



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 11:06 PM EDT

PDB ID : 6DD8 / pdb_00006dd8
Title : Structure of mouse SYCP3, P21 form
Authors : Rosenberg, S.C.; Munoz, I.C.; Uson, I.; Corbett, K.D.
Deposited on : 2018-05-09
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

<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
Mogul	:	2022.3.0, CSD as543be (2022)
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

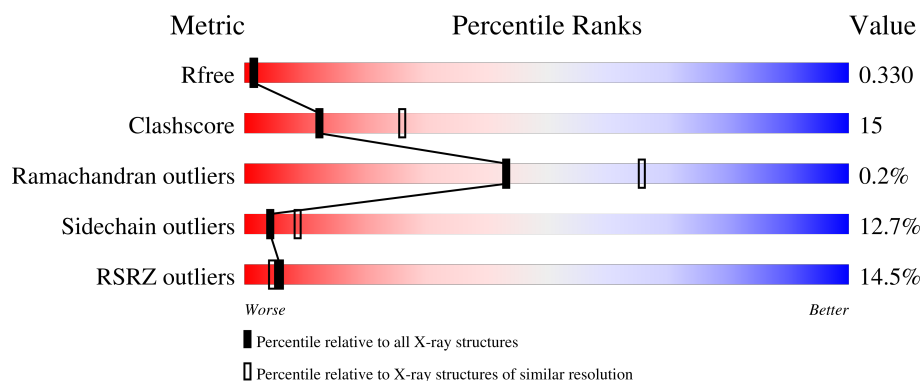
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (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 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	144	14% 60% 26% 5% 9%
1	B	144	15% 52% 28% 6% 15%
1	C	144	12% 50% 33% • 15%
1	D	144	6% 49% 29% • 19%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 4123 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.

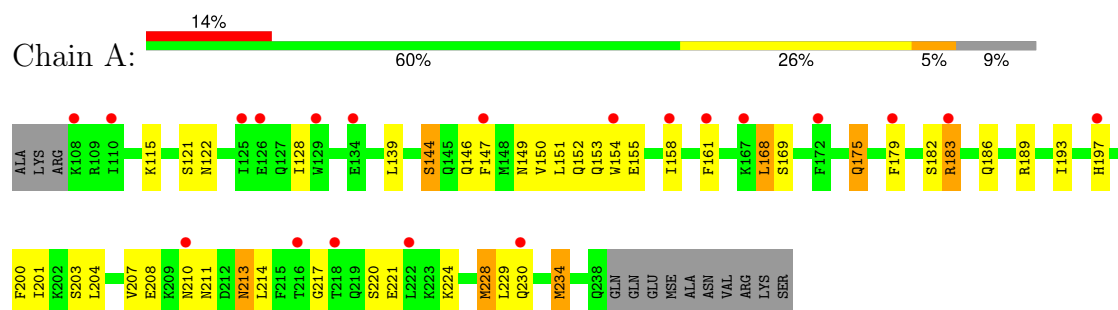
- Molecule 1 is a protein called Synaptonemal complex protein 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	131	Total	C	N	O	Se	0	0	0
			1072	673	187	206	6			
1	B	123	Total	C	N	O	Se	0	0	0
			1017	640	179	193	5			
1	C	123	Total	C	N	O	Se	0	0	0
			1048	659	188	195	6			
1	D	117	Total	C	N	O	Se	0	0	0
			986	618	174	188	6			

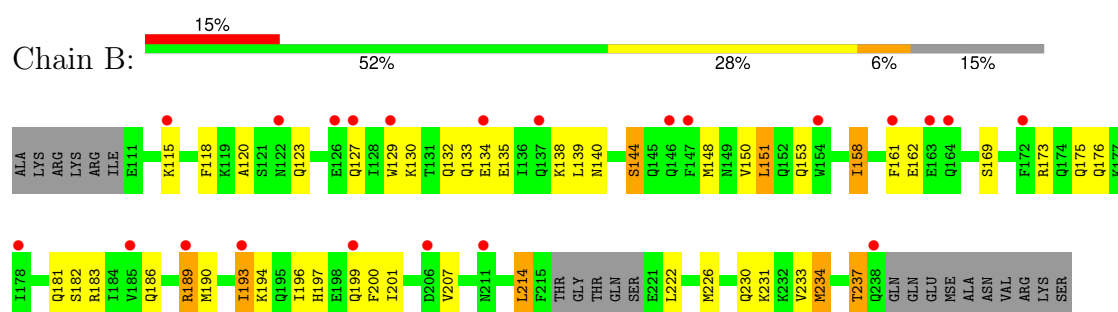
3 Residue-property plots

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.

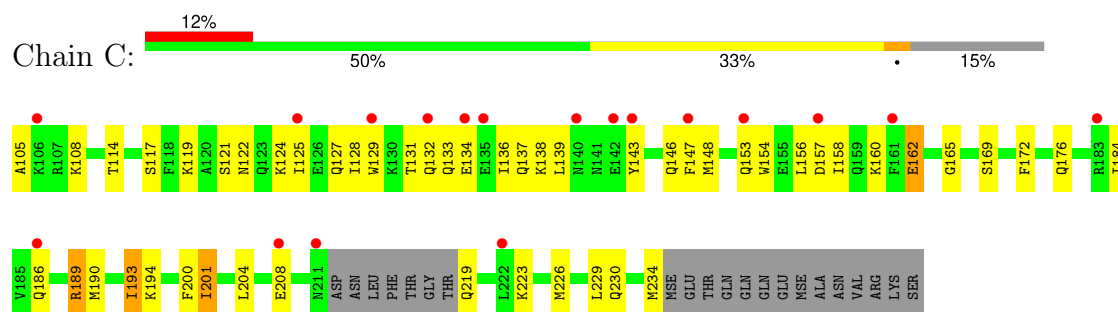
• Molecule 1: Synaptonemal complex protein 3



• Molecule 1: Synaptonemal complex protein 3

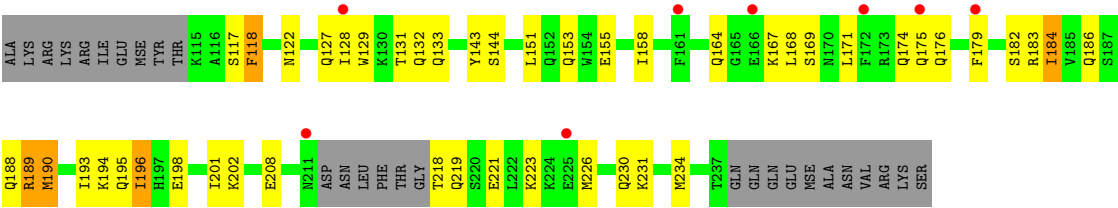


• Molecule 1: Synaptonemal complex protein 3



• Molecule 1: Synaptonemal complex protein 3





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	45.81Å 49.40Å 150.26Å 90.00° 90.80° 90.00°	Depositor
Resolution (Å)	46.92 – 2.60 46.92 – 2.60	Depositor EDS
% Data completeness (in resolution range)	97.9 (46.92-2.60) 99.1 (46.92-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.67 (at 2.61Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.254 , 0.323 0.263 , 0.330	Depositor DCC
R_{free} test set	1127 reflections (5.36%)	wwPDB-VP
Wilson B-factor (Å ²)	65.1	Xtriage
Anisotropy	0.517	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 62.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4123	wwPDB-VP
Average B, all atoms (Å ²)	89.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.90% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.41	0/1078	0.56	0/1430
1	B	0.38	0/1021	0.52	0/1349
1	C	0.40	0/1053	0.54	0/1385
1	D	0.49	2/990 (0.2%)	0.59	0/1305
All	All	0.42	2/4142 (0.0%)	0.55	0/5469

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	190	MSE	CG-SE	-5.49	1.78	1.95
1	D	190	MSE	SE-CE	-5.45	1.79	1.95

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	1072	0	1043	52	0
1	B	1017	0	1001	54	0
1	C	1048	0	1070	45	0
1	D	986	0	991	55	0
All	All	4123	0	4105	127	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 15.

All (127) 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:233:VAL:HG22	1:C:114:THR:HG22	1.55	0.87
1:C:201:ILE:HD11	1:D:144:SER:HB2	1.63	0.80
1:C:190:MSE:HE2	1:D:155:GLU:HB2	1.62	0.80
1:C:154:TRP:HE1	1:D:186:GLN:HE21	1.27	0.79
1:C:176:GLN:HE21	1:D:169:SER:HB2	1.51	0.76
1:C:121:SER:HA	1:C:124:LYS:HD2	1.76	0.68
1:A:175:GLN:HB3	1:D:168:LEU:HD21	1.75	0.68
1:A:183:ARG:NH2	1:B:158:ILE:O	2.22	0.67
1:B:237:THR:O	1:B:237:THR:OG1	2.13	0.65
1:C:137:GLN:NE2	1:D:208:GLU:OE2	2.30	0.63
1:A:149:ASN:O	1:A:152:GLN:HG2	1.98	0.62
1:A:150:VAL:HG11	1:D:193:ILE:HG13	1.81	0.62
1:D:127:GLN:O	1:D:131:THR:HG23	2.01	0.61
1:A:183:ARG:CZ	1:B:162:GLU:HB2	2.31	0.60
1:C:122:ASN:ND2	1:D:223:LYS:HG2	2.18	0.58
1:A:175:GLN:HB3	1:D:168:LEU:CD2	2.33	0.57
1:C:129:TRP:O	1:C:132:GLN:HG3	2.03	0.57
1:A:183:ARG:HH21	1:B:161:PHE:HB3	1.68	0.57
1:B:153:GLN:HB3	1:C:189:ARG:NH1	2.20	0.56
1:C:156:LEU:HB3	1:C:160:LYS:HZ2	1.70	0.56
1:A:183:ARG:NE	1:B:162:GLU:HB2	2.21	0.55
1:B:129:TRP:HB2	1:D:129:TRP:CH2	2.41	0.55
1:A:230:GLN:HE21	1:A:234:MSE:HE3	1.71	0.54
1:B:197:HIS:HD2	1:C:143:TYR:OH	1.90	0.54
1:A:221:GLU:HB3	1:D:128:ILE:HD13	1.89	0.54
1:B:186:GLN:NE2	1:D:186:GLN:HG2	2.23	0.54
1:B:161:PHE:HB2	1:C:186:GLN:HE22	1.73	0.54
1:B:169:SER:O	1:B:173:ARG:HD2	2.08	0.54
1:C:108:LYS:H	1:C:108:LYS:HD2	1.72	0.54
1:C:122:ASN:HD21	1:D:223:LYS:HG2	1.73	0.53
1:A:197:HIS:CE1	1:B:144:SER:HB2	2.44	0.53
1:B:132:GLN:HE22	1:D:133:GLN:HE21	1.55	0.53
1:B:132:GLN:OE1	1:D:133:GLN:NE2	2.42	0.53
1:C:134:GLU:O	1:C:138:LYS:HD3	2.09	0.53
1:C:105:ALA:N	1:C:108:LYS:HZ3	2.07	0.53
1:A:182:SER:O	1:A:186:GLN:HG2	2.09	0.52
1:A:168:LEU:HD11	1:D:174:GLN:HB3	1.90	0.52
1:B:176:GLN:HG3	1:D:175:GLN:HE22	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:179:PHE:HD1	1:D:164:GLN:HB3	1.74	0.52
1:D:230:GLN:HG2	1:D:234:MSE:HE2	1.90	0.52
1:A:149:ASN:OD1	1:A:152:GLN:NE2	2.42	0.52
1:A:214:LEU:O	1:A:220:SER:OG	2.25	0.52
1:A:201:ILE:HD11	1:B:144:SER:HB2	1.92	0.51
1:A:122:ASN:OD1	1:B:226:MSE:HG3	2.11	0.51
1:B:189:ARG:HG3	1:C:153:GLN:HE21	1.76	0.51
1:A:155:GLU:N	1:B:190:MSE:HE1	2.26	0.51
1:B:196:ILE:HD13	1:C:146:GLN:HB3	1.92	0.50
1:A:204:LEU:HD13	1:B:140:ASN:ND2	2.27	0.50
1:A:197:HIS:O	1:A:200:PHE:HB3	2.11	0.50
1:B:120:ALA:HA	1:B:123:GLN:OE1	2.12	0.49
1:B:139:LEU:HD12	1:C:204:LEU:HD23	1.93	0.49
1:C:190:MSE:HE1	1:D:151:LEU:HG	1.93	0.49
1:A:154:TRP:CD2	1:B:190:MSE:HE3	2.47	0.49
1:A:168:LEU:HD21	1:D:174:GLN:OE1	2.12	0.49
1:A:144:SER:OG	1:B:197:HIS:HE1	1.94	0.49
1:B:189:ARG:NH1	1:C:157:ASP:HB2	2.27	0.49
1:D:184:ILE:O	1:D:188:GLN:HG3	2.12	0.49
1:C:162:GLU:HA	1:D:179:PHE:HZ	1.78	0.49
1:A:151:LEU:HD23	1:B:194:LYS:HD2	1.95	0.49
1:B:150:VAL:HG11	1:C:193:ILE:HG22	1.95	0.48
1:A:161:PHE:HD1	1:B:183:ARG:HD3	1.78	0.48
1:C:127:GLN:O	1:C:131:THR:HG23	2.12	0.48
1:C:229:LEU:HG	1:D:118:PHE:HZ	1.78	0.48
1:A:155:GLU:HG3	1:B:190:MSE:SE	2.64	0.47
1:A:229:LEU:HD21	1:D:118:PHE:CE1	2.49	0.47
1:A:153:GLN:HB3	1:D:189:ARG:NH1	2.30	0.47
1:B:175:GLN:OE1	1:D:175:GLN:HB3	2.15	0.46
1:B:190:MSE:HA	1:B:193:ILE:HG22	1.96	0.46
1:C:162:GLU:HG2	1:D:183:ARG:HD3	1.98	0.46
1:D:195:GLN:O	1:D:198:GLU:N	2.49	0.46
1:B:132:GLN:NE2	1:D:133:GLN:HE21	2.14	0.46
1:A:147:PHE:CE1	1:C:147:PHE:HE1	2.33	0.46
1:B:197:HIS:O	1:B:200:PHE:HB3	2.17	0.45
1:B:132:GLN:HG3	1:B:133:GLN:N	2.30	0.45
1:C:200:PHE:O	1:C:204:LEU:HG	2.16	0.45
1:A:144:SER:OG	1:B:197:HIS:CE1	2.69	0.45
1:C:122:ASN:OD1	1:D:226:MSE:HG3	2.17	0.45
1:D:189:ARG:HA	1:D:189:ARG:HD3	1.30	0.45
1:D:194:LYS:HB2	1:D:194:LYS:HE3	1.72	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:230:GLN:HG3	1:A:234:MSE:HE3	1.98	0.44
1:C:200:PHE:CZ	1:C:204:LEU:HD11	2.51	0.44
1:C:176:GLN:NE2	1:D:169:SER:HB2	2.27	0.44
1:C:162:GLU:HA	1:D:179:PHE:CZ	2.53	0.44
1:A:115:LYS:HA	1:B:230:GLN:NE2	2.32	0.44
1:C:230:GLN:HB2	1:D:118:PHE:CE2	2.53	0.44
1:A:161:PHE:CD2	1:D:182:SER:HB2	2.53	0.44
1:A:168:LEU:HD23	1:A:168:LEU:HA	1.76	0.43
1:B:222:LEU:HD12	1:C:125:ILE:HG12	2.00	0.43
1:C:132:GLN:NE2	1:C:133:GLN:HG2	2.32	0.43
1:A:230:GLN:HE21	1:B:115:LYS:HG2	1.83	0.43
1:A:211:ASN:ND2	1:D:132:GLN:HE21	2.17	0.43
1:B:130:LYS:O	1:B:134:GLU:HG3	2.17	0.43
1:D:167:LYS:O	1:D:171:LEU:HG	2.19	0.43
1:A:197:HIS:HA	1:D:143:TYR:CE1	2.53	0.43
1:C:158:ILE:HD11	1:D:186:GLN:HB3	2.01	0.43
1:C:172:PHE:O	1:C:176:GLN:HB2	2.18	0.43
1:C:219:GLN:HG2	1:C:223:LYS:HE3	2.00	0.43
1:B:214:LEU:HD13	1:C:128:ILE:HG23	2.01	0.43
1:B:151:LEU:HD23	1:B:151:LEU:HA	1.83	0.42
1:A:128:ILE:HD13	1:A:128:ILE:HG21	1.78	0.42
1:D:176:GLN:O	1:D:179:PHE:HB3	2.19	0.42
1:D:218:THR:HA	1:D:221:GLU:HB2	2.01	0.42
1:A:213:ASN:O	1:A:217:GLY:N	2.52	0.42
1:A:153:GLN:HB3	1:D:189:ARG:HH12	1.85	0.42
1:A:201:ILE:HD11	1:B:144:SER:CB	2.50	0.42
1:D:151:LEU:HD12	1:D:151:LEU:HA	1.75	0.42
1:A:146:GLN:HB3	1:D:196:ILE:HD13	2.01	0.42
1:A:115:LYS:HA	1:B:230:GLN:HE21	1.85	0.42
1:A:154:TRP:HE1	1:A:158:ILE:HD11	1.85	0.41
1:A:189:ARG:NH1	1:D:153:GLN:OE1	2.53	0.41
1:B:132:GLN:NE2	1:B:133:GLN:OE1	2.53	0.41
1:C:230:GLN:HB2	1:D:118:PHE:CD2	2.55	0.41
1:A:234:MSE:HE1	1:B:115:LYS:HG2	2.02	0.41
1:C:165:GLY:HA3	1:D:179:PHE:CZ	2.55	0.41
1:A:161:PHE:CD1	1:B:183:ARG:HD3	2.55	0.41
1:B:129:TRP:HD1	1:D:129:TRP:CZ2	2.39	0.41
1:B:132:GLN:HG3	1:B:133:GLN:H	1.86	0.41
1:B:231:LYS:HA	1:B:234:MSE:HE2	2.02	0.41
1:A:154:TRP:HE1	1:B:186:GLN:NE2	2.19	0.41
1:B:175:GLN:HE22	1:D:176:GLN:HG3	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:147:PHE:HZ	1:D:193:ILE:HG23	1.85	0.41
1:C:226:MSE:HG3	1:D:122:ASN:OD1	2.21	0.41
1:B:190:MSE:O	1:B:193:ILE:HG22	2.21	0.40
1:C:132:GLN:HG3	1:C:133:GLN:N	2.36	0.40
1:A:154:TRP:O	1:A:158:ILE:HG12	2.21	0.40
1:A:197:HIS:HA	1:D:143:TYR:HE1	1.86	0.40
1:A:224:LYS:HG3	1:A:228:MSE:HE2	2.03	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	129/144 (90%)	126 (98%)	3 (2%)	0	100	100
1	B	119/144 (83%)	111 (93%)	8 (7%)	0	100	100
1	C	119/144 (83%)	113 (95%)	6 (5%)	0	100	100
1	D	113/144 (78%)	102 (90%)	10 (9%)	1 (1%)	14	30
All	All	480/576 (83%)	452 (94%)	27 (6%)	1 (0%)	43	66

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	196	ILE

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	115/128 (90%)	100 (87%)	15 (13%)	4	8
1	B	109/128 (85%)	91 (84%)	18 (16%)	2	4
1	C	116/128 (91%)	102 (88%)	14 (12%)	5	10
1	D	110/128 (86%)	100 (91%)	10 (9%)	9	19
All	All	450/512 (88%)	393 (87%)	57 (13%)	4	9

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	121	SER
1	A	139	LEU
1	A	144	SER
1	A	168	LEU
1	A	169	SER
1	A	175	GLN
1	A	183	ARG
1	A	193	ILE
1	A	203	SER
1	A	207	VAL
1	A	208	GLU
1	A	210	ASN
1	A	213	ASN
1	A	228	MSE
1	A	234	MSE
1	B	118	PHE
1	B	127	GLN
1	B	135	GLU
1	B	138	LYS
1	B	144	SER
1	B	148	MSE
1	B	151	LEU
1	B	158	ILE
1	B	181	GLN
1	B	182	SER
1	B	189	ARG
1	B	193	ILE
1	B	199	GLN
1	B	201	ILE
1	B	207	VAL

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Mol	Chain	Res	Type
1	B	214	LEU
1	B	234	MSE
1	B	237	THR
1	C	117	SER
1	C	119	LYS
1	C	136	ILE
1	C	139	LEU
1	C	148	MSE
1	C	162	GLU
1	C	169	SER
1	C	184	ILE
1	C	189	ARG
1	C	193	ILE
1	C	194	LYS
1	C	201	ILE
1	C	208	GLU
1	C	234	MSE
1	D	117	SER
1	D	118	PHE
1	D	158	ILE
1	D	184	ILE
1	D	189	ARG
1	D	190	MSE
1	D	201	ILE
1	D	202	LYS
1	D	219	GLN
1	D	231	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	123	GLN
1	A	137	GLN
1	A	149	ASN
1	A	152	GLN
1	A	175	GLN
1	A	230	GLN
1	B	127	GLN
1	B	132	GLN
1	B	186	GLN
1	B	197	HIS
1	B	230	GLN

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Mol	Chain	Res	Type
1	C	153	GLN
1	C	186	GLN
1	C	188	GLN
1	C	195	GLN
1	C	211	ASN
1	C	230	GLN
1	D	132	GLN
1	D	133	GLN
1	D	152	GLN
1	D	175	GLN
1	D	176	GLN
1	D	186	GLN

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](#)

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	124/144 (86%)	0.94	20 (16%) 4 3	60, 83, 108, 129	0
1	B	116/144 (80%)	1.20	22 (18%) 3 2	61, 91, 118, 138	0
1	C	117/144 (81%)	0.95	18 (15%) 5 4	61, 92, 121, 132	0
1	D	111/144 (77%)	0.85	8 (7%) 21 17	55, 84, 104, 123	0
All	All	468/576 (81%)	0.98	68 (14%) 6 4	55, 87, 114, 138	0

All (68) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	211	ASN	5.4
1	C	135	GLU	4.7
1	D	161	PHE	4.7
1	A	222	LEU	4.6
1	B	129	TRP	4.6
1	A	161	PHE	4.6
1	B	122	ASN	4.5
1	C	132	GLN	4.4
1	A	183	ARG	4.3
1	A	172	PHE	4.2
1	B	161	PHE	3.9
1	C	222	LEU	3.8
1	D	128	ILE	3.6
1	C	125	ILE	3.5
1	D	225	GLU	3.5
1	C	208	GLU	3.4
1	B	193	ILE	3.4
1	C	129	TRP	3.2
1	A	179	PHE	3.2
1	A	125	ILE	3.1
1	D	211	ASN	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	146	GLN	3.0
1	A	216	THR	3.0
1	A	218	THR	3.0
1	D	179	PHE	2.9
1	B	147	PHE	2.8
1	D	172	PHE	2.8
1	B	115	LYS	2.8
1	C	106	LYS	2.7
1	A	154	TRP	2.6
1	C	161	PHE	2.6
1	C	134	GLU	2.6
1	B	154	TRP	2.5
1	B	126	GLU	2.5
1	D	166	GLU	2.5
1	A	129	TRP	2.5
1	C	186	GLN	2.5
1	A	230	GLN	2.4
1	B	199	GLN	2.4
1	B	172	PHE	2.4
1	B	189	ARG	2.4
1	A	158	ILE	2.4
1	B	164	GLN	2.4
1	C	147	PHE	2.4
1	C	183	ARG	2.3
1	B	206	ASP	2.3
1	C	157	ASP	2.3
1	A	167	LYS	2.2
1	A	210	ASN	2.2
1	B	185	VAL	2.2
1	A	147	PHE	2.2
1	C	143	TYR	2.2
1	A	134	GLU	2.2
1	D	175	GLN	2.2
1	A	108	LYS	2.2
1	C	211	ASN	2.1
1	A	197	HIS	2.1
1	B	178	ILE	2.1
1	A	126	GLU	2.1
1	B	127	GLN	2.1
1	A	110	ILE	2.1
1	B	163	GLU	2.1
1	C	142	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	238	GLN	2.1
1	C	153	GLN	2.0
1	B	134	GLU	2.0
1	B	137	GLN	2.0
1	C	140	ASN	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 oligosaccharides 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.