARG
1	B	44	ARG
1	B	49	THR
1	B	51	HIS
1	B	53	ASP
1	B	59	GLU
1	B	110	ARG
1	B	116	LEU
1	B	123	MSE
1	B	125	THR
1	B	126	LEU
1	B	128	VAL
1	B	143	LYS

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Mol	Chain	Res	Type
1	B	146	LEU
1	B	149	GLU
1	B	153	LEU
1	B	164	ARG
1	B	166	ARG
1	B	171	LEU
1	B	174	VAL
1	B	187	TYR
1	B	203	LEU
1	B	208	MSE
1	B	211	GLN
1	B	241	GLU
1	B	242	ARG
1	C	56	ARG
1	C	76	THR
1	C	85	LYS
1	C	94	ILE
1	C	104	ILE
1	C	123	MSE
1	C	126	LEU
1	C	164	ARG
1	C	184	ILE
1	C	187	TYR
1	C	193	ARG
1	C	227	GLN
1	C	228	GLU
1	C	240	LEU
1	C	243	VAL
1	D	27	LYS
1	D	38	ARG
1	D	44	ARG
1	D	76	THR
1	D	84	GLU
1	D	94	ILE
1	D	110	ARG
1	D	125	THR
1	D	143	LYS
1	D	146	LEU
1	D	153	LEU
1	D	164	ARG
1	D	187	TYR
1	D	193	ARG

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Mol	Chain	Res	Type
1	D	201	SER
1	D	236	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	120	GLN
1	A	181	HIS
1	A	222	HIS
1	B	32	HIS
1	B	96	ASN
1	B	98	GLN
1	B	115	ASN
1	B	120	GLN
1	B	181	HIS
1	B	211	GLN
1	B	222	HIS
1	C	32	HIS
1	C	96	ASN
1	C	98	GLN
1	C	120	GLN
1	C	222	HIS
1	D	96	ASN

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](#)

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	233/256 (91%)	0.47	20 (8%) 11 7	51, 64, 94, 120	0
1	B	218/256 (85%)	0.65	29 (13%) 4 2	49, 68, 101, 124	0
1	C	227/256 (88%)	0.39	14 (6%) 21 16	49, 63, 95, 104	0
1	D	235/256 (91%)	0.51	17 (7%) 16 12	51, 68, 99, 111	0
All	All	913/1024 (89%)	0.50	80 (8%) 11 7	49, 66, 98, 124	0

All (80) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	74	SER	5.9
1	B	24	ILE	5.4
1	D	14	THR	5.1
1	C	73	GLN	5.0
1	D	176	ASP	4.4
1	A	12	ALA	4.3
1	A	169	GLU	3.9
1	B	26	GLY	3.8
1	C	174	VAL	3.7
1	C	168	ALA	3.7
1	B	239	ASP	3.6
1	B	70	ALA	3.5
1	D	171	LEU	3.4
1	A	170	GLY	3.3
1	C	131	HIS	3.2
1	D	74	SER	3.1
1	C	16	LEU	3.1
1	C	245	ALA	3.1
1	A	13	SER	3.0
1	C	226	ALA	3.0
1	D	172	GLU	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	53	ASP	2.9
1	B	51	HIS	2.9
1	B	25	ASN	2.8
1	B	169	GLU	2.8
1	D	43	GLU	2.8
1	B	50	ASP	2.7
1	A	2	SER	2.7
1	D	205	HIS	2.7
1	D	229	VAL	2.7
1	D	76	THR	2.7
1	B	242	ARG	2.7
1	B	60	ALA	2.7
1	D	197	ASN	2.7
1	B	131	HIS	2.6
1	C	164	ARG	2.6
1	A	245	ALA	2.6
1	A	122	GLY	2.6
1	C	132	ASN	2.6
1	D	232	THR	2.5
1	A	52	GLU	2.5
1	B	176	ASP	2.5
1	B	245	ALA	2.5
1	B	10	ARG	2.5
1	A	14	THR	2.5
1	A	235	ASP	2.5
1	B	246	GLU	2.5
1	D	12	ALA	2.5
1	B	30	ILE	2.4
1	B	183	GLY	2.4
1	A	11	TYR	2.4
1	B	52	GLU	2.4
1	A	174	VAL	2.4
1	B	243	VAL	2.3
1	A	186	GLY	2.3
1	B	170	GLY	2.3
1	C	176	ASP	2.3
1	B	168	ALA	2.2
1	B	7	ILE	2.2
1	C	235	ASP	2.2
1	D	136	ALA	2.2
1	D	118	GLN	2.2
1	A	200	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	227	GLN	2.2
1	B	69	ARG	2.2
1	D	116	LEU	2.2
1	B	6	ILE	2.1
1	C	205	HIS	2.1
1	B	76	THR	2.1
1	A	132	ASN	2.1
1	A	75	GLY	2.1
1	A	176	ASP	2.1
1	B	200	PRO	2.1
1	A	5	VAL	2.1
1	D	112	VAL	2.1
1	B	132	ASN	2.0
1	A	131	HIS	2.0
1	A	238	GLU	2.0
1	D	238	GLU	2.0
1	B	54	VAL	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.