



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:14 PM GMT

PDB ID : 4O93
Title : Crystal structure of Thermus thermophilis transhydrogenase domain II dimer
Authors : Leung, J.H.; Yamaguchi, M.; Moeller, A.; Schurig-Briccio, L.A.; Gennis, R.B.;
Potter, C.S.; Carragher, B.; Stout, C.D.
Deposited on : 2013-12-31
Resolution : 2.77 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

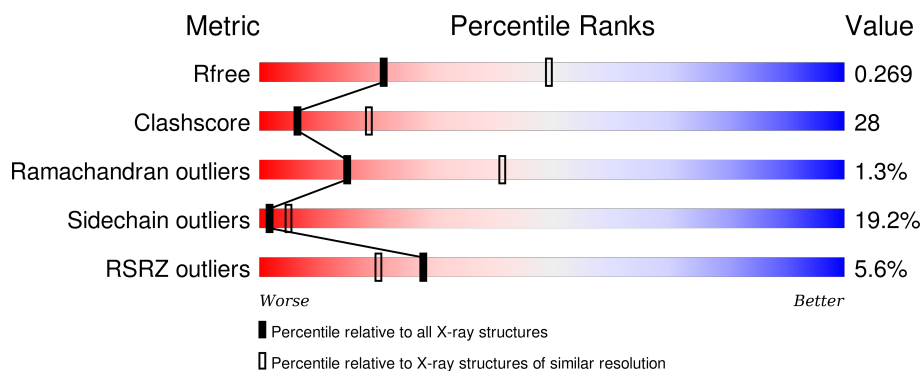
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.77 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	3004 (2.80-2.76)
Clashscore	102246	3480 (2.80-2.76)
Ramachandran outliers	100387	3423 (2.80-2.76)
Sidechain outliers	100360	3425 (2.80-2.76)
RSRZ outliers	91569	3016 (2.80-2.76)

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	94	<div> <div>4%</div> <div>61% 28% 12%</div> </div>
1	C	94	<div> <div>%</div> <div>45% 39% 11% . .</div> </div>
2	B	270	<div> <div>4%</div> <div>56% 32% 10% .</div> </div>
2	D	270	<div> <div>9%</div> <div>53% 33% 10% .</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5212 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 NAD(P) transhydrogenase subunit alpha 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	94	Total	C	N	O	S	0	0	0
			714	475	114	119	6			
1	C	90	Total	C	N	O	S	0	0	0
			678	453	106	113	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	16	CYS	ALA	CONFLICT	UNP Q72GR9
C	16	CYS	ALA	CONFLICT	UNP Q72GR9

- Molecule 2 is a protein called NAD(P) transhydrogenase subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	264	Total	C	N	O	S	0	0	0
			1916	1277	306	317	16			
2	D	260	Total	C	N	O	S	0	0	0
			1893	1262	302	313	16			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	258	ILE	-	EXPRESSION TAG	UNP Q72GS0
B	265	HIS	-	EXPRESSION TAG	UNP Q72GS0
B	266	HIS	-	EXPRESSION TAG	UNP Q72GS0
B	267	HIS	-	EXPRESSION TAG	UNP Q72GS0
B	268	HIS	-	EXPRESSION TAG	UNP Q72GS0
B	269	HIS	-	EXPRESSION TAG	UNP Q72GS0
B	270	HIS	-	EXPRESSION TAG	UNP Q72GS0
D	258	ILE	-	EXPRESSION TAG	UNP Q72GS0
D	265	HIS	-	EXPRESSION TAG	UNP Q72GS0
D	266	HIS	-	EXPRESSION TAG	UNP Q72GS0

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Chain	Residue	Modelled	Actual	Comment	Reference
D	267	HIS	-	EXPRESSION TAG	UNP Q72GS0
D	268	HIS	-	EXPRESSION TAG	UNP Q72GS0
D	269	HIS	-	EXPRESSION TAG	UNP Q72GS0
D	270	HIS	-	EXPRESSION TAG	UNP Q72GS0

- Molecule 3 is MERCURY (II) ION (three-letter code: HG) (formula: Hg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Hg 1 1	0	0
3	C	1	Total Hg 1 1	0	0

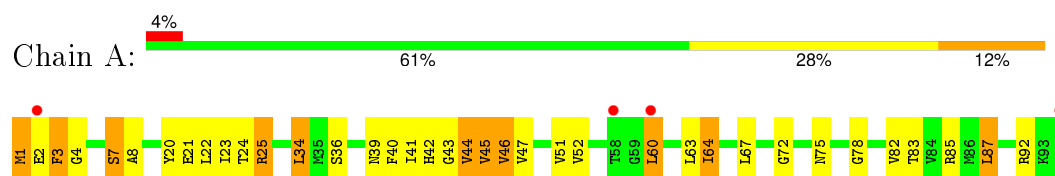
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O 1 1	0	0
4	B	2	Total O 2 2	0	0
4	C	2	Total O 2 2	0	0
4	D	4	Total O 4 4	0	0

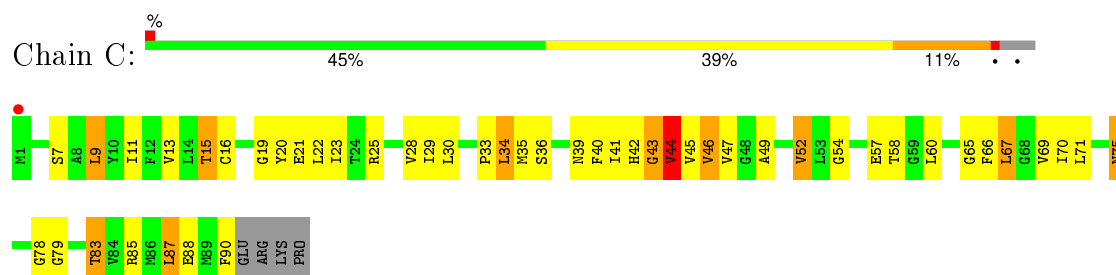
3 Residue-property plots [i](#)

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.

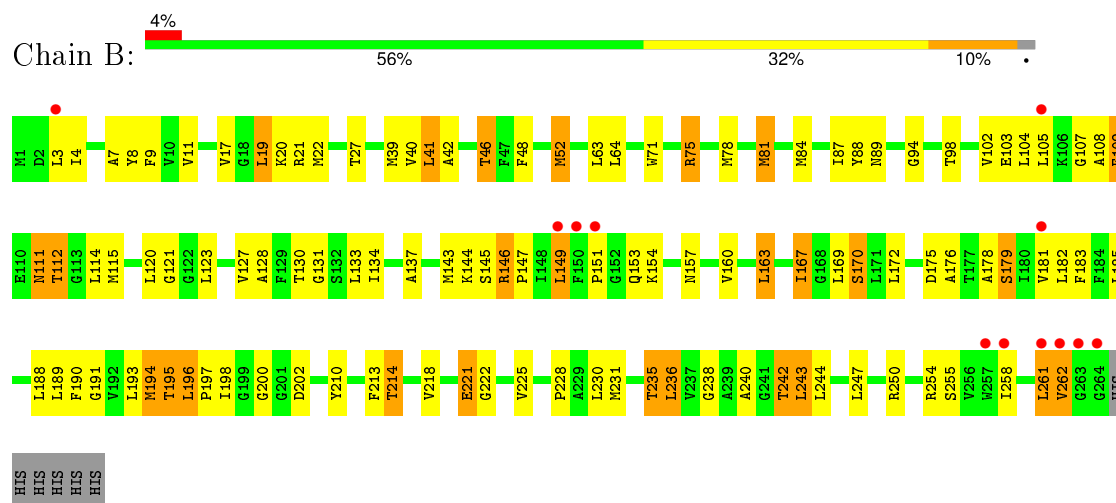
- Molecule 1: NAD(P) transhydrogenase subunit alpha 2



- Molecule 1: NAD(P) transhydrogenase subunit alpha 2

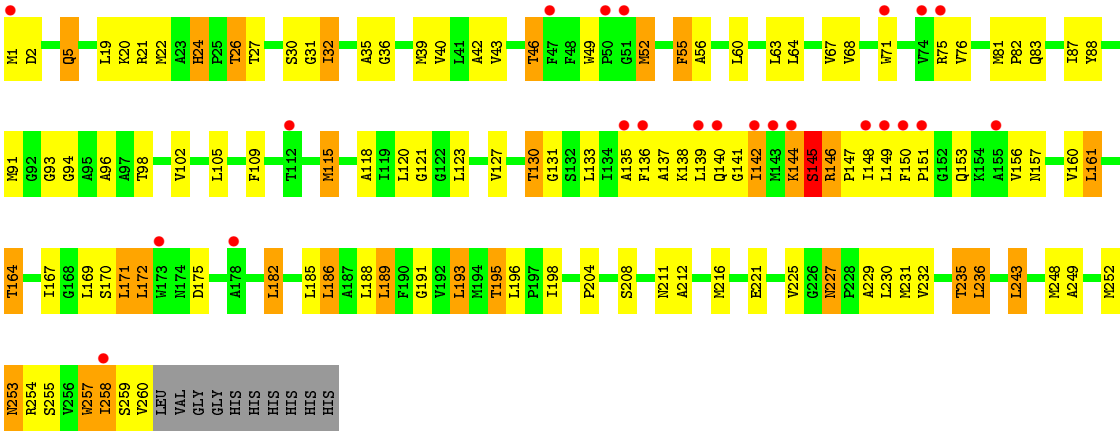


- Molecule 2: NAD(P) transhydrogenase subunit beta



- Molecule 2: NAD(P) transhydrogenase subunit beta





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	125.41 Å 86.92 Å 98.98 Å 90.00° 94.55° 90.00°	Depositor
Resolution (Å)	98.67 – 2.77 39.75 – 2.77	Depositor EDS
% Data completeness (in resolution range)	96.6 (98.67-2.77) 96.6 (39.75-2.77)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.70 (at 2.77 Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.204 , 0.269 0.204 , 0.269	Depositor DCC
R_{free} test set	1354 reflections (5.45%)	DCC
Wilson B-factor (Å ²)	90.1	Xtriage
Anisotropy	0.121	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 72.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 26219 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5212	wwPDB-VP
Average B, all atoms (Å ²)	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.15% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: HG

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	0.69	0/731	0.92	0/991
1	C	0.58	0/694	0.82	2/942 (0.2%)
2	B	0.65	0/1957	0.85	0/2666
2	D	0.60	0/1934	0.80	0/2635
All	All	0.63	0/5316	0.84	2/7234 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	D	0	1

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	C	87	LEU	CA-CB-CG	5.89	128.84	115.30
1	C	44	VAL	CB-CA-C	-5.87	100.26	111.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	142	ILE	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	714	0	739	55	0
1	C	678	0	700	54	0
2	B	1916	0	2032	117	0
2	D	1893	0	2006	122	0
3	A	1	0	0	0	0
3	C	1	0	0	1	0
4	A	1	0	0	0	0
4	B	2	0	0	0	0
4	C	2	0	0	0	0
4	D	4	0	0	0	0
All	All	5212	0	5477	294	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 28.

All (294) 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)
2:D:141:GLY:HA2	2:D:144:LYS:HB2	1.21	1.15
1:A:64:ILE:HD12	2:B:102:VAL:HG23	1.24	1.11
2:D:63:LEU:O	2:D:67:VAL:HG22	1.50	1.10
2:D:32:ILE:H	2:D:32:ILE:HD13	1.15	1.10
1:C:79:GLY:O	1:C:83:THR:HG22	1.52	1.10
2:B:115:MET:HG2	2:B:172:LEU:HD23	1.33	1.05
2:B:42:ALA:O	2:B:46:THR:HG22	1.60	1.02
2:D:157:ASN:HD21	2:D:193:LEU:HD22	1.19	1.01
2:B:19:LEU:HA	2:B:22:MET:HE2	1.39	1.00
2:B:255:SER:OG	2:B:258:ILE:HG13	1.62	0.99
2:D:149:LEU:HA	2:D:153:GLN:HE22	1.28	0.98
1:A:1:MET:H2	1:A:8:ALA:HB1	1.35	0.91
1:A:64:ILE:CD1	2:B:102:VAL:HG23	1.99	0.91
1:A:64:ILE:HD12	2:B:102:VAL:CG2	2.01	0.91
2:D:130:THR:CG2	2:D:191:GLY:HA3	2.02	0.90
2:D:157:ASN:ND2	2:D:193:LEU:HD22	1.90	0.85
2:B:19:LEU:HA	2:B:22:MET:CE	2.06	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:164:THR:HA	2:D:167:ILE:HD12	1.60	0.84
1:A:60:LEU:O	1:A:64:ILE:HG22	1.78	0.84
2:D:153:GLN:HA	2:D:156:VAL:HG13	1.59	0.84
2:B:231:MET:O	2:B:235:THR:HG23	1.78	0.83
2:B:131:GLY:HA2	2:B:195:THR:HG21	1.61	0.82
1:C:41:ILE:O	1:C:44:VAL:HG22	1.79	0.81
1:A:1:MET:H2	1:A:8:ALA:CB	1.92	0.81
1:A:1:MET:N	1:A:8:ALA:HB1	1.95	0.80
2:B:115:MET:HG2	2:B:172:LEU:CD2	2.12	0.79
2:D:21:ARG:O	2:D:27:THR:HG23	1.82	0.79
1:A:3:PHE:H	1:A:4:GLY:HA2	1.47	0.79
2:B:9:PHE:HZ	1:C:13:VAL:HG21	1.48	0.79
2:D:121:GLY:HA3	2:D:221:GLU:OE2	1.83	0.79
2:D:32:ILE:N	2:D:32:ILE:HD13	1.97	0.79
2:D:87:ILE:O	2:D:91:MET:HG2	1.83	0.78
2:D:27:THR:O	2:D:30:SER:HB3	1.83	0.78
2:D:32:ILE:H	2:D:32:ILE:CD1	1.97	0.77
2:D:109:PHE:CB	2:D:115:MET:HG3	2.15	0.76
2:B:19:LEU:HD23	2:B:22:MET:HE3	1.68	0.76
2:B:157:ASN:OD1	2:B:193:LEU:HB3	1.85	0.76
2:D:21:ARG:NH1	2:D:27:THR:OG1	2.19	0.75
2:D:144:LYS:HG2	2:D:145:SER:N	2.01	0.75
2:D:167:ILE:HD11	2:D:186:LEU:HD12	1.68	0.75
2:B:261:LEU:CD2	2:B:262:VAL:H	2.00	0.75
1:C:87:LEU:HD23	2:D:32:ILE:HD12	1.66	0.75
2:B:17:VAL:O	2:B:21:ARG:HG3	1.87	0.75
1:A:47:VAL:HG22	2:B:46:THR:HG21	1.69	0.74
1:A:85:ARG:CZ	2:B:78:MET:HE3	2.18	0.74
2:D:191:GLY:O	2:D:195:THR:HG22	1.88	0.74
1:C:29:ILE:HD12	1:C:29:ILE:H	1.52	0.73
2:B:19:LEU:HD23	2:B:22:MET:CE	2.18	0.73
2:D:138:LYS:HA	2:D:144:LYS:HA	1.70	0.73
2:B:94:GLY:O	2:B:98:THR:HG23	1.89	0.73
1:C:16:CYS:SG	3:C:500:HG:HG	2.06	0.72
2:B:255:SER:H	2:B:258:ILE:HD12	1.55	0.71
1:A:46:VAL:HG13	1:A:72:GLY:HA3	1.71	0.71
2:B:103:GLU:HG3	2:B:108:ALA:HB3	1.70	0.71
2:D:167:ILE:CD1	2:D:186:LEU:HD12	2.20	0.71
1:A:25:ARG:HA	1:A:25:ARG:NE	2.06	0.70
2:D:141:GLY:CA	2:D:144:LYS:HB2	2.11	0.70
2:D:150:PHE:CZ	2:D:153:GLN:HB2	2.27	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:146:ARG:CB	2:D:147:PRO:CD	2.70	0.69
1:C:87:LEU:CD2	2:D:32:ILE:HD12	2.23	0.69
2:D:160:VAL:O	2:D:164:THR:HG22	1.93	0.69
2:D:231:MET:O	2:D:235:THR:CG2	2.41	0.68
2:B:71:TRP:O	2:B:75:ARG:HG2	1.94	0.67
1:C:11:ILE:O	1:C:15:THR:HG23	1.94	0.67
2:B:178:ALA:O	2:B:181:VAL:HG22	1.95	0.67
2:D:5:GLN:HE21	2:D:5:GLN:HA	1.58	0.66
1:A:23:ILE:CG1	2:B:240:ALA:HB1	2.25	0.66
1:A:23:ILE:HG13	2:B:240:ALA:HB1	1.78	0.66
2:B:238:GLY:O	2:B:242:THR:HG23	1.96	0.66
2:B:128:ALA:HB1	2:B:214:THR:HG22	1.77	0.65
1:A:40:PHE:CZ	2:B:39:MET:HG3	2.31	0.65
2:D:146:ARG:HB2	2:D:147:PRO:HD2	1.77	0.65
2:D:94:GLY:O	2:D:98:THR:HG23	1.96	0.65
2:D:204:PRO:HG2	2:D:252:MET:HE1	1.79	0.65
2:D:71:TRP:HE1	2:D:75:ARG:HD2	1.62	0.64
2:D:191:GLY:O	2:D:195:THR:CG2	2.45	0.64
2:B:163:LEU:HD22	2:B:167:ILE:HG22	1.79	0.64
1:C:87:LEU:HD23	2:D:32:ILE:CD1	2.28	0.63
2:D:167:ILE:O	2:D:170:SER:OG	2.12	0.63
2:D:130:THR:HG22	2:D:191:GLY:HA3	1.78	0.63
2:B:11:VAL:HG23	2:B:41:LEU:HD13	1.81	0.63
2:B:222:GLY:O	2:B:225:VAL:O	2.17	0.62
2:B:144:LYS:HE3	2:B:146:ARG:HB2	1.80	0.62
2:D:146:ARG:HB2	2:D:147:PRO:CD	2.29	0.62
2:D:204:PRO:HG2	2:D:252:MET:CE	2.29	0.62
2:D:149:LEU:HA	2:D:153:GLN:NE2	2.07	0.62
1:A:45:VAL:HG13	2:B:218:VAL:HB	1.82	0.62
2:D:144:LYS:HG2	2:D:145:SER:H	1.65	0.61
1:C:71:LEU:HD23	2:D:91:MET:HE3	1.83	0.61
2:D:153:GLN:HA	2:D:156:VAL:CG1	2.31	0.61
2:D:231:MET:O	2:D:235:THR:HG23	2.01	0.61
2:D:71:TRP:NE1	2:D:75:ARG:HD2	2.15	0.61
2:D:164:THR:HB	2:D:186:LEU:HB3	1.82	0.61
1:A:2:GLU:HG2	2:B:114:LEU:HD21	1.82	0.61
2:B:221:GLU:O	2:B:225:VAL:HG22	2.00	0.60
2:D:221:GLU:O	2:D:225:VAL:HG22	2.00	0.60
1:A:25:ARG:HD3	1:C:25:ARG:HH21	1.66	0.60
1:A:3:PHE:N	1:A:4:GLY:HA2	2.14	0.60
2:B:261:LEU:HD23	2:B:262:VAL:H	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:111:ASN:HD22	2:B:111:ASN:C	2.05	0.60
1:C:36:SER:OG	1:C:83:THR:HB	2.02	0.59
1:C:71:LEU:HD22	2:D:91:MET:HA	1.84	0.59
1:A:25:ARG:HA	1:A:25:ARG:CZ	2.33	0.59
1:C:35:MET:HE3	2:D:248:MET:SD	2.42	0.59
2:B:81:MET:HE3	2:B:84:MET:HG3	1.83	0.59
1:A:23:ILE:HD12	1:A:34:LEU:HD11	1.83	0.59
2:B:8:TYR:OH	2:B:46:THR:HB	2.01	0.59
1:A:42:HIS:HD1	1:A:75:ASN:HD21	1.51	0.59
2:B:261:LEU:HD22	2:B:262:VAL:H	1.67	0.59
1:C:43:GLY:O	1:C:46:VAL:HG23	2.02	0.59
2:B:9:PHE:CZ	1:C:13:VAL:HG21	2.32	0.59
2:D:160:VAL:O	2:D:164:THR:CG2	2.51	0.58
2:D:127:VAL:HG13	2:D:191:GLY:HA2	1.86	0.58
1:A:46:VAL:HG13	1:A:72:GLY:CA	2.34	0.58
2:B:149:LEU:HA	2:B:153:GLN:HE22	1.68	0.58
1:A:83:THR:HG22	1:A:87:LEU:HD22	1.85	0.58
1:A:85:ARG:NE	2:B:78:MET:HE3	2.17	0.58
1:C:22:LEU:HD22	2:D:20:LYS:HG2	1.87	0.56
1:C:71:LEU:HD23	2:D:91:MET:CE	2.36	0.56
2:B:210:TYR:HA	2:B:213:PHE:HB2	1.87	0.56
1:A:78:GLY:O	1:A:82:VAL:HG23	2.06	0.56
2:D:185:LEU:O	2:D:189:LEU:HB2	2.06	0.56
2:D:150:PHE:HB2	2:D:151:PRO:HD2	1.89	0.55
2:B:4:ILE:HD11	2:B:48:PHE:O	2.07	0.55
1:A:47:VAL:HG13	2:B:46:THR:HG21	1.88	0.55
2:B:175:ASP:N	2:B:175:ASP:OD1	2.40	0.55
2:D:109:PHE:HB2	2:D:115:MET:HG3	1.86	0.54
2:B:238:GLY:O	2:B:242:THR:CG2	2.54	0.54
1:A:41:ILE:O	1:A:44:VAL:HG22	2.08	0.54
1:C:42:HIS:HE1	2:D:211:ASN:OD1	1.90	0.54
2:D:130:THR:HG21	2:D:188:LEU:O	2.07	0.54
2:B:131:GLY:CA	2:B:195:THR:HG21	2.34	0.54
1:A:2:GLU:HB2	2:B:114:LEU:HD11	1.89	0.54
1:A:85:ARG:NH2	2:B:78:MET:HE3	2.22	0.54
2:D:182:LEU:HD22	2:D:186:LEU:HG	1.90	0.53
1:C:11:ILE:O	1:C:15:THR:CG2	2.56	0.53
1:A:25:ARG:HG3	1:C:25:ARG:HE	1.72	0.53
2:B:21:ARG:HB3	2:B:27:THR:HB	1.91	0.53
2:D:148:ILE:HG12	2:D:196:LEU:HG	1.90	0.53
2:D:135:ALA:O	2:D:139:LEU:HD12	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:128:ALA:CB	2:B:214:THR:HG22	2.39	0.52
2:D:148:ILE:HD12	2:D:150:PHE:H	1.75	0.52
2:D:109:PHE:HB3	2:D:115:MET:HG3	1.90	0.52
2:D:71:TRP:CD1	2:D:75:ARG:HD2	2.45	0.52
1:C:42:HIS:HD2	1:C:75:ASN:OD1	1.92	0.51
2:B:42:ALA:O	2:B:46:THR:CG2	2.46	0.51
1:C:30:LEU:HD23	1:C:33:PRO:HG2	1.91	0.51
2:D:156:VAL:HG22	2:D:157:ASN:N	2.25	0.51
2:B:147:PRO:HB3	2:B:197:PRO:O	2.11	0.51
2:B:103:GLU:HG2	2:B:109:PHE:CE2	2.45	0.51
1:A:46:VAL:HG13	1:A:72:GLY:C	2.30	0.51
1:C:35:MET:CE	2:D:248:MET:SD	2.98	0.51
2:D:150:PHE:CZ	2:D:153:GLN:CB	2.93	0.51
2:D:81:MET:N	2:D:82:PRO:HD2	2.25	0.51
2:B:19:LEU:HD12	2:B:236:LEU:HD13	1.92	0.51
2:D:231:MET:O	2:D:235:THR:HG22	2.10	0.51
1:A:23:ILE:HG12	2:B:240:ALA:HB1	1.92	0.51
2:B:144:LYS:CE	2:B:146:ARG:HB2	2.41	0.51
1:A:64:ILE:C	1:A:64:ILE:HD13	2.31	0.51
2:B:7:ALA:O	2:B:11:VAL:HG23	2.10	0.51
2:D:146:ARG:HG2	2:D:146:ARG:HH11	1.76	0.51
1:C:39:ASN:HA	1:C:42:HIS:CE1	2.46	0.50
2:D:156:VAL:CG2	2:D:157:ASN:N	2.75	0.50
2:B:130:THR:O	2:B:134:ILE:HG12	2.12	0.50
2:B:195:THR:HA	2:B:198:ILE:HD12	1.93	0.50
1:C:21:GLU:OE1	1:C:21:GLU:HA	2.10	0.50
2:D:161:LEU:O	2:D:164:THR:HG23	2.11	0.49
1:A:47:VAL:O	1:A:51:VAL:HG23	2.12	0.49
2:B:137:ALA:HB1	2:B:143:MET:HB2	1.95	0.49
1:C:29:ILE:CD1	1:C:29:ILE:H	2.21	0.49
2:B:111:ASN:HD22	2:B:112:THR:N	2.10	0.49
2:B:9:PHE:CZ	1:C:9:LEU:HD13	2.47	0.49
1:C:49:ALA:O	1:C:52:VAL:HG12	2.13	0.49
2:B:190:PHE:CE2	2:B:194:MET:HG3	2.48	0.49
2:B:8:TYR:HD2	2:B:228:PRO:HD2	1.76	0.49
1:C:23:ILE:CD1	1:C:34:LEU:HD11	2.42	0.49
2:D:71:TRP:HE1	2:D:75:ARG:CD	2.26	0.49
2:D:255:SER:H	2:D:258:ILE:HG22	1.77	0.49
2:B:163:LEU:HD22	2:B:163:LEU:O	2.12	0.48
2:D:49:TRP:HB3	2:D:52:MET:HG3	1.95	0.48
1:A:24:THR:HG22	2:B:243:LEU:HD11	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:254:ARG:HE	2:B:258:ILE:HG21	1.78	0.48
2:D:131:GLY:HA2	2:D:195:THR:HG21	1.95	0.48
2:D:146:ARG:HG2	2:D:146:ARG:NH1	2.28	0.48
2:D:198:ILE:HD12	2:D:259:SER:O	2.14	0.48
2:B:81:MET:HE2	2:B:84:MET:HB2	1.96	0.48
2:D:36:GLY:O	2:D:40:VAL:HG23	2.14	0.48
1:A:43:GLY:O	1:A:46:VAL:HG22	2.14	0.47
2:B:89:ASN:HD21	2:B:214:THR:HG23	1.80	0.47
2:D:153:GLN:CA	2:D:156:VAL:HG13	2.38	0.47
2:D:257:TRP:HA	2:D:260:VAL:HG12	1.96	0.47
1:A:3:PHE:H	1:A:4:GLY:CA	2.20	0.47
2:B:81:MET:HE3	2:B:84:MET:CG	2.44	0.47
2:B:130:THR:OG1	2:B:191:GLY:HA3	2.15	0.47
1:C:40:PHE:HE2	2:D:35:ALA:HB1	1.79	0.47
1:C:42:HIS:CE1	2:D:211:ASN:OD1	2.67	0.47
2:D:91:MET:HB3	2:D:91:MET:HE2	1.66	0.47
1:A:85:ARG:CZ	2:B:78:MET:CE	2.89	0.46
2:B:167:ILE:HD11	2:B:183:PHE:N	2.31	0.46
2:D:130:THR:CG2	2:D:191:GLY:CA	2.84	0.46
2:B:146:ARG:CZ	2:B:146:ARG:HA	2.45	0.46
2:D:102:VAL:HA	2:D:105:LEU:HD12	1.97	0.46
2:D:227:ASN:HD21	2:D:229:ALA:HB3	1.81	0.46
2:B:163:LEU:O	2:B:167:ILE:HG22	2.16	0.46
2:B:191:GLY:O	2:B:195:THR:HG22	2.16	0.46
1:A:45:VAL:CG1	2:B:218:VAL:HB	2.45	0.46
2:D:212:ALA:O	2:D:216:MET:HG3	2.16	0.46
1:A:3:PHE:N	1:A:4:GLY:CA	2.79	0.46
2:B:81:MET:HA	2:B:81:MET:CE	2.46	0.45
2:D:140:GLN:HB3	2:D:142:ILE:HG12	1.98	0.45
1:A:21:GLU:HG3	1:C:21:GLU:HG3	1.97	0.45
1:A:51:VAL:HA	2:B:52:MET:HE1	1.98	0.45
2:D:123:LEU:HD23	2:D:123:LEU:O	2.16	0.45
1:A:45:VAL:HG13	2:B:218:VAL:CB	2.46	0.45
1:C:35:MET:CE	2:D:208:SER:HB2	2.46	0.45
2:D:39:MET:O	2:D:43:VAL:HG23	2.17	0.45
1:C:9:LEU:HA	1:C:9:LEU:HD23	1.70	0.45
2:D:169:LEU:O	2:D:172:LEU:HB2	2.17	0.45
2:B:191:GLY:O	2:B:195:THR:CG2	2.65	0.45
1:C:67:LEU:HA	1:C:67:LEU:HD22	1.80	0.45
1:C:20:TYR:CZ	2:D:243:LEU:HG	2.52	0.44
1:A:7:SER:HB3	1:C:7:SER:HB3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:23:ILE:HD12	1:C:34:LEU:HD11	1.98	0.44
1:A:20:TYR:CE2	2:B:243:LEU:HG	2.52	0.44
2:D:123:LEU:C	2:D:123:LEU:HD23	2.38	0.44
2:B:9:PHE:CE1	1:C:9:LEU:HD13	2.53	0.44
2:D:253:ASN:N	2:D:253:ASN:OD1	2.49	0.44
2:B:154:LYS:HE3	2:B:154:LYS:HB2	1.87	0.44
2:D:22:MET:HG3	2:D:31:GLY:HA3	1.99	0.44
1:A:47:VAL:CG2	2:B:46:THR:HG21	2.43	0.43
2:B:78:MET:HE2	2:B:78:MET:HA	1.99	0.43
2:D:146:ARG:CG	2:D:146:ARG:HH11	2.31	0.43
2:B:71:TRP:CD1	2:B:75:ARG:CZ	3.00	0.43
2:B:149:LEU:HA	2:B:153:GLN:NE2	2.33	0.43
1:C:42:HIS:CD2	1:C:75:ASN:OD1	2.72	0.43
2:B:81:MET:CE	2:B:84:MET:HG3	2.47	0.43
1:C:30:LEU:O	1:C:34:LEU:HB2	2.19	0.43
2:D:64:LEU:O	2:D:68:VAL:HG23	2.19	0.43
1:C:85:ARG:O	1:C:88:GLU:HB2	2.19	0.43
2:B:176:ALA:O	2:B:179:SER:N	2.52	0.43
2:D:24:HIS:HB2	2:D:27:THR:HG22	2.00	0.43
1:C:28:VAL:C	1:C:30:LEU:H	2.22	0.43
2:B:127:VAL:HG13	2:B:191:GLY:HA2	2.01	0.43
1:A:39:ASN:ND2	1:A:42:HIS:CE1	2.87	0.43
2:B:39:MET:O	2:B:40:VAL:C	2.55	0.43
2:B:169:LEU:O	2:B:170:SER:C	2.57	0.43
2:D:123:LEU:O	2:D:127:VAL:HG23	2.19	0.42
2:D:252:MET:C	2:D:254:ARG:H	2.23	0.42
1:A:45:VAL:HG13	2:B:218:VAL:CG1	2.49	0.42
2:D:83:GLN:HB2	2:D:136:PHE:CD1	2.54	0.42
1:A:22:LEU:HD22	2:B:20:LYS:HG3	2.01	0.42
2:D:249:ALA:O	2:D:252:MET:O	2.36	0.42
1:C:65:GLY:O	1:C:69:VAL:HG23	2.19	0.42
2:D:148:ILE:HD12	2:D:149:LEU:N	2.34	0.42
2:D:115:MET:O	2:D:118:ALA:HB3	2.19	0.42
1:C:43:GLY:C	1:C:45:VAL:N	2.72	0.42
1:A:78:GLY:HA3	2:B:88:TYR:CE2	2.55	0.42
1:C:66:PHE:CE2	1:C:70:ILE:HD11	2.55	0.42
2:B:193:LEU:HA	2:B:196:LEU:HD22	2.01	0.42
2:B:130:THR:HG23	2:B:188:LEU:HD22	2.01	0.42
2:B:131:GLY:HA2	2:B:195:THR:CG2	2.40	0.42
2:D:232:VAL:O	2:D:236:LEU:HB2	2.19	0.42
1:C:19:GLY:HA2	2:D:236:LEU:HD22	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:148:ILE:HG12	2:D:196:LEU:CG	2.49	0.42
2:B:145:SER:HB2	2:B:146:ARG:NH1	2.35	0.42
2:D:227:ASN:HD22	2:D:230:LEU:H	1.67	0.42
1:C:75:ASN:C	1:C:75:ASN:HD22	2.23	0.42
1:C:47:VAL:HG22	2:D:46:THR:HG21	2.02	0.42
1:C:78:GLY:HA3	2:D:88:TYR:CZ	2.55	0.42
2:B:255:SER:CB	2:B:258:ILE:HG13	2.49	0.42
1:A:1:MET:N	1:A:8:ALA:CB	2.67	0.41
2:B:167:ILE:HD11	2:B:182:LEU:HB3	2.01	0.41
2:B:231:MET:O	2:B:235:THR:CG2	2.59	0.41
2:B:130:THR:HG23	2:B:188:LEU:CD2	2.50	0.41
2:B:103:GLU:HG2	2:B:109:PHE:HE2	1.84	0.41
2:D:171:LEU:HD12	2:D:175:ASP:HA	2.02	0.41
2:B:87:ILE:HD12	2:B:133:LEU:HD23	2.02	0.41
2:B:111:ASN:ND2	2:B:111:ASN:C	2.71	0.41
2:D:42:ALA:O	2:D:46:THR:CG2	2.69	0.41
2:B:121:GLY:HA3	2:B:221:GLU:OE1	2.20	0.41
1:A:36:SER:O	1:A:39:ASN:HB3	2.20	0.41
2:D:55:PHE:O	2:D:56:ALA:C	2.59	0.41
2:D:204:PRO:HG2	2:D:252:MET:HE3	2.03	0.41
2:D:144:LYS:O	2:D:145:SER:CB	2.69	0.41
2:B:160:VAL:HG21	2:B:193:LEU:HD11	2.03	0.41
1:C:78:GLY:HA3	2:D:88:TYR:CE2	2.56	0.41
2:B:202:ASP:OD1	2:B:254:ARG:NH2	2.54	0.41
1:A:23:ILE:HG12	2:B:240:ALA:CB	2.50	0.40
1:A:39:ASN:HD21	2:B:89:ASN:HA	1.86	0.40
2:D:136:PHE:O	2:D:137:ALA:C	2.60	0.40
1:C:36:SER:O	1:C:39:ASN:HB3	2.21	0.40
2:B:19:LEU:HD12	2:B:236:LEU:CD1	2.52	0.40
1:C:34:LEU:HD23	2:D:22:MET:O	2.20	0.40
2:D:93:GLY:O	2:D:96:ALA:HB3	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	92/94 (98%)	80 (87%)	11 (12%)	1 (1%)	17	47
1	C	88/94 (94%)	79 (90%)	7 (8%)	2 (2%)	8	24
2	B	262/270 (97%)	236 (90%)	22 (8%)	4 (2%)	13	37
2	D	258/270 (96%)	229 (89%)	27 (10%)	2 (1%)	24	56
All	All	700/728 (96%)	624 (89%)	67 (10%)	9 (1%)	15	41

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3	PHE
2	B	107	GLY
1	C	43	GLY
2	D	26	THR
2	D	145	SER
2	B	151	PRO
2	B	200	GLY
1	C	54	GLY
2	B	262	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	74/74 (100%)	60 (81%)	14 (19%)	2	5
1	C	70/74 (95%)	57 (81%)	13 (19%)	2	5
2	B	189/195 (97%)	151 (80%)	38 (20%)	1	4
2	D	187/195 (96%)	152 (81%)	35 (19%)	2	5
All	All	520/538 (97%)	420 (81%)	100 (19%)	2	5

All (100) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	7	SER
1	A	25	ARG
1	A	34	LEU
1	A	44	VAL
1	A	45	VAL
1	A	46	VAL
1	A	52	VAL
1	A	60	LEU
1	A	63	LEU
1	A	64	ILE
1	A	67	LEU
1	A	87	LEU
1	A	92	ARG
2	B	3	LEU
2	B	19	LEU
2	B	41	LEU
2	B	46	THR
2	B	52	MET
2	B	63	LEU
2	B	64	LEU
2	B	75	ARG
2	B	81	MET
2	B	104	LEU
2	B	105	LEU
2	B	109	PHE
2	B	111	ASN
2	B	112	THR
2	B	120	LEU
2	B	123	LEU
2	B	146	ARG
2	B	149	LEU
2	B	163	LEU
2	B	167	ILE
2	B	170	SER
2	B	179	SER
2	B	185	LEU
2	B	189	LEU
2	B	194	MET
2	B	195	THR
2	B	196	LEU
2	B	214	THR
2	B	221	GLU

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Mol	Chain	Res	Type
2	B	230	LEU
2	B	235	THR
2	B	236	LEU
2	B	242	THR
2	B	243	LEU
2	B	244	LEU
2	B	247	LEU
2	B	250	ARG
2	B	261	LEU
1	C	9	LEU
1	C	15	THR
1	C	34	LEU
1	C	44	VAL
1	C	46	VAL
1	C	52	VAL
1	C	57	GLU
1	C	58	THR
1	C	60	LEU
1	C	67	LEU
1	C	75	ASN
1	C	83	THR
1	C	90	PHE
2	D	1	MET
2	D	2	ASP
2	D	5	GLN
2	D	19	LEU
2	D	24	HIS
2	D	26	THR
2	D	32	ILE
2	D	46	THR
2	D	52	MET
2	D	55	PHE
2	D	60	LEU
2	D	76	VAL
2	D	115	MET
2	D	120	LEU
2	D	130	THR
2	D	133	LEU
2	D	144	LYS
2	D	145	SER
2	D	146	ARG
2	D	161	LEU

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Mol	Chain	Res	Type
2	D	164	THR
2	D	171	LEU
2	D	172	LEU
2	D	182	LEU
2	D	186	LEU
2	D	189	LEU
2	D	193	LEU
2	D	195	THR
2	D	227	ASN
2	D	235	THR
2	D	236	LEU
2	D	243	LEU
2	D	253	ASN
2	D	257	TRP
2	D	258	ILE

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

Mol	Chain	Res	Type
1	A	39	ASN
2	B	24	HIS
2	B	89	ASN
2	B	111	ASN
2	B	153	GLN
1	C	42	HIS
1	C	75	ASN
2	D	5	GLN
2	D	140	GLN
2	D	153	GLN
2	D	157	ASN
2	D	174	ASN
2	D	227	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	94/94 (100%)	0.14	4 (4%) 39 31	58, 72, 108, 137	0
1	C	90/94 (95%)	0.07	1 (1%) 82 77	65, 81, 117, 133	0
2	B	264/270 (97%)	0.03	12 (4%) 37 29	59, 75, 100, 136	0
2	D	260/270 (96%)	0.24	23 (8%) 12 7	64, 86, 120, 138	0
All	All	708/728 (97%)	0.13	40 (5%) 28 20	58, 79, 114, 138	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	149	LEU	7.7
2	D	142	ILE	6.2
1	A	60	LEU	6.0
2	D	148	ILE	5.6
2	B	262	VAL	5.5
2	D	151	PRO	5.3
2	D	50	PRO	4.5
2	B	263	GLY	4.2
2	D	150	PHE	4.1
2	D	71	TRP	4.0
2	B	261	LEU	3.9
2	D	155	ALA	3.4
2	B	3	LEU	3.4
2	D	173	TRP	3.3
2	B	150	PHE	3.1
2	B	181	VAL	3.0
2	D	1	MET	2.9
1	A	94	PRO	2.8
2	D	75	ARG	2.8
2	B	258	ILE	2.7
2	D	139	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
2	B	149	LEU	2.7
2	B	105	LEU	2.6
1	A	2	GLU	2.5
2	D	51	GLY	2.5
2	D	258	ILE	2.5
2	D	144	LYS	2.5
2	D	74	VAL	2.5
2	B	257	TRP	2.4
2	D	136	PHE	2.4
1	C	1	MET	2.3
2	D	140	GLN	2.3
2	D	178	ALA	2.2
2	D	112	THR	2.2
1	A	58	THR	2.1
2	D	135	ALA	2.1
2	B	264	GLY	2.1
2	B	151	PRO	2.1
2	D	47	PHE	2.1
2	D	143	MET	2.1

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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	HG	C	500	1/1	0.99	0.10	-	82,82,82,82	1
3	HG	A	500	1/1	0.99	0.09	-	78,78,78,78	1

6.5 Other polymers [i](#)

There are no such residues in this entry.