



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 08:36 AM UTC

PDB ID : 3E8Z / pdb_00003e8z
Title : X-ray structure of rat arginase I-N130A mutant: the unliganded complex
Authors : Shishova, E.Y.; Di Costanzo, L.; Christianson, D.W.
Deposited on : 2008-08-20
Resolution : 2.00 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

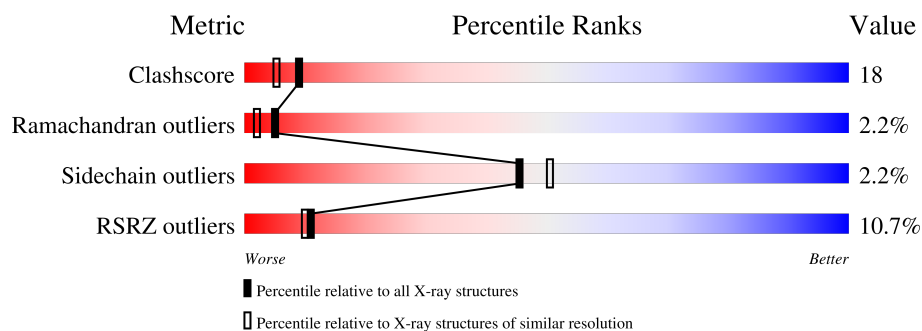
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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))
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	323	
1	B	323	
1	C	323	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7348 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 Arginase-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	308	Total	C	N	O	S	0	0	0
			2341	1494	398	442	7			
1	B	308	Total	C	N	O	S	0	0	0
			2341	1494	398	442	7			
1	C	308	Total	C	N	O	S	0	0	0
			2341	1494	398	442	7			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	130	ALA	ASN	engineered mutation	UNP P07824
B	130	ALA	ASN	engineered mutation	UNP P07824
C	130	ALA	ASN	engineered mutation	UNP P07824

- Molecule 2 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Mn	0	0
			2	2		
2	B	2	Total	Mn	0	0
			2	2		
2	C	2	Total	Mn	0	0
			2	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	134	Total	O	0	0
			134	134		
3	B	111	Total	O	0	0
			111	111		

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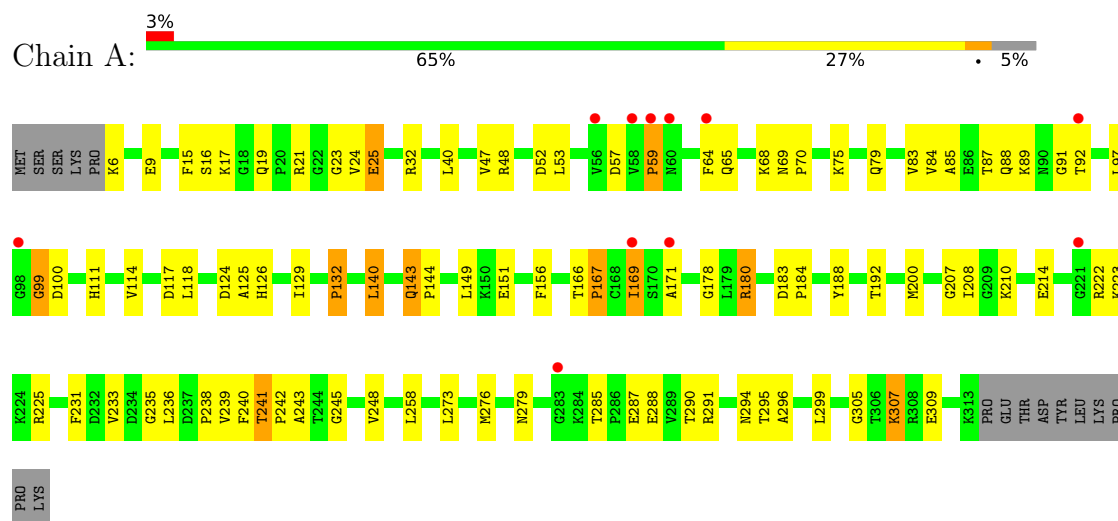
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	74	Total	O	0	0
			74	74		

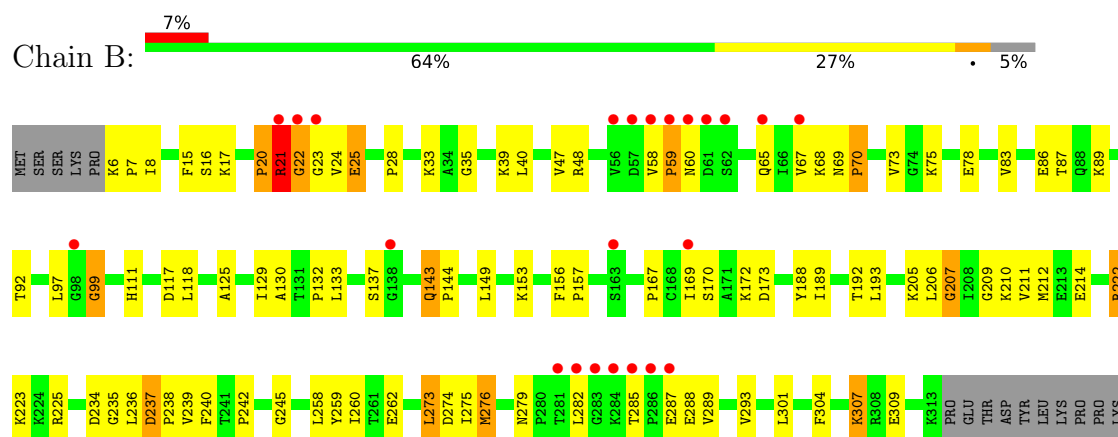
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

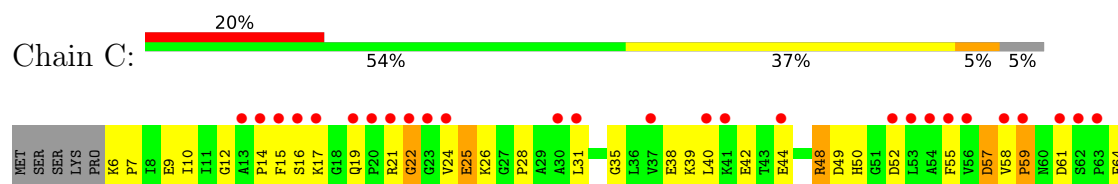
• Molecule 1: Arginase-1

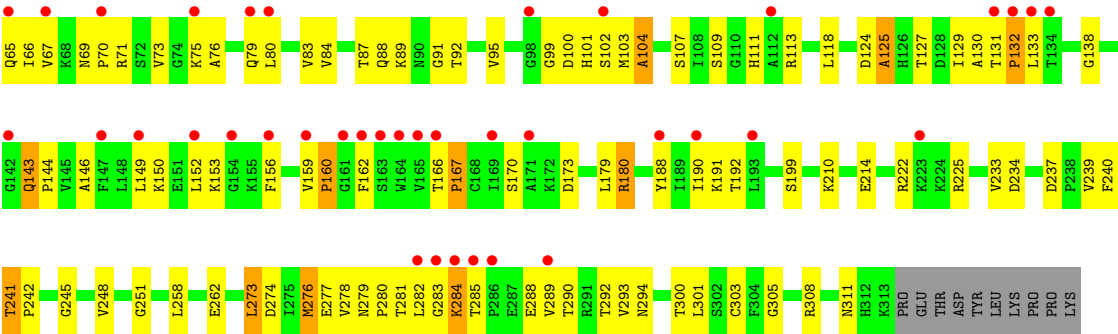


• Molecule 1: Arginase-1



• Molecule 1: Arginase-1





4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	87.50Å 87.50Å 100.11Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	41.77 – 2.00 41.77 – 2.00	Depositor EDS
% Data completeness (in resolution range)	91.7 (41.77-2.00) 91.8 (41.77-2.00)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.16 (at 2.00Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.236 , 0.280 0.245 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	20.0	Xtriage
Anisotropy	0.633	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 54.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.21$	Xtriage
Estimated twinning fraction	0.097 for -h,-k,l 0.308 for h,-h-k,-l 0.097 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	7348	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.52% 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 ⓘ

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

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	0.46	0/2392	1.01	14/3247 (0.4%)
1	B	0.45	0/2392	0.98	11/3247 (0.3%)
1	C	0.40	0/2392	0.97	9/3247 (0.3%)
All	All	0.44	0/7176	0.99	34/9741 (0.3%)

There are no bond length outliers.

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	207	GLY	N-CA-C	-8.38	102.35	112.48
1	A	125	ALA	N-CA-C	-7.64	103.42	112.89
1	B	125	ALA	N-CA-C	-7.23	104.46	113.28
1	C	125	ALA	N-CA-C	-7.20	104.30	113.23
1	B	276	MET	N-CA-C	7.11	120.60	110.14
1	A	305	GLY	N-CA-C	7.11	122.11	113.79
1	A	207	GLY	N-CA-C	-6.89	104.15	112.48
1	A	241	THR	CA-C-N	6.63	126.41	119.05
1	A	241	THR	C-N-CA	6.63	126.41	119.05
1	B	235	GLY	N-CA-C	-6.35	106.47	114.16
1	A	97	LEU	N-CA-C	-6.34	98.91	109.24
1	C	245	GLY	N-CA-C	6.25	119.75	112.50
1	A	276	MET	N-CA-C	6.20	119.30	109.81
1	B	245	GLY	N-CA-C	6.19	121.66	113.37
1	A	99	GLY	N-CA-C	-5.99	98.97	113.18
1	C	276	MET	N-CA-C	5.95	118.51	109.95
1	C	225	ARG	N-CA-C	5.87	113.30	108.07
1	B	237	ASP	CA-C-N	5.85	125.53	119.56
1	B	237	ASP	C-N-CA	5.85	125.53	119.56
1	A	140	LEU	N-CA-C	5.75	119.39	112.38
1	A	245	GLY	N-CA-C	5.65	120.00	112.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	65	GLN	CB-CA-C	-5.65	109.55	117.23
1	A	231	PHE	N-CA-C	5.56	117.79	108.73
1	C	102	SER	N-CA-C	-5.47	105.47	111.82
1	C	241	THR	CA-C-N	5.46	124.92	119.24
1	C	241	THR	C-N-CA	5.46	124.92	119.24
1	C	104	ALA	N-CA-C	-5.39	105.97	112.54
1	C	305	GLY	N-CA-C	5.32	121.07	114.37
1	B	206	LEU	N-CA-C	5.16	118.73	112.23
1	B	21	ARG	N-CA-C	5.15	121.78	110.80
1	A	183	ASP	CA-C-N	5.09	124.53	119.24
1	A	183	ASP	C-N-CA	5.09	124.53	119.24
1	A	169	ILE	N-CA-C	5.04	115.97	108.46
1	B	99	GLY	N-CA-C	-5.02	101.29	113.18

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	2341	0	2375	72	0
1	B	2341	0	2375	78	0
1	C	2341	0	2375	112	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
3	A	134	0	0	2	0
3	B	111	0	0	4	0
3	C	74	0	0	1	0
All	All	7348	0	7125	260	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 18.

All (260) 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:B:222:ARG:HD3	1:B:223:LYS:HG2	1.21	1.12
1:A:238:PRO:O	1:A:242:PRO:HG3	1.64	0.95
1:B:7:PRO:HG2	1:B:92:THR:HG22	1.56	0.88
1:A:15:PHE:O	1:A:99:GLY:HA3	1.77	0.85
1:B:117:ASP:O	1:B:225:ARG:HD2	1.76	0.85
1:B:170:SER:HB3	1:B:173:ASP:OD2	1.78	0.83
1:C:21:ARG:HH21	1:C:282:LEU:HD22	1.47	0.79
1:C:9:GLU:HG2	1:C:87:THR:HG21	1.65	0.79
1:C:210:LYS:HE3	1:C:214:GLU:OE2	1.83	0.77
1:B:149:LEU:HD23	1:B:169:ILE:HG13	1.66	0.76
1:C:21:ARG:NH2	1:C:282:LEU:HD22	2.02	0.73
1:C:35:GLY:O	1:C:39:LYS:HG3	1.89	0.72
1:B:15:PHE:CZ	1:B:17:LYS:HB2	2.25	0.72
1:A:75:LYS:O	1:A:79:GLN:HG3	1.89	0.71
1:B:21:ARG:NH2	1:B:282:LEU:HD22	2.05	0.71
1:C:143:GLN:N	1:C:144:PRO:HD2	2.05	0.71
1:A:15:PHE:CZ	1:A:17:LYS:HB2	2.26	0.70
1:A:143:GLN:N	1:A:144:PRO:HD2	2.05	0.70
1:C:40:LEU:HD23	1:C:301:LEU:HD23	1.73	0.70
1:A:117:ASP:O	1:A:225:ARG:HD2	1.91	0.70
1:C:146:ALA:HA	1:C:152:LEU:HD12	1.72	0.70
1:B:15:PHE:O	1:B:99:GLY:HA3	1.92	0.69
1:B:25:GLU:H	1:B:25:GLU:CD	2.01	0.69
1:C:150:LYS:HA	1:C:167:PRO:HB3	1.74	0.69
1:C:25:GLU:CD	1:C:25:GLU:H	2.01	0.68
1:B:24:VAL:HG22	1:B:99:GLY:HA2	1.76	0.68
1:A:53:LEU:HD21	1:A:83:VAL:HG21	1.75	0.67
1:C:24:VAL:HG22	1:C:99:GLY:HA2	1.75	0.67
1:C:240:PHE:C	1:C:242:PRO:HD3	2.19	0.67
1:C:290:THR:HG22	1:C:294:ASN:ND2	2.10	0.67
1:B:39:LYS:HE2	1:B:301:LEU:HD11	1.78	0.66
1:A:290:THR:HG22	1:A:294:ASN:ND2	2.11	0.66
1:C:12:GLY:HA3	1:C:52:ASP:OD1	1.96	0.66
1:A:290:THR:HG22	1:A:294:ASN:HD21	1.61	0.65
1:B:205:LYS:HA	3:B:600:HOH:O	1.96	0.65
1:B:258:LEU:O	1:B:262:GLU:HG3	1.98	0.64
1:B:210:LYS:HE3	1:B:214:GLU:OE2	1.98	0.64
1:B:222:ARG:HG3	3:B:605:HOH:O	1.97	0.64
1:A:143:GLN:N	1:A:144:PRO:CD	2.61	0.63
1:B:21:ARG:HH21	1:B:282:LEU:HD22	1.63	0.63
1:C:9:GLU:HG2	1:C:87:THR:CG2	2.29	0.63
1:C:16:SER:HB2	1:C:19:GLN:HE22	1.64	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:10:ILE:HD11	1:C:40:LEU:HD12	1.81	0.63
1:B:222:ARG:HD3	1:B:223:LYS:CG	2.14	0.63
1:A:69:ASN:N	1:A:70:PRO:HD3	2.13	0.62
1:C:143:GLN:H	1:C:144:PRO:CD	2.12	0.62
1:B:143:GLN:N	1:B:144:PRO:HD2	2.14	0.62
1:C:79:GLN:O	1:C:83:VAL:HG23	2.00	0.62
1:C:143:GLN:N	1:C:144:PRO:CD	2.62	0.62
1:B:7:PRO:CG	1:B:92:THR:HG22	2.27	0.62
1:C:9:GLU:OE2	1:C:50:HIS:HB2	1.99	0.61
1:C:25:GLU:O	1:C:28:PRO:HD2	2.01	0.61
1:C:39:LYS:HE2	1:C:301:LEU:HD11	1.82	0.61
1:B:143:GLN:N	1:B:144:PRO:CD	2.65	0.60
1:B:20:PRO:O	1:B:21:ARG:O	2.20	0.60
1:C:69:ASN:N	1:C:70:PRO:HD3	2.17	0.59
1:C:170:SER:HB3	1:C:173:ASP:OD2	2.02	0.59
1:A:287:GLU:OE1	1:A:291:ARG:NH2	2.34	0.59
1:B:222:ARG:O	1:B:223:LYS:HD3	2.03	0.59
1:B:273:LEU:HD23	1:B:274:ASP:N	2.18	0.59
1:B:40:LEU:HB3	1:B:47:VAL:HG21	1.84	0.59
1:C:109:SER:O	1:C:113:ARG:HG3	2.01	0.59
1:A:240:PHE:C	1:A:242:PRO:HD3	2.28	0.58
1:A:241:THR:N	1:A:242:PRO:HD3	2.18	0.58
1:B:275:ILE:C	1:B:276:MET:HE2	2.29	0.58
1:A:239:VAL:O	1:A:291:ARG:HD3	2.04	0.58
1:C:180:ARG:HG3	1:C:248:VAL:HG11	1.85	0.58
1:A:285:THR:OG1	1:A:287:GLU:HG3	2.03	0.57
1:C:15:PHE:CZ	1:C:17:LYS:HB2	2.38	0.57
1:C:31:LEU:HD23	1:C:293:VAL:HG13	1.85	0.57
1:C:69:ASN:O	1:C:73:VAL:HG23	2.03	0.57
1:C:233:VAL:HG11	1:C:278:VAL:HG22	1.87	0.57
1:B:23:GLY:HA2	1:B:25:GLU:OE2	2.05	0.57
1:C:132:PRO:HD2	1:C:156:PHE:CD2	2.39	0.57
1:C:75:LYS:NZ	1:C:79:GLN:HG2	2.20	0.56
1:C:188:TYR:CZ	1:C:192:THR:HG21	2.40	0.56
1:B:39:LYS:HE2	1:B:301:LEU:CD1	2.36	0.56
1:B:307:LYS:HZ3	1:B:309:GLU:CG	2.18	0.56
1:B:275:ILE:O	1:B:276:MET:HE2	2.06	0.56
1:A:9:GLU:HG2	1:A:87:THR:HG21	1.88	0.56
1:B:83:VAL:O	1:B:87:THR:HG23	2.05	0.56
1:C:118:LEU:C	1:C:118:LEU:HD12	2.32	0.55
1:A:21:ARG:HG3	1:A:21:ARG:HH11	1.70	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:24:VAL:HG22	1:A:99:GLY:HA2	1.89	0.55
1:A:143:GLN:H	1:A:144:PRO:CD	2.19	0.55
1:B:238:PRO:O	1:B:242:PRO:HG3	2.06	0.55
1:B:240:PHE:C	1:B:242:PRO:HD3	2.31	0.55
1:A:296:ALA:HB2	3:A:629:HOH:O	2.06	0.55
1:A:118:LEU:C	1:A:118:LEU:HD12	2.32	0.55
1:B:153:LYS:HB2	1:B:167:PRO:HG2	1.88	0.54
1:A:233:VAL:HG11	3:A:629:HOH:O	2.07	0.54
1:C:38:GLU:O	1:C:42:GLU:HG3	2.07	0.54
1:B:307:LYS:HB2	1:B:307:LYS:NZ	2.24	0.53
1:C:146:ALA:HA	1:C:152:LEU:CD1	2.39	0.53
1:B:279:ASN:C	1:B:279:ASN:HD22	2.15	0.53
1:C:25:GLU:CD	1:C:25:GLU:N	2.67	0.53
1:C:285:THR:OG1	1:C:288:GLU:HG3	2.08	0.53
1:A:208:ILE:HG23	3:B:600:HOH:O	2.08	0.53
1:A:210:LYS:HE3	1:A:214:GLU:OE2	2.08	0.53
1:B:68:LYS:NZ	1:B:137:SER:O	2.42	0.53
1:C:80:LEU:O	1:C:84:VAL:HG23	2.09	0.53
1:C:279:ASN:ND2	1:C:281:THR:H	2.07	0.53
1:C:237:ASP:OD1	1:C:239:VAL:HG23	2.09	0.52
1:C:290:THR:HG22	1:C:294:ASN:HD21	1.75	0.52
1:C:258:LEU:HD13	1:C:308:ARG:HD3	1.92	0.52
1:A:21:ARG:HG3	1:A:21:ARG:NH1	2.25	0.52
1:A:85:ALA:O	1:A:89:LYS:HG3	2.10	0.52
1:B:188:TYR:CZ	1:B:192:THR:HG21	2.45	0.52
1:A:149:LEU:HD21	1:A:171:ALA:HA	1.91	0.51
1:A:149:LEU:HD23	1:A:169:ILE:O	2.10	0.51
1:C:258:LEU:O	1:C:262:GLU:HG3	2.09	0.51
1:A:9:GLU:HG2	1:A:87:THR:CG2	2.40	0.51
1:C:26:LYS:HB2	1:C:280:PRO:CG	2.41	0.51
1:C:273:LEU:HD22	1:C:274:ASP:N	2.26	0.51
1:A:6:LYS:HG3	1:A:91:GLY:O	2.11	0.51
1:A:40:LEU:HB3	1:A:47:VAL:HG21	1.92	0.51
1:B:307:LYS:HZ3	1:B:309:GLU:HG2	1.75	0.51
1:C:190:ILE:HG13	1:C:191:LYS:N	2.25	0.51
1:C:283:GLY:O	1:C:284:LYS:C	2.54	0.51
1:B:118:LEU:HD12	1:B:118:LEU:C	2.35	0.51
1:C:279:ASN:C	1:C:279:ASN:HD22	2.17	0.50
1:C:14:PRO:HB2	1:C:25:GLU:HB3	1.93	0.50
1:A:25:GLU:CD	1:A:25:GLU:H	2.20	0.50
1:A:75:LYS:NZ	1:A:79:GLN:OE1	2.43	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:130:ALA:O	1:C:143:GLN:HG2	2.12	0.50
1:C:132:PRO:HD2	1:C:156:PHE:CG	2.46	0.49
1:C:24:VAL:HG22	1:C:24:VAL:O	2.11	0.49
1:C:129:ILE:HD11	1:C:149:LEU:CD1	2.43	0.49
1:A:184:PRO:HA	1:C:311:ASN:O	2.13	0.49
1:A:17:LYS:HE3	1:A:57:ASP:OD1	2.12	0.49
1:C:15:PHE:CZ	1:C:73:VAL:HA	2.48	0.49
1:C:290:THR:CG2	1:C:294:ASN:HD21	2.26	0.48
1:A:16:SER:HB3	1:A:25:GLU:HG3	1.95	0.48
1:B:130:ALA:O	1:B:143:GLN:HG2	2.13	0.48
1:B:133:LEU:HD11	1:B:157:PRO:HD3	1.95	0.48
1:C:129:ILE:HD11	1:C:149:LEU:HD12	1.95	0.48
1:B:279:ASN:CG	1:B:282:LEU:HG	2.38	0.48
1:C:289:VAL:O	1:C:293:VAL:HG23	2.14	0.48
1:A:124:ASP:HB3	1:A:126:HIS:O	2.14	0.48
1:C:280:PRO:HA	1:C:289:VAL:HG13	1.96	0.48
1:B:111:HIS:HB2	3:B:560:HOH:O	2.13	0.47
1:A:23:GLY:N	1:A:25:GLU:OE2	2.42	0.47
1:C:24:VAL:HG13	1:C:99:GLY:HA3	1.95	0.47
1:A:64:PHE:O	1:A:65:GLN:HB2	2.15	0.47
1:B:129:ILE:HG12	1:B:129:ILE:O	2.15	0.47
1:C:84:VAL:HG21	1:C:107:SER:HA	1.97	0.47
1:C:180:ARG:CZ	1:C:251:GLY:HA2	2.43	0.47
1:A:307:LYS:HB2	1:A:307:LYS:NZ	2.29	0.47
1:B:207:GLY:O	1:B:211:VAL:HG23	2.14	0.47
1:C:58:VAL:HG21	1:C:71:ARG:HB3	1.97	0.47
1:C:241:THR:N	1:C:242:PRO:HD3	2.30	0.47
1:A:222:ARG:C	1:A:223:LYS:HD3	2.39	0.47
1:B:86:GLU:O	1:B:89:LYS:HB3	2.14	0.46
1:B:289:VAL:O	1:B:293:VAL:HG23	2.15	0.46
1:C:258:LEU:HD11	3:C:524:HOH:O	2.13	0.46
1:B:69:ASN:O	1:B:73:VAL:HG23	2.16	0.46
1:C:16:SER:HB3	1:C:24:VAL:HG12	1.98	0.46
1:C:70:PRO:O	1:C:162:PHE:HE1	1.99	0.46
1:C:129:ILE:HG12	1:C:129:ILE:O	2.16	0.46
1:A:180:ARG:NH2	1:A:235:GLY:O	2.43	0.45
1:C:88:GLN:HG3	1:C:111:HIS:HA	1.98	0.45
1:A:166:THR:O	1:A:167:PRO:C	2.60	0.45
1:A:16:SER:HB3	1:A:24:VAL:HG12	1.98	0.45
1:B:273:LEU:HD23	1:B:274:ASP:H	1.81	0.45
1:C:55:PHE:CD1	1:C:76:ALA:HB1	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:239:VAL:O	1:A:291:ARG:CD	2.64	0.45
1:C:166:THR:O	1:C:167:PRO:C	2.60	0.45
1:B:35:GLY:O	1:B:39:LYS:HG3	2.17	0.45
1:B:132:PRO:HD2	1:B:156:PHE:CD2	2.52	0.45
1:A:129:ILE:HG12	1:A:129:ILE:O	2.17	0.45
1:C:80:LEU:HD22	1:C:103:MET:HE3	1.99	0.45
1:A:180:ARG:HG3	1:A:248:VAL:HG11	1.98	0.44
1:B:47:VAL:HG12	1:B:48:ARG:N	2.33	0.44
1:C:50:HIS:O	1:C:50:HIS:ND1	2.49	0.44
1:A:149:LEU:HD21	1:A:171:ALA:CA	2.47	0.44
1:B:8:ILE:HD11	1:B:304:PHE:CD1	2.53	0.44
1:A:68:LYS:C	1:A:70:PRO:HD3	2.43	0.44
1:A:149:LEU:HD21	1:A:171:ALA:N	2.32	0.44
1:A:307:LYS:HZ3	1:A:309:GLU:HG2	1.83	0.44
1:C:89:LYS:C	1:C:91:GLY:H	2.25	0.44
1:B:237:ASP:OD1	1:B:239:VAL:HG23	2.18	0.44
1:A:285:THR:OG1	1:A:288:GLU:HG3	2.18	0.44
1:A:307:LYS:NZ	1:A:307:LYS:CB	2.81	0.44
1:A:178:GLY:HA2	1:A:200:MET:SD	2.58	0.43
1:B:69:ASN:N	1:B:70:PRO:HD3	2.33	0.43
1:C:279:ASN:HD22	1:C:281:THR:H	1.66	0.43
1:A:236:LEU:HD12	1:A:295:THR:HG21	1.99	0.43
1:A:258:LEU:HD23	1:A:299:LEU:HD23	1.99	0.43
1:C:17:LYS:NZ	1:C:57:ASP:OD2	2.50	0.43
1:C:143:GLN:O	1:C:146:ALA:HB3	2.18	0.43
1:B:234:ASP:OD1	1:B:234:ASP:C	2.61	0.43
1:A:84:VAL:O	1:A:88:GLN:HG2	2.17	0.43
1:B:28:PRO:HG3	1:B:97:LEU:O	2.18	0.43
1:C:103:MET:HB2	1:C:276:MET:CE	2.48	0.43
1:C:150:LYS:HE2	1:C:167:PRO:O	2.17	0.43
1:C:61:ASP:OD2	1:C:69:ASN:HA	2.19	0.43
1:B:23:GLY:H	1:B:279:ASN:HD21	1.66	0.43
1:B:279:ASN:HB3	1:B:282:LEU:HD12	2.00	0.43
1:C:21:ARG:O	1:C:22:GLY:C	2.61	0.43
1:C:242:PRO:HD2	1:C:292:THR:OG1	2.18	0.43
1:A:16:SER:CB	1:A:25:GLU:HG3	2.49	0.43
1:A:132:PRO:HD2	1:A:156:PHE:CD2	2.54	0.43
1:C:131:THR:C	1:C:133:LEU:H	2.27	0.42
1:B:33:LYS:C	1:B:35:GLY:H	2.28	0.42
1:C:48:ARG:HD2	1:C:49:ASP:N	2.34	0.42
1:C:277:GLU:HA	1:C:277:GLU:OE1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:189:ILE:HG23	1:B:193:LEU:HD22	2.00	0.42
1:C:101:HIS:CD2	1:C:104:ALA:HB2	2.54	0.42
1:C:67:VAL:HA	1:C:138:GLY:O	2.19	0.42
1:C:87:THR:HB	1:C:92:THR:OG1	2.20	0.42
1:B:21:ARG:O	1:B:22:GLY:O	2.38	0.42
1:C:64:PHE:O	1:C:65:GLN:HB2	2.20	0.42
1:A:149:LEU:HD22	1:A:151:GLU:OE1	2.20	0.42
1:B:222:ARG:HH11	1:B:222:ARG:HG2	1.84	0.42
1:B:273:LEU:CD2	1:B:274:ASP:N	2.83	0.42
1:A:180:ARG:HA	1:C:308:ARG:O	2.18	0.42
1:C:127:THR:HB	1:C:129:ILE:HG22	2.01	0.42
1:A:16:SER:HB3	1:A:24:VAL:CG1	2.50	0.42
1:A:307:LYS:NZ	1:A:309:GLU:CG	2.83	0.42
1:B:285:THR:OG1	1:B:288:GLU:HG3	2.20	0.42
1:A:188:TYR:O	1:A:192:THR:HG23	2.20	0.41
1:C:95:VAL:HG13	1:C:273:LEU:HD13	2.02	0.41
1:B:39:LYS:CE	1:B:301:LEU:HD11	2.49	0.41
1:B:75:LYS:O	1:B:78:GLU:HB3	2.19	0.41
1:A:24:VAL:HG22	1:A:99:GLY:CA	2.49	0.41
1:B:210:LYS:HE3	1:B:214:GLU:HG3	2.02	0.41
1:A:88:GLN:HG3	1:A:111:HIS:HA	2.02	0.41
1:B:212:MET:HE2	1:B:260:ILE:HA	2.02	0.41
1:B:287:GLU:OE2	1:B:288:GLU:HG2	2.20	0.41
1:C:153:LYS:HD2	1:C:167:PRO:HG2	2.02	0.41
1:C:300:THR:O	1:C:303:CYS:HB2	2.20	0.41
1:A:243:ALA:HB1	1:A:279:ASN:O	2.21	0.41
1:B:16:SER:HB3	1:B:25:GLU:HG3	2.02	0.41
1:C:6:LYS:HD2	1:C:91:GLY:O	2.21	0.41
1:C:233:VAL:HG11	1:C:278:VAL:CG2	2.51	0.41
1:B:58:VAL:HG13	1:B:59:PRO:HD2	2.03	0.41
1:C:19:GLN:HG3	1:C:100:ASP:HB3	2.03	0.41
1:C:179:LEU:HB2	1:C:199:SER:HA	2.02	0.41
1:A:19:GLN:HG2	1:A:100:ASP:HB3	2.02	0.40
1:A:140:LEU:O	1:A:144:PRO:HD3	2.20	0.40
1:B:170:SER:C	1:B:172:LYS:H	2.28	0.40
1:C:124:ASP:OD1	1:C:125:ALA:N	2.54	0.40
1:B:24:VAL:HG22	1:B:99:GLY:CA	2.45	0.40
1:B:209:GLY:HA2	1:B:259:TYR:CE2	2.57	0.40
1:B:274:ASP:HB3	1:B:276:MET:HE3	2.03	0.40
1:C:44:GLU:HA	1:C:44:GLU:OE1	2.20	0.40
1:C:258:LEU:CD1	1:C:308:ARG:HD3	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88:GLN:HB2	1:A:114:VAL:HG21	2.04	0.40
1:B:67:VAL:HG12	1:B:70:PRO:HG3	2.03	0.40
1:C:59:PRO:C	1:C:61:ASP:H	2.29	0.40
1:C:234:ASP:OD1	1:C:234:ASP:C	2.64	0.40
1:A:32:ARG:NH1	1:A:52:ASP:OD1	2.51	0.40
1:B:307:LYS:NZ	1:B:309:GLU:CG	2.83	0.40
1:C:7:PRO:HG2	1:C:92:THR:HG22	2.03	0.40
1:C:21:ARG:O	1:C:22:GLY:O	2.38	0.40
1:C:131:THR:O	1:C:133:LEU:N	2.54	0.40
1:C:64:PHE:O	1:C:66:ILE:N	2.52	0.40
1:C:70:PRO:HB3	1:C:159:VAL:CG1	2.51	0.40
1:C:159:VAL:HA	1:C:160:PRO:HD3	1.95	0.40
1:C:279:ASN:ND2	1:C:279:ASN:C	2.80	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	306/323 (95%)	290 (95%)	12 (4%)	4 (1%)	9	5
1	B	306/323 (95%)	288 (94%)	11 (4%)	7 (2%)	5	2
1	C	306/323 (95%)	279 (91%)	18 (6%)	9 (3%)	3	1
All	All	918/969 (95%)	857 (93%)	41 (4%)	20 (2%)	5	2

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	59	PRO
1	B	20	PRO
1	B	21	ARG
1	B	22	GLY

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Mol	Chain	Res	Type
1	B	59	PRO
1	C	59	PRO
1	C	22	GLY
1	C	284	LYS
1	C	143	GLN
1	C	180	ARG
1	C	222	ARG
1	A	143	GLN
1	A	180	ARG
1	B	60	ASN
1	B	143	GLN
1	C	160	PRO
1	C	132	PRO
1	C	167	PRO
1	B	70	PRO
1	A	167	PRO

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	257/272 (94%)	250 (97%)	7 (3%)	39	42
1	B	257/272 (94%)	251 (98%)	6 (2%)	44	49
1	C	257/272 (94%)	253 (98%)	4 (2%)	55	62
All	All	771/816 (94%)	754 (98%)	17 (2%)	45	50

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	GLU
1	A	48	ARG
1	A	59	PRO
1	A	92	THR
1	A	132	PRO
1	A	273	LEU

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Mol	Chain	Res	Type
1	A	307	LYS
1	B	6	LYS
1	B	25	GLU
1	B	222	ARG
1	B	236	LEU
1	B	273	LEU
1	B	307	LYS
1	C	25	GLU
1	C	48	ARG
1	C	57	ASP
1	C	273	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	294	ASN
1	B	279	ASN
1	C	19	GLN
1	C	65	GLN
1	C	88	GLN
1	C	90	ASN
1	C	279	ASN
1	C	294	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 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	308/323 (95%)	0.39	11 (3%) 46 45	10, 20, 33, 46	0
1	B	308/323 (95%)	0.65	23 (7%) 20 19	11, 21, 39, 56	0
1	C	308/323 (95%)	1.20	65 (21%) 2 2	11, 30, 47, 55	0
All	All	924/969 (95%)	0.75	99 (10%) 11 10	10, 23, 44, 56	0

All (99) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	58	VAL	5.7
1	C	14	PRO	4.2
1	A	59	PRO	4.0
1	C	63	PRO	4.0
1	C	21	ARG	3.8
1	B	285	THR	3.7
1	C	282	LEU	3.7
1	B	59	PRO	3.7
1	C	59	PRO	3.6
1	C	134	THR	3.6
1	C	22	GLY	3.5
1	C	159	VAL	3.5
1	C	53	LEU	3.3
1	C	58	VAL	3.3
1	C	40	LEU	3.3
1	C	67	VAL	3.2
1	C	162	PHE	3.2
1	A	58	VAL	3.2
1	C	56	VAL	3.2
1	A	283	GLY	3.2
1	C	142	GLY	3.2
1	C	15	PHE	3.1
1	C	70	PRO	3.1

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Mol	Chain	Res	Type	RSRZ
1	C	169	ILE	3.0
1	B	98	GLY	3.0
1	B	287	GLU	3.0
1	C	62	SER	2.9
1	C	171	ALA	2.9
1	B	281	THR	2.8
1	B	286	PRO	2.8
1	C	61	ASP	2.8
1	C	165	VAL	2.8
1	C	161	GLY	2.7
1	C	283	GLY	2.7
1	C	149	LEU	2.7
1	C	20	PRO	2.7
1	A	92	THR	2.7
1	C	133	LEU	2.7
1	C	24	VAL	2.7
1	B	163	SER	2.7
1	C	37	VAL	2.7
1	B	284	LYS	2.7
1	B	22	GLY	2.7
1	C	17	LYS	2.6
1	C	164	TRP	2.6
1	B	57	ASP	2.6
1	B	67	VAL	2.6
1	C	75	LYS	2.6
1	C	163	SER	2.6
1	C	16	SER	2.5
1	C	284	LYS	2.5
1	C	188	TYR	2.5
1	C	19	GLN	2.5
1	B	56	VAL	2.4
1	C	285	THR	2.4
1	C	112	ALA	2.4
1	C	52	ASP	2.4
1	B	283	GLY	2.4
1	B	60	ASN	2.4
1	A	169	ILE	2.4
1	C	31	LEU	2.4
1	C	147	PHE	2.4
1	C	131	THR	2.4
1	C	54	ALA	2.3
1	C	223	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	13	ALA	2.3
1	C	152	LEU	2.3
1	C	98	GLY	2.3
1	A	64	PHE	2.3
1	C	289	VAL	2.3
1	A	60	ASN	2.3
1	C	193	LEU	2.3
1	A	56	VAL	2.2
1	B	65	GLN	2.2
1	B	138	GLY	2.2
1	C	65	GLN	2.2
1	B	61	ASP	2.2
1	B	62	SER	2.2
1	C	154	GLY	2.1
1	C	30	ALA	2.1
1	C	166	THR	2.1
1	C	55	PHE	2.1
1	A	221	GLY	2.1
1	B	169	ILE	2.1
1	C	190	ILE	2.1
1	C	41	LYS	2.1
1	A	171	ALA	2.1
1	B	21	ARG	2.1
1	C	23	GLY	2.1
1	C	156	PHE	2.1
1	C	80	LEU	2.0
1	C	132	PRO	2.0
1	C	286	PRO	2.0
1	A	98	GLY	2.0
1	C	44	GLU	2.0
1	C	102	SER	2.0
1	B	282	LEU	2.0
1	C	79	GLN	2.0
1	B	23	GLY	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 [i](#)

There are no oligosaccharides 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. 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	B-factors($\text{\AA}^2$)	Q<0.9
2	MN	A	500	1/1	0.99	0.04	15,15,15,15	0
2	MN	B	500	1/1	0.99	0.03	16,16,16,16	0
2	MN	C	500	1/1	0.99	0.07	24,24,24,24	0
2	MN	C	501	1/1	0.99	0.02	18,18,18,18	0
2	MN	A	501	1/1	1.00	0.04	16,16,16,16	0
2	MN	B	501	1/1	1.00	0.01	14,14,14,14	0

6.5 Other polymers [i](#)

There are no such residues in this entry.