



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:56 AM GMT

PDB ID : 2OR9
Title : The structure of the anti-c-myc antibody 9E10 Fab fragment/epitope peptide complex reveals a novel binding mode dominated by the heavy chain hyper-variable loops
Authors : Krauss, N.; Scheerer, P.; Hoehne, W.
Deposited on : 2007-02-02
Resolution : 2.70 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

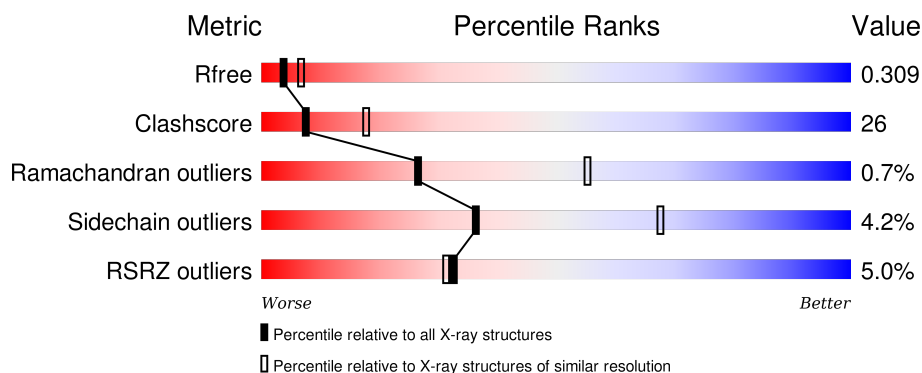
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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	L	218	<div> <div>3%</div> <div>61%</div> <div>36%</div> <div>..</div> </div>
1	M	218	<div> <div>%</div> <div>63%</div> <div>33%</div> <div>.</div> </div>
2	H	228	<div> <div>14%</div> <div>50%</div> <div>44%</div> <div>..</div> </div>
2	I	228	<div> <div>2%</div> <div>58%</div> <div>37%</div> <div>.</div> </div>
3	P	11	<div> <div>55%</div> <div>45%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7182 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 Monoclonal anti-c-myc antibody 9E10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	216	Total	C	N	O	S	0	0	0
			1671	1045	284	335	7			
1	M	218	Total	C	N	O	S	0	0	0
			1687	1053	286	340	8			

- Molecule 2 is a protein called Monoclonal anti-c-myc antibody 9E10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	221	Total	C	N	O	S	0	0	0
			1698	1079	278	332	9			
2	I	228	Total	C	N	O	S	0	0	0
			1752	1108	290	345	9			

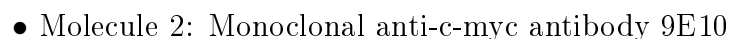
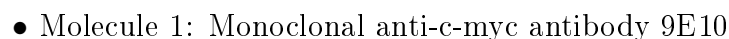
- Molecule 3 is a protein called synthetic epitope peptide of 9E10.

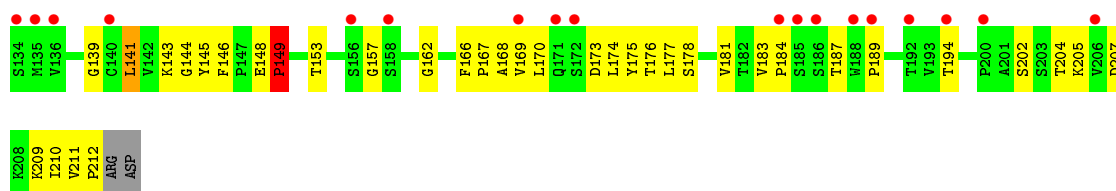
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	P	11	Total	C	N	O	0	0	0
			92	55	14	23			

- Molecule 4 is water.

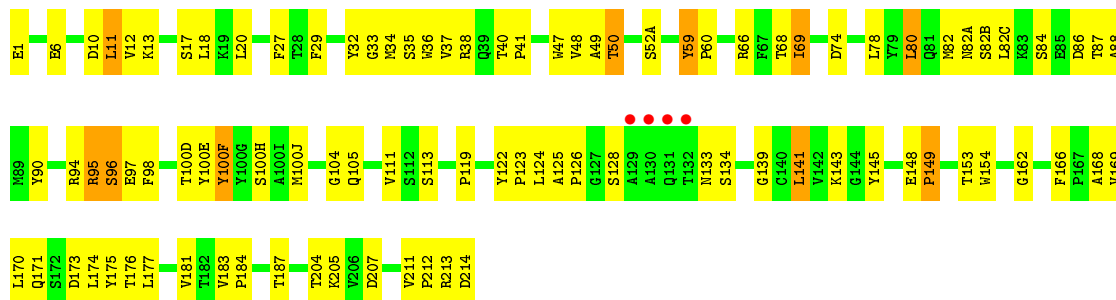
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	H	35	Total	O	0	0
			35	35		
4	I	94	Total	O	0	0
			94	94		
4	L	48	Total	O	0	0
			48	48		
4	M	91	Total	O	0	0
			91	91		
4	P	14	Total	O	0	0
			14	14		

- Molecule 1: Monoclonal anti-c-myc antibody 9E10

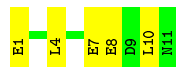




• Molecule 2: Monoclonal anti-c-myc antibody 9E10



• Molecule 3: synthetic epitope peptide of 9E10



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	76.07Å 111.88Å 134.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.70 19.36 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.4 (20.00-2.70) 99.4 (19.36-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.94 (at 2.70Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.252 , 0.310 0.252 , 0.309	Depositor DCC
R_{free} test set	1623 reflections (5.09%)	DCC
Wilson B-factor (Å ²)	57.0	Xtriage
Anisotropy	0.460	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 49.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 31878 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	7182	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 3.70% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

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	L	0.41	0/1712	0.65	0/2325
1	M	0.44	0/1728	0.68	0/2345
2	H	0.40	0/1747	0.64	0/2384
2	I	0.41	0/1802	0.67	0/2459
3	P	0.49	0/91	0.60	0/119
All	All	0.41	0/7080	0.66	0/9632

There are no bond length outliers.

There are no bond angle outliers.

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	L	1671	0	1598	74	0
1	M	1687	0	1609	75	0
2	H	1698	0	1633	111	0
2	I	1752	0	1682	96	0
3	P	92	0	89	7	0
4	H	35	0	0	5	0
4	I	94	0	0	3	0
4	L	48	0	0	0	0
4	M	91	0	0	0	0
4	P	14	0	0	0	0
All	All	7182	0	6611	345	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 26.

All (345) 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:H:87:THR:HG22	2:H:111:VAL:H	0.97	1.12
2:H:87:THR:CG2	2:H:111:VAL:H	1.65	1.10
2:H:87:THR:HG22	2:H:111:VAL:N	1.72	1.02
2:H:49:ALA:HB1	2:H:69:ILE:HD13	1.44	1.00
2:I:87:THR:HG22	2:I:111:VAL:H	1.33	0.94
2:I:34:MET:HE1	2:I:94:ARG:HA	1.52	0.92
1:L:34:ASN:HD22	1:L:49:TYR:HA	1.36	0.91
2:I:49:ALA:HB1	2:I:69:ILE:HD13	1.53	0.90
1:M:51:ILE:HD11	1:M:65:SER:C	1.91	0.89
2:I:119:PRO:HB3	2:I:145:TYR:HB3	1.58	0.84
2:I:34:MET:HE3	2:I:94:ARG:HG3	1.59	0.84
2:H:119:PRO:HB3	2:H:145:TYR:HB3	1.60	0.82
1:L:24:ARG:HH11	1:L:24:ARG:HB3	1.43	0.82
1:M:24:ARG:HB3	1:M:24:ARG:NH1	1.96	0.80
2:H:33:GLY:O	2:H:95:ARG:HB2	1.83	0.78
1:L:33:MET:HE3	1:L:34:ASN:H	1.47	0.77
1:M:24:ARG:HH11	1:M:24:ARG:HB3	1.49	0.76
2:H:84:SER:HA	2:H:111:VAL:HB	1.68	0.76
2:H:40:THR:HB	2:H:41:PRO:HD2	1.68	0.75
2:I:87:THR:CG2	2:I:111:VAL:H	2.00	0.74
2:I:96:SER:O	2:I:100(H):SER:HA	1.88	0.74
2:I:87:THR:HG22	2:I:111:VAL:N	2.04	0.73
1:M:16:GLY:HA2	1:M:77:PRO:HB2	1.69	0.73
2:H:34:MET:HE2	2:H:94:ARG:HA	1.69	0.72
2:I:211:VAL:HG13	2:I:212:PRO:HD2	1.71	0.72
1:L:18:ARG:HB2	1:L:76:HIS:HD2	1.53	0.72
1:L:94:VAL:HG13	2:H:47:TRP:HZ3	1.55	0.71
1:M:193:THR:HG22	1:M:208:SER:CB	2.19	0.71
1:L:133:VAL:HG21	2:H:124:LEU:HD21	1.73	0.71
1:M:210:ASN:HB2	1:M:213:GLU:HB2	1.72	0.70
2:I:40:THR:HB	2:I:41:PRO:HD2	1.73	0.70
1:L:94:VAL:HG13	2:H:47:TRP:CZ3	2.27	0.69
1:M:156:GLN:HA	1:M:156:GLN:HE21	1.57	0.69
2:I:47:TRP:HE1	2:I:50:THR:CG2	2.05	0.69
2:H:34:MET:HE1	2:H:94:ARG:HG3	1.73	0.68
1:L:21:ILE:HG12	1:L:102:THR:HG21	1.73	0.68
2:H:20:LEU:HG	2:H:82:MET:CE	2.23	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:34:MET:CE	2:I:94:ARG:HA	2.23	0.68
1:L:33:MET:CE	1:L:88:CYS:HB2	2.24	0.68
1:L:33:MET:HE3	1:L:34:ASN:N	2.09	0.67
2:I:47:TRP:HE1	2:I:50:THR:HG22	1.59	0.67
1:L:193:THR:HG22	1:L:208:SER:CB	2.25	0.66
2:I:12:VAL:O	2:I:111:VAL:HA	1.95	0.66
2:H:189:PRO:HD2	4:H:239:HOH:O	1.96	0.66
1:M:150:ILE:HG23	1:M:192:TYR:CE2	2.31	0.66
1:L:149:LYS:HB2	1:L:193:THR:OG1	1.96	0.66
2:H:20:LEU:HG	2:H:82:MET:HE2	1.78	0.65
2:I:47:TRP:NE1	2:I:50:THR:HG22	2.11	0.65
1:L:197:THR:HG22	1:L:204:PRO:HG3	1.78	0.65
2:I:47:TRP:NE1	2:I:50:THR:CG2	2.60	0.65
1:M:193:THR:HG22	1:M:208:SER:HB3	1.78	0.65
1:M:18:ARG:HB2	1:M:76:HIS:HD2	1.61	0.64
1:L:33:MET:HE2	1:L:88:CYS:HB2	1.79	0.64
1:L:80:GLU:O	1:L:83:PRO:HD2	1.97	0.64
2:H:84:SER:O	2:H:87:THR:HG23	1.97	0.64
2:H:82:MET:HB3	2:H:82(C):LEU:HD21	1.79	0.64
2:I:96:SER:HB3	2:I:98:PHE:HE1	1.62	0.63
1:M:197:THR:HG22	1:M:204:PRO:HG3	1.80	0.63
2:H:34:MET:HB3	2:H:78:LEU:HD22	1.81	0.63
1:L:24:ARG:HG3	1:L:70:ASP:OD1	1.99	0.63
2:H:148:GLU:OE1	2:H:149:PRO:HA	1.98	0.63
1:L:14:SER:HB2	1:L:17:GLN:HG3	1.82	0.62
1:L:31:SER:OG	1:L:51:ILE:HD11	1.99	0.62
1:M:131:SER:OG	1:M:180:THR:HG22	1.98	0.62
1:M:14:SER:HB2	1:M:17:GLN:HG3	1.81	0.62
1:L:94:VAL:HG13	1:L:95:PRO:HA	1.82	0.62
2:I:82:MET:HB3	2:I:82(C):LEU:HD21	1.82	0.62
2:I:10:ASP:OD1	2:I:11:LEU:N	2.33	0.62
2:H:6:GLU:OE2	2:H:91:TYR:HA	2.00	0.62
2:H:143:LYS:HG3	2:H:176:THR:CG2	2.29	0.62
2:H:211:VAL:HG13	2:H:212:PRO:HD2	1.82	0.61
2:I:124:LEU:HB2	2:I:139:GLY:O	2.01	0.61
1:M:51:ILE:HD12	1:M:71:PHE:HD2	1.64	0.61
1:M:123:GLU:N	1:M:123:GLU:OE1	2.34	0.61
2:I:94:ARG:O	2:I:100(J):MET:HA	2.00	0.61
1:M:211:ARG:HG2	1:M:211:ARG:HH11	1.66	0.61
2:H:39:GLN:O	2:H:88:ALA:HB1	2.01	0.61
2:H:177:LEU:HD12	2:H:177:LEU:C	2.21	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:177:LEU:C	2:I:177:LEU:HD12	2.22	0.60
1:L:34:ASN:ND2	1:L:49:TYR:HA	2.14	0.60
2:H:37:VAL:HG21	2:H:100(J):MET:HE1	1.84	0.59
1:M:214:CYS:SG	2:I:128:SER:HA	2.42	0.59
2:H:125:ALA:HB1	2:H:126:PRO:HD2	1.84	0.59
2:I:84:SER:O	2:I:87:THR:HG23	2.01	0.59
2:I:148:GLU:OE1	2:I:149:PRO:HA	2.03	0.59
2:H:87:THR:HA	2:H:109:VAL:O	2.02	0.59
1:M:94:VAL:HG23	3:P:1:GLU:OE2	2.03	0.59
2:H:184:PRO:HG2	2:H:187:THR:HG23	1.84	0.59
1:M:27(B):VAL:HG22	1:M:90:GLN:HG2	1.85	0.59
1:M:33:MET:HE3	1:M:89:GLN:O	2.03	0.58
1:L:89:GLN:HG2	1:L:90:GLN:N	2.17	0.58
2:H:124:LEU:HD11	2:H:141:LEU:HB2	1.84	0.58
2:H:51:ILE:HG13	2:H:57:THR:HG22	1.85	0.58
2:H:100:TYR:HB3	2:H:100(E):TYR:CE1	2.39	0.58
2:H:170:LEU:HD13	2:H:175:TYR:CE1	2.39	0.58
1:L:48:ILE:HA	1:L:53:ASN:O	2.04	0.58
1:L:123:GLU:N	1:L:123:GLU:OE1	2.36	0.58
2:I:125:ALA:HB1	2:I:126:PRO:HD2	1.85	0.58
2:H:58:HIS:CD2	2:H:59:TYR:H	2.22	0.57
1:L:193:THR:HG22	1:L:208:SER:HB3	1.86	0.57
1:M:34:ASN:OD1	1:M:49:TYR:HA	2.04	0.57
2:H:37:VAL:HG22	2:H:47:TRP:HA	1.86	0.57
1:L:2:ILE:HG12	1:L:27:GLU:OE2	2.04	0.57
2:I:170:LEU:HD13	2:I:175:TYR:CE1	2.39	0.57
1:M:136:LEU:HD21	1:M:196:ALA:HB2	1.87	0.57
1:M:50:ALA:O	1:M:51:ILE:HG22	2.05	0.57
1:M:51:ILE:HD11	1:M:66:GLY:N	2.19	0.57
2:H:168:ALA:HA	2:H:177:LEU:HB3	1.86	0.57
2:I:143:LYS:HG3	2:I:176:THR:CG2	2.35	0.56
2:H:50:THR:C	2:H:69:ILE:HD12	2.26	0.56
2:I:36:TRP:CE2	2:I:80:LEU:HB2	2.41	0.56
2:I:119:PRO:CB	2:I:145:TYR:HB3	2.32	0.56
2:H:210:ILE:HG13	4:H:234:HOH:O	2.05	0.56
2:H:12:VAL:O	2:H:111:VAL:HA	2.06	0.56
2:I:34:MET:HB3	2:I:78:LEU:HD22	1.88	0.56
2:H:63:VAL:HG11	2:H:67:PHE:CE2	2.40	0.56
2:H:10:ASP:OD1	2:H:11:LEU:N	2.38	0.55
2:H:169:VAL:O	2:H:175:TYR:HA	2.06	0.55
1:L:131:SER:OG	1:L:180:THR:HG22	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:211:ARG:HH11	1:L:211:ARG:HG2	1.70	0.55
1:M:124:GLN:HE22	1:M:131:SER:CB	2.20	0.55
2:H:31:HIS:CD2	3:P:8:GLU:HG3	2.42	0.54
2:H:96:SER:HB3	3:P:4:LEU:HB3	1.88	0.54
1:M:117:ILE:HD13	1:M:208:SER:HA	1.89	0.54
2:H:183:VAL:HB	2:H:184:PRO:HD2	1.88	0.54
2:H:31:HIS:CG	3:P:8:GLU:HG3	2.43	0.54
2:H:168:ALA:HB2	2:H:177:LEU:HD23	1.90	0.54
1:M:182:THR:HG23	1:M:185:GLU:OE2	2.08	0.54
1:L:170:ASP:O	1:L:172:THR:HG23	2.07	0.53
2:I:184:PRO:HG2	2:I:187:THR:HG23	1.90	0.53
1:M:27(C):ASP:O	1:M:27(D):ASN:HB2	2.07	0.53
2:H:116:THR:HG22	2:H:202:SER:HB3	1.90	0.53
1:M:38:GLN:O	1:M:84:ALA:HB1	2.09	0.53
2:H:119:PRO:HB3	2:H:145:TYR:CB	2.37	0.53
1:L:162:SER:OG	2:H:166:PHE:HB3	2.08	0.53
1:L:110:ASP:OD2	1:L:199:LYS:HE3	2.07	0.53
1:L:105:GLU:CD	1:L:173:TYR:HH	2.12	0.53
1:M:96:TRP:CZ2	2:I:100(H):SER:HB2	2.44	0.53
1:L:15:LEU:HD21	1:L:80:GLU:CD	2.28	0.53
1:L:27(B):VAL:HG12	1:L:27(B):VAL:O	2.08	0.53
1:L:124:GLN:HE22	1:L:131:SER:CB	2.23	0.52
1:L:199:LYS:HD2	1:L:199:LYS:O	2.09	0.52
2:I:169:VAL:O	2:I:175:TYR:HA	2.10	0.52
2:I:168:ALA:HA	2:I:177:LEU:HB3	1.91	0.52
2:H:53:ARG:HD3	4:H:246:HOH:O	2.09	0.52
2:H:119:PRO:CB	2:H:145:TYR:HB3	2.35	0.52
1:L:80:GLU:O	1:L:83:PRO:CD	2.58	0.52
2:H:143:LYS:HG3	2:H:176:THR:HG21	1.90	0.52
2:I:32:TYR:O	2:I:52(A):SER:HA	2.08	0.52
2:H:60:PRO:HA	4:H:245:HOH:O	2.09	0.52
1:M:150:ILE:HD11	1:M:155:ARG:HG2	1.91	0.52
1:L:61:ARG:NH2	1:L:82:ASP:OD2	2.43	0.52
1:L:82:ASP:N	1:L:83:PRO:HD2	2.25	0.52
2:H:173:ASP:O	2:H:174:LEU:HG	2.10	0.52
1:M:18:ARG:HB2	1:M:76:HIS:CD2	2.42	0.52
2:I:183:VAL:HB	2:I:184:PRO:HD2	1.91	0.52
1:L:27(B):VAL:HG12	1:L:32:PHE:H	1.74	0.51
1:L:50:ALA:HB3	1:L:53:ASN:HD22	1.75	0.51
2:H:124:LEU:HB2	2:H:139:GLY:O	2.10	0.51
2:I:211:VAL:CG1	2:I:212:PRO:HD2	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:87:THR:HG22	2:H:110:THR:HA	1.92	0.51
2:I:34:MET:CE	2:I:94:ARG:HG3	2.36	0.51
1:M:33:MET:HE3	1:M:89:GLN:C	2.31	0.51
1:L:105:GLU:OE2	1:L:173:TYR:OH	2.25	0.50
2:I:33:GLY:O	2:I:34:MET:HE1	2.12	0.50
1:L:13:VAL:CG1	1:L:17:GLN:HB2	2.41	0.50
1:L:18:ARG:HB2	1:L:76:HIS:CD2	2.42	0.50
1:M:156:GLN:HA	1:M:156:GLN:NE2	2.26	0.50
2:I:124:LEU:HD11	2:I:141:LEU:HB2	1.92	0.50
1:L:136:LEU:HD21	1:L:196:ALA:HB2	1.94	0.50
1:M:80:GLU:O	1:M:83:PRO:HD2	2.11	0.50
2:I:84:SER:HA	2:I:111:VAL:HB	1.93	0.50
1:L:33:MET:HE3	1:L:89:GLN:O	2.11	0.50
1:M:169:LYS:NZ	1:M:169:LYS:HB3	2.27	0.50
2:H:17:SER:HB2	2:H:82(A):ASN:HD22	1.77	0.50
2:H:34:MET:CE	2:H:94:ARG:HA	2.40	0.50
2:I:50:THR:O	2:I:69:ILE:CD1	2.61	0.49
2:H:103:TRP:N	2:H:103:TRP:CD1	2.80	0.49
2:H:123:PRO:O	2:H:124:LEU:HD12	2.13	0.49
2:I:13:LYS:HG2	2:I:113:SER:HA	1.94	0.49
1:M:156:GLN:CA	1:M:156:GLN:HE21	2.19	0.49
2:I:105:GLN:N	2:I:105:GLN:OE1	2.44	0.49
1:M:51:ILE:HD12	1:M:71:PHE:CD2	2.47	0.49
2:I:6:GLU:H	2:I:105:GLN:HE22	1.60	0.49
1:M:21:ILE:HG12	1:M:102:THR:HG21	1.95	0.49
2:I:33:GLY:O	2:I:34:MET:CE	2.61	0.49
1:M:61:ARG:NH2	1:M:82:ASP:OD1	2.40	0.49
2:I:27:PHE:CE1	2:I:29:PHE:HA	2.48	0.49
1:M:42:GLN:HB3	1:M:43:PRO:HD2	1.95	0.48
2:I:47:TRP:NE1	2:I:50:THR:HG23	2.28	0.48
1:M:54:ARG:HD2	1:M:58:VAL:O	2.14	0.48
2:H:83:LYS:O	2:H:111:VAL:HG21	2.13	0.48
1:M:24:ARG:HG3	1:M:70:ASP:OD1	2.13	0.48
1:M:61:ARG:NH2	1:M:82:ASP:OD2	2.46	0.48
2:H:48:VAL:O	2:H:60:PRO:HD2	2.14	0.48
2:I:97:GLU:HG3	2:I:100(H):SER:HB3	1.95	0.48
2:I:20:LEU:HG	2:I:82:MET:CE	2.42	0.48
2:H:66:ARG:NH2	2:H:86:ASP:OD2	2.47	0.48
2:H:9:GLY:O	2:H:10:ASP:HB2	2.13	0.48
1:L:133:VAL:HG11	2:H:124:LEU:HD23	1.96	0.48
1:M:82:ASP:N	1:M:83:PRO:HD2	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:36:TRP:CE2	2:H:80:LEU:HB2	2.48	0.48
2:H:32:TYR:HD2	2:H:95:ARG:O	1.96	0.47
3:P:10:LEU:HD23	3:P:10:LEU:C	2.34	0.47
1:M:149:LYS:HA	1:M:153:SER:O	2.14	0.47
2:I:166:PHE:CD1	2:I:166:PHE:N	2.82	0.47
2:H:204:THR:HG22	2:H:205:LYS:N	2.29	0.47
1:M:33:MET:CE	1:M:89:GLN:C	2.83	0.47
2:I:173:ASP:O	2:I:174:LEU:HG	2.14	0.47
1:L:175:MET:HG2	1:L:176:SER:N	2.29	0.47
2:H:50:THR:H	2:H:69:ILE:CD1	2.28	0.47
1:M:13:VAL:CG1	1:M:17:GLN:HB2	2.44	0.47
1:M:200:THR:O	1:M:201:SER:HB2	2.14	0.47
2:I:36:TRP:CD1	2:I:69:ILE:HG22	2.49	0.47
2:I:119:PRO:HB3	2:I:145:TYR:CB	2.37	0.47
2:H:6:GLU:OE1	2:H:90:TYR:O	2.32	0.47
2:I:143:LYS:HG3	2:I:176:THR:HG21	1.97	0.47
3:P:7:GLU:O	3:P:10:LEU:HB3	2.14	0.47
2:I:100(E):TYR:O	2:I:100(F):TYR:C	2.54	0.47
1:M:193:THR:HG22	1:M:208:SER:HB2	1.95	0.47
1:L:61:ARG:NH2	1:L:82:ASP:OD1	2.45	0.47
2:H:114:ALA:HB3	2:H:146:PHE:CE2	2.50	0.47
2:I:33:GLY:O	2:I:95:ARG:N	2.39	0.46
1:L:50:ALA:O	1:L:51:ILE:HB	2.15	0.46
1:L:27(C):ASP:O	1:L:27(D):ASN:HB2	2.15	0.46
2:H:37:VAL:CG2	2:H:100(J):MET:HE1	2.46	0.46
2:I:66:ARG:HG2	2:I:82(B):SER:HB2	1.97	0.46
1:M:136:LEU:HD23	1:M:144:ILE:CD1	2.46	0.46
2:I:37:VAL:HG22	2:I:47:TRP:HA	1.97	0.46
2:I:168:ALA:HB2	2:I:177:LEU:HD23	1.98	0.45
2:I:100(D):THR:HG22	2:I:100(E):TYR:O	2.16	0.45
2:I:66:ARG:NH2	2:I:86:ASP:OD2	2.49	0.45
1:L:158:GLY:O	1:L:179:LEU:HA	2.17	0.45
2:H:143:LYS:HG3	2:H:176:THR:HG22	1.99	0.45
2:I:171:GLN:HG2	4:I:229:HOH:O	2.17	0.45
2:H:11:LEU:HD23	2:H:12:VAL:H	1.82	0.45
2:H:59:TYR:CE2	2:H:69:ILE:HG12	2.51	0.45
1:L:162:SER:OG	2:H:167:PRO:HD2	2.17	0.45
1:L:32:PHE:HA	2:H:100(G):TYR:OH	2.16	0.45
2:I:204:THR:HG22	2:I:205:LYS:N	2.31	0.45
1:L:200:THR:O	1:L:201:SER:HB2	2.17	0.45
2:H:60:PRO:HG2	2:H:62:SER:HB3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:38:ARG:NH1	2:I:86:ASP:HA	2.32	0.45
1:L:182:THR:HG23	1:L:185:GLU:OE2	2.16	0.45
1:L:88:CYS:O	1:L:99:GLY:N	2.47	0.45
2:H:94:ARG:O	2:H:100(J):MET:HA	2.16	0.45
2:I:40:THR:CB	2:I:41:PRO:HD2	2.44	0.45
2:H:98:PHE:HB2	2:H:100(G):TYR:HB2	1.98	0.45
2:H:178:SER:HB3	4:H:247:HOH:O	2.17	0.45
1:L:33:MET:HE1	1:L:88:CYS:HB2	1.95	0.44
2:I:47:TRP:HE1	2:I:50:THR:HG23	1.81	0.44
1:M:27(B):VAL:HG22	1:M:90:GLN:CG	2.47	0.44
2:H:31:HIS:HA	3:P:8:GLU:CG	2.47	0.44
2:H:166:PHE:N	2:H:166:PHE:CD1	2.85	0.44
2:H:177:LEU:HD12	2:H:177:LEU:O	2.18	0.44
2:I:6:GLU:OE1	2:I:90:TYR:O	2.34	0.44
1:M:37:GLN:HB2	1:M:47:LEU:HD11	1.99	0.44
2:I:35:SER:HA	2:I:50:THR:HA	2.00	0.44
2:H:40:THR:CB	2:H:41:PRO:HD2	2.42	0.44
1:M:211:ARG:HG2	1:M:211:ARG:NH1	2.32	0.44
1:M:80:GLU:O	1:M:83:PRO:CD	2.65	0.44
1:M:118:PHE:HA	1:M:119:PRO:HD3	1.82	0.44
1:L:2:ILE:HG23	1:L:27:GLU:H	1.82	0.44
2:H:83:LYS:O	2:H:111:VAL:HG11	2.18	0.44
2:I:96:SER:HB3	2:I:98:PHE:CE1	2.49	0.44
2:H:22:CYS:HB3	2:H:78:LEU:HB3	1.99	0.44
1:M:43:PRO:HB3	2:I:104:GLY:O	2.17	0.44
2:I:48:VAL:O	2:I:60:PRO:HD2	2.17	0.44
2:H:162:GLY:O	2:H:181:VAL:HA	2.18	0.44
2:H:211:VAL:CG1	2:H:212:PRO:HD2	2.48	0.44
1:M:39:LYS:NZ	1:M:81:ASP:OD1	2.51	0.44
1:M:125:LEU:O	1:M:183:LYS:HD2	2.17	0.44
2:H:12:VAL:HG11	2:H:82(C):LEU:HD12	2.00	0.43
2:I:50:THR:C	2:I:69:ILE:HD12	2.39	0.43
1:M:51:ILE:CD1	1:M:66:GLY:O	2.66	0.43
1:M:51:ILE:HD13	1:M:66:GLY:O	2.18	0.43
2:H:144:GLY:C	2:H:174:LEU:HD22	2.38	0.43
2:H:20:LEU:HG	2:H:82:MET:HE1	1.97	0.43
2:I:87:THR:O	2:I:88:ALA:HB2	2.18	0.43
2:I:13:LYS:HE3	2:I:113:SER:O	2.18	0.43
2:H:40:THR:HB	2:H:41:PRO:CD	2.44	0.43
2:I:153:THR:HG22	2:I:154:TRP:N	2.34	0.43
1:L:159:VAL:HA	1:L:178:THR:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:50:THR:O	2:I:69:ILE:HD12	2.18	0.43
1:M:51:ILE:HD11	1:M:65:SER:CA	2.47	0.43
2:H:102:TYR:C	2:H:103:TRP:CD1	2.92	0.43
1:L:16:GLY:HA2	1:L:77:PRO:HB2	2.01	0.43
2:I:20:LEU:HG	2:I:82:MET:HE2	1.99	0.43
1:L:105:GLU:CD	1:L:173:TYR:OH	2.55	0.43
1:L:12:ALA:HA	1:L:105:GLU:O	2.18	0.43
2:I:59:TYR:CD1	2:I:59:TYR:N	2.87	0.43
1:L:167:ASP:OD2	1:L:168:SER:N	2.52	0.43
2:I:11:LEU:HD23	2:I:12:VAL:H	1.84	0.42
1:M:24:ARG:HH11	1:M:24:ARG:CB	2.25	0.42
1:M:118:PHE:CD2	2:I:124:LEU:HB3	2.54	0.42
1:L:32:PHE:HB3	1:L:91:THR:OG1	2.18	0.42
2:I:17:SER:HB2	2:I:82(A):ASN:HD22	1.84	0.42
1:L:37:GLN:HB2	1:L:47:LEU:HD11	2.01	0.42
2:H:39:GLN:NE2	2:H:43:LYS:O	2.45	0.42
2:I:36:TRP:HD1	2:I:69:ILE:CG2	2.33	0.42
2:I:97:GLU:HG2	4:I:258:HOH:O	2.19	0.42
2:H:100(G):TYR:O	2:H:100(H):SER:HB3	2.20	0.42
1:M:131:SER:HA	1:M:179:LEU:O	2.19	0.42
2:H:1:GLU:HG3	2:H:2:VAL:N	2.35	0.42
1:M:96:TRP:CH2	2:I:100(H):SER:HB2	2.54	0.42
2:I:123:PRO:O	2:I:124:LEU:HD12	2.20	0.42
1:M:106:ILE:HG22	1:M:107:LYS:N	2.35	0.42
2:I:162:GLY:O	2:I:181:VAL:HA	2.19	0.42
1:L:193:THR:HG22	1:L:208:SER:HB2	1.99	0.42
1:M:123:GLU:O	1:M:124:GLN:C	2.58	0.42
1:M:124:GLN:HG2	1:M:129:GLY:C	2.40	0.42
2:H:105:GLN:OE1	2:H:105:GLN:N	2.53	0.42
1:M:124:GLN:HB2	2:I:122:TYR:CE2	2.55	0.42
2:H:11:LEU:HD23	2:H:12:VAL:N	2.35	0.41
1:L:89:GLN:CG	1:L:90:GLN:N	2.82	0.41
1:L:27(C):ASP:OD1	1:L:68:GLY:N	2.52	0.41
2:H:194:THR:HG23	2:H:209:LYS:N	2.35	0.41
1:L:124:GLN:HG2	1:L:129:GLY:C	2.40	0.41
1:M:81:ASP:C	1:M:83:PRO:HD2	2.40	0.41
2:I:6:GLU:H	2:I:105:GLN:NE2	2.18	0.41
1:L:149:LYS:HA	1:L:153:SER:O	2.20	0.41
2:H:59:TYR:CD1	2:H:59:TYR:N	2.88	0.41
2:I:36:TRP:HD1	2:I:69:ILE:HG22	1.85	0.41
1:M:124:GLN:HE22	1:M:131:SER:HB2	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:59:TYR:CE2	2:I:68:THR:HA	2.55	0.41
1:L:42:GLN:HB3	1:L:43:PRO:HD2	2.02	0.41
2:H:39:GLN:C	2:H:88:ALA:HB1	2.41	0.41
2:H:87:THR:O	2:H:88:ALA:HB2	2.21	0.41
1:M:76:HIS:HA	1:M:77:PRO:HA	1.94	0.41
2:H:194:THR:HG23	2:H:209:LYS:HA	2.03	0.41
2:I:213:ARG:O	2:I:214:ASP:HB2	2.21	0.41
1:M:175:MET:HG2	1:M:176:SER:N	2.36	0.41
2:I:133:ASN:OD1	2:I:134:SER:N	2.48	0.41
2:H:83:LYS:C	2:H:111:VAL:HG11	2.41	0.41
1:L:125:LEU:HD12	1:L:125:LEU:HA	1.91	0.41
1:L:136:LEU:N	1:L:136:LEU:HD12	2.36	0.40
2:H:63:VAL:HB	2:H:67:PHE:CG	2.57	0.40
2:H:177:LEU:CD1	2:H:177:LEU:C	2.89	0.40
2:H:100(E):TYR:CD1	2:H:100(E):TYR:N	2.90	0.40
1:M:175:MET:CE	1:M:177:SER:HB2	2.51	0.40
2:H:153:THR:CG2	2:H:157:GLY:N	2.85	0.40
2:I:1:GLU:HB2	4:I:303:HOH:O	2.21	0.40
2:H:93:ALA:HB3	2:H:100(J):MET:CE	2.52	0.40
2:I:40:THR:HB	2:I:41:PRO:CD	2.48	0.40
1:L:183:LYS:HG2	1:L:187:GLU:OE2	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	L	214/218 (98%)	190 (89%)	23 (11%)	1 (0%)	34	63
1	M	216/218 (99%)	199 (92%)	15 (7%)	2 (1%)	21	49
2	H	217/228 (95%)	198 (91%)	17 (8%)	2 (1%)	21	49
2	I	226/228 (99%)	211 (93%)	14 (6%)	1 (0%)	39	69

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	P	9/11 (82%)	8 (89%)	1 (11%)	0	100	100
All	All	882/903 (98%)	806 (91%)	70 (8%)	6 (1%)	26	55

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	171	SER
2	H	62	SER
1	M	51	ILE
1	M	27(D)	ASN
2	I	100(F)	TYR
2	H	149	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	L	189/191 (99%)	184 (97%)	5 (3%)	54	83
1	M	191/191 (100%)	184 (96%)	7 (4%)	41	72
2	H	191/196 (97%)	182 (95%)	9 (5%)	32	63
2	I	196/196 (100%)	184 (94%)	12 (6%)	23	49
3	P	11/11 (100%)	11 (100%)	0	100	100
All	All	778/785 (99%)	745 (96%)	33 (4%)	36	68

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	24	ARG
1	L	73	LEU
1	L	90	GLN
1	L	176	SER
1	L	179	LEU
2	H	11	LEU

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Mol	Chain	Res	Type
2	H	18	LEU
2	H	59	TYR
2	H	69	ILE
2	H	74	ASP
2	H	80	LEU
2	H	141	LEU
2	H	149	PRO
2	H	207	ASP
1	M	24	ARG
1	M	27(B)	VAL
1	M	73	LEU
1	M	156	GLN
1	M	157	ASN
1	M	169	LYS
1	M	179	LEU
2	I	11	LEU
2	I	18	LEU
2	I	50	THR
2	I	59	TYR
2	I	69	ILE
2	I	74	ASP
2	I	80	LEU
2	I	95	ARG
2	I	96	SER
2	I	141	LEU
2	I	149	PRO
2	I	207	ASP

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

Mol	Chain	Res	Type
1	L	34	ASN
1	L	53	ASN
1	L	76	HIS
1	L	89	GLN
1	L	90	GLN
1	L	137	ASN
2	H	31	HIS
2	H	58	HIS
2	H	81	GLN
2	H	82(A)	ASN
1	M	53	ASN

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Mol	Chain	Res	Type
1	M	76	HIS
1	M	137	ASN
1	M	156	GLN
2	I	31	HIS
2	I	81	GLN
2	I	82(A)	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	L	216/218 (99%)	0.21	7 (3%) 51 51	35, 61, 82, 99	0
1	M	218/218 (100%)	-0.12	2 (0%) 85 86	25, 45, 75, 99	0
2	H	221/228 (96%)	0.89	32 (14%) 3 2	23, 72, 92, 102	0
2	I	228/228 (100%)	0.03	4 (1%) 71 72	23, 55, 82, 111	0
3	P	11/11 (100%)	-0.42	0 100 100	35, 40, 59, 61	0
All	All	894/903 (99%)	0.24	45 (5%) 32 31	23, 58, 86, 111	0

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	I	131	GLN	5.5
2	H	206	VAL	5.5
2	I	130	ALA	4.9
2	H	134	SER	4.5
1	M	214	CYS	4.0
2	H	126	PRO	3.6
2	H	136	VAL	3.5
2	H	200	PRO	3.5
2	H	184	PRO	3.3
2	H	186	SER	3.3
1	L	3	VAL	3.2
2	H	128	SER	3.1
1	L	121	SER	3.0
2	H	15	GLY	3.0
2	H	188	TRP	2.9
2	H	158	SER	2.9
2	H	172	SER	2.9
2	H	185	SER	2.8
2	H	192	THR	2.8
2	H	156	SER	2.8

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Mol	Chain	Res	Type	RSRZ
2	H	127	GLY	2.8
2	H	83	LYS	2.6
2	I	129	ALA	2.5
2	H	112	SER	2.5
1	L	126	THR	2.5
2	H	86	ASP	2.5
2	H	111	VAL	2.4
2	H	122	TYR	2.3
2	H	135	MET	2.3
2	H	171	GLN	2.3
2	H	118	PRO	2.3
2	H	119	PRO	2.3
2	H	189	PRO	2.2
2	H	82(C)	LEU	2.2
2	H	169	VAL	2.2
1	L	80	GLU	2.2
1	M	213	GLU	2.1
2	H	194	THR	2.1
2	I	132	THR	2.1
1	L	24	ARG	2.1
2	H	120	SER	2.1
1	L	103	LYS	2.1
1	L	211	ARG	2.1
2	H	140	CYS	2.0
2	H	58	HIS	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.