



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:39 PM GMT

PDB ID : 4PK7
Title : crystal structure of human Stromal Antigen 2 (SA2) in complex with Sister Chromatid Cohesion protein 1 (Scc1) with bound MES, native proteins
Authors : Hara, K.; Chen, Z.; Tomchick, D.R.; Yu, H.
Deposited on : 2014-05-13
Resolution : 2.95 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

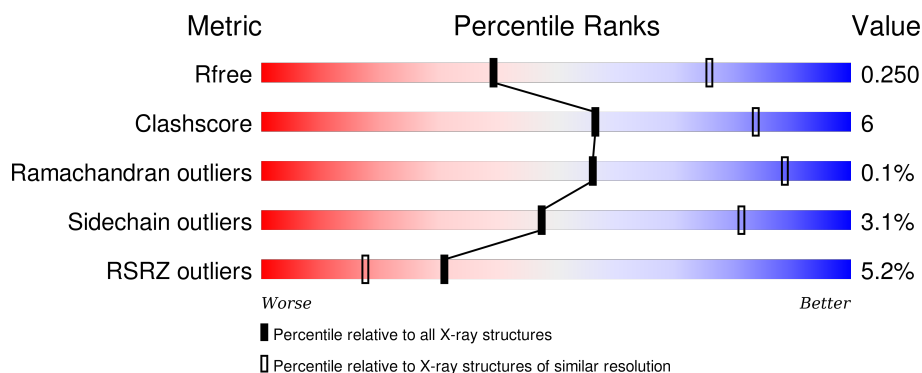
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.95 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	2184 (3.00-2.92)
Clashscore	102246	2552 (3.00-2.92)
Ramachandran outliers	100387	2468 (3.00-2.92)
Sidechain outliers	100360	2471 (3.00-2.92)
RSRZ outliers	91569	2201 (3.00-2.92)

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	994	
2	B	148	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 16049 atoms, of which 8063 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 Cohesin subunit SA-2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	903	Total	C	H	N	O	S	0	0	0
			14756	4702	7393	1226	1381	54			

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	67	GLY	-	expression tag	UNP Q8N3U4
A	68	ALA	-	expression tag	UNP Q8N3U4
A	69	MET	-	expression tag	UNP Q8N3U4
A	70	ASP	-	expression tag	UNP Q8N3U4
A	71	PRO	-	expression tag	UNP Q8N3U4
A	72	GLU	-	expression tag	UNP Q8N3U4
A	73	PHE	-	expression tag	UNP Q8N3U4
A	74	GLY	-	expression tag	UNP Q8N3U4
A	75	ARG	-	expression tag	UNP Q8N3U4
A	76	PRO	-	expression tag	UNP Q8N3U4
A	77	GLY	-	expression tag	UNP Q8N3U4
A	78	ARG	-	expression tag	UNP Q8N3U4
A	79	PRO	-	expression tag	UNP Q8N3U4

- Molecule 2 is a protein called Double-strand-break repair protein rad21 homolog.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	76	Total	C	H	N	O	S	0	0	0
			1268	396	657	103	109	3			

There are 8 discrepancies between the modelled and reference sequences:

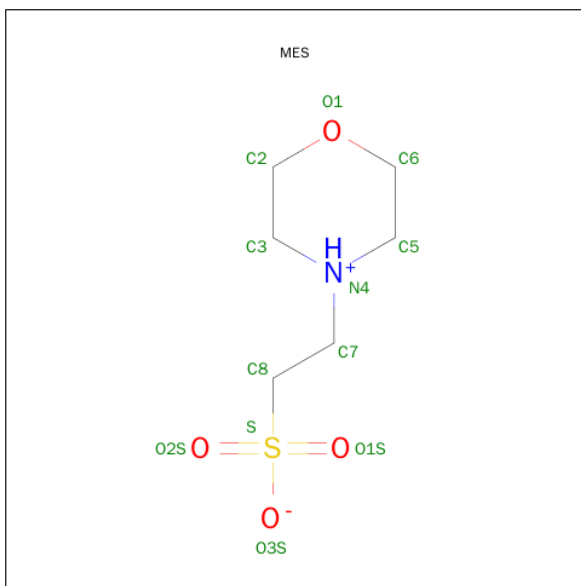
Chain	Residue	Modelled	Actual	Comment	Reference
B	273	GLY	-	expression tag	UNP O60216
B	274	PRO	-	expression tag	UNP O60216
B	275	LEU	-	expression tag	UNP O60216

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Chain	Residue	Modelled	Actual	Comment	Reference
B	276	GLY	-	expression tag	UNP O60216
B	277	SER	-	expression tag	UNP O60216
B	278	GLY	-	expression tag	UNP O60216
B	279	ARG	-	expression tag	UNP O60216
B	280	PRO	-	expression tag	UNP O60216

- Molecule 3 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C₆H₁₃NO₄S).

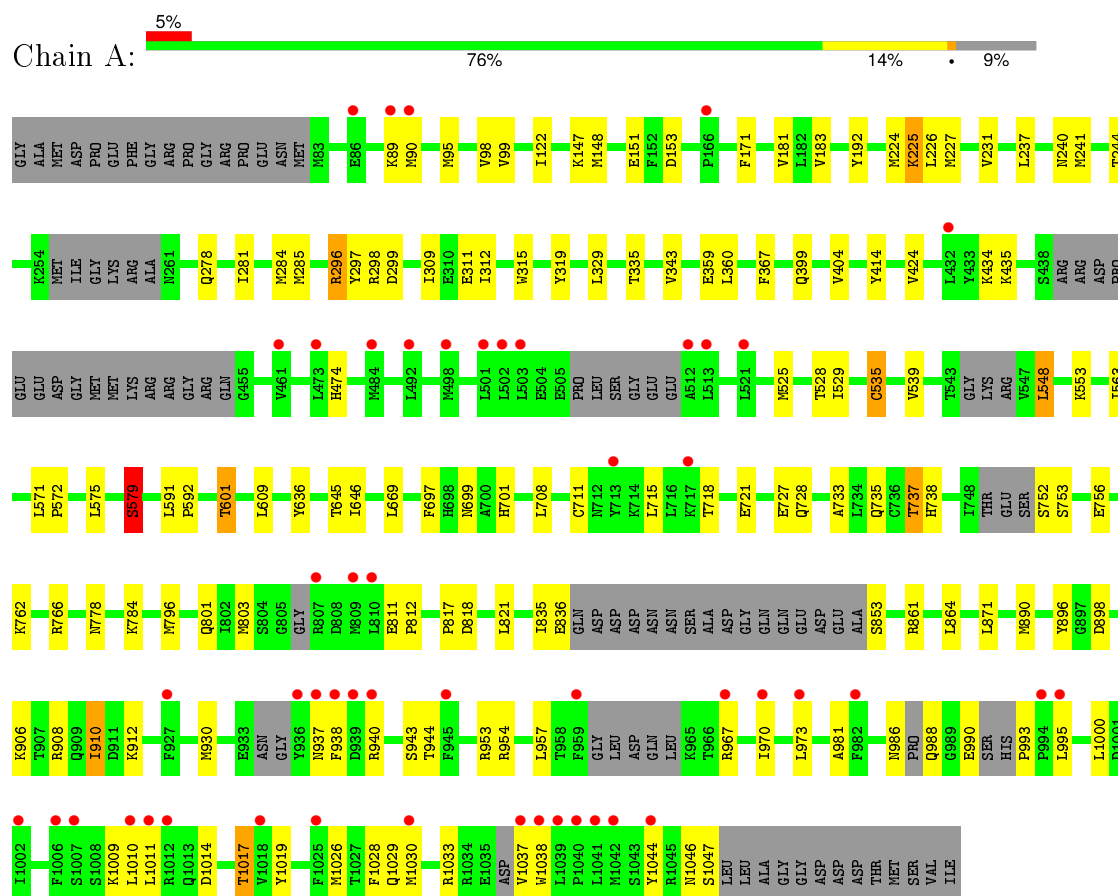


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	N	O	S	
3	A	1	25	6	13	1	4	1	0

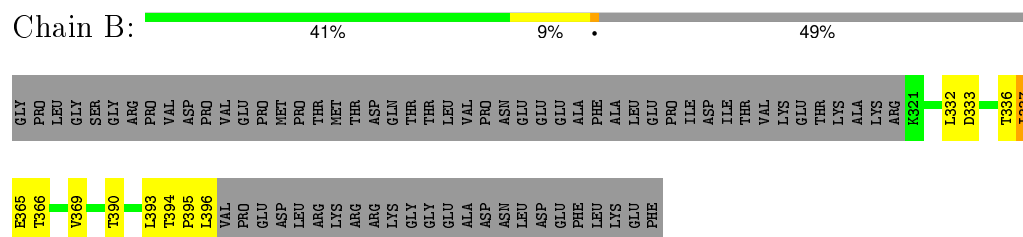
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Cohesin subunit SA-2



• Molecule 2: Double-strand-break repair protein rad21 homolog



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	78.45Å 107.28Å 180.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.68 – 2.95 47.68 – 2.95	Depositor EDS
% Data completeness (in resolution range)	99.8 (47.68-2.95) 99.9 (47.68-2.95)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.22 (at 2.96Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.188 , 0.251 0.186 , 0.250	Depositor DCC
R_{free} test set	1636 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	67.9	Xtriage
Anisotropy	0.248	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 47.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 32816 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	16049	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.76% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.45	0/7486	0.61	1/10079 (0.0%)
2	B	0.46	0/622	0.68	0/841
All	All	0.45	0/8108	0.62	1/10920 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	579	SER	CB-CA-C	-5.42	99.81	110.10

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	7363	7393	7371	90	1
2	B	611	657	657	15	0
3	A	12	13	13	1	0
All	All	7986	8063	8041	97	1

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 6.

All (97) 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:A:756:GLU:N	1:A:756:GLU:OE2	2.29	0.65
1:A:548:LEU:HD23	1:A:553:LYS:HG3	1.77	0.65
1:A:525:MET:O	1:A:528:THR:OG1	2.15	0.63
2:B:349:THR:OG1	2:B:350:THR:N	2.31	0.63
1:A:981:ALA:HB1	1:A:1000:LEU:HD11	1.81	0.62
1:A:890:MET:SD	1:A:954:ARG:NH2	2.72	0.61
1:A:224:MET:HB3	1:A:311:GLU:HG3	1.82	0.60
1:A:988:GLN:N	1:A:988:GLN:OE1	2.35	0.60
1:A:535:CYS:HB3	1:A:548:LEU:HD11	1.85	0.59
1:A:954:ARG:HA	1:A:957:LEU:CD1	2.35	0.56
1:A:296:ARG:NH1	1:A:299:ASP:OD2	2.38	0.56
1:A:241:MET:HG3	1:A:278:GLN:NE2	2.20	0.56
1:A:752:SER:N	1:A:753:SER:HA	2.19	0.56
1:A:937:ASN:HB3	1:A:938:PHE:HD2	1.71	0.56
1:A:591:LEU:HB2	1:A:592:PRO:HD3	1.88	0.55
1:A:99:VAL:HG21	1:A:181:VAL:HG12	1.88	0.55
1:A:225:LYS:NZ	1:A:311:GLU:OE2	2.40	0.55
1:A:733:ALA:O	1:A:737:THR:HG22	2.07	0.55
1:A:609:LEU:HD21	1:A:646:ILE:HG23	1.89	0.54
1:A:298:ARG:HG3	2:B:337:ILE:HD11	1.88	0.54
2:B:393:LEU:C	2:B:395:PRO:CD	2.76	0.54
2:B:390:THR:HA	2:B:393:LEU:HD12	1.91	0.53
1:A:89:LYS:HG3	1:A:90:MET:N	2.23	0.53
1:A:95:MET:HE3	1:A:98:VAL:HG11	1.91	0.53
1:A:937:ASN:CB	1:A:938:PHE:HB3	2.39	0.53
1:A:227:MET:HG2	1:A:315:TRP:CZ2	2.43	0.52
1:A:399:GLN:OE1	1:A:434:LYS:NZ	2.42	0.52
1:A:811:GLU:N	1:A:812:PRO:HD2	2.24	0.52
1:A:762:LYS:O	1:A:766:ARG:HG2	2.10	0.52
1:A:89:LYS:HB3	1:A:171:PHE:HD1	1.75	0.52
1:A:796:MET:HE1	2:B:393:LEU:HD23	1.92	0.51
1:A:986:ASN:HA	1:A:995:LEU:HD21	1.93	0.51
1:A:970:ILE:HD13	1:A:1009:LYS:HB3	1.92	0.50
1:A:801:GLN:CG	2:B:395:PRO:HG3	2.42	0.50
1:A:1030:MET:HG2	1:A:1038:TRP:CZ3	2.47	0.49
1:A:601:THR:HG21	1:A:645:THR:HB	1.94	0.49
1:A:359:GLU:O	1:A:360:LEU:HG	2.12	0.49
1:A:967:ARG:HB3	1:A:1010:LEU:HD13	1.94	0.49
1:A:937:ASN:HB3	1:A:938:PHE:CD2	2.48	0.48
1:A:122:ILE:HG21	1:A:148:MET:CE	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:990:GLU:HB2	1:A:993:PRO:N	2.28	0.48
1:A:801:GLN:HG2	2:B:395:PRO:HG3	1.95	0.48
1:A:89:LYS:HB3	1:A:171:PHE:CD1	2.49	0.48
1:A:122:ILE:HG21	1:A:148:MET:HE2	1.95	0.48
1:A:309:ILE:HG13	1:A:335:THR:HG21	1.96	0.48
1:A:861:ARG:HA	1:A:864:LEU:HD12	1.95	0.48
2:B:393:LEU:C	2:B:395:PRO:HD2	2.34	0.47
1:A:937:ASN:HB3	1:A:938:PHE:HB3	1.95	0.47
1:A:535:CYS:CB	1:A:548:LEU:HD11	2.44	0.47
1:A:953:ARG:O	1:A:957:LEU:HD12	2.15	0.47
1:A:796:MET:HG2	1:A:871:LEU:HD23	1.97	0.46
1:A:147:LYS:HE3	1:A:151:GLU:HG3	1.96	0.46
1:A:898:ASP:HB3	2:B:369:VAL:CG1	2.45	0.46
1:A:1046:ASN:O	1:A:1047:SER:OG	2.24	0.45
1:A:835:ILE:HG22	1:A:836:GLU:N	2.32	0.45
1:A:241:MET:HA	1:A:244:THR:HG22	1.98	0.45
1:A:298:ARG:CG	2:B:337:ILE:HD11	2.47	0.45
1:A:335:THR:HG22	1:A:343:VAL:HG12	1.98	0.44
1:A:529:ILE:HG23	1:A:563:ILE:HD13	1.98	0.44
1:A:940:ARG:NH2	1:A:1037:VAL:HA	2.32	0.44
1:A:539:VAL:HG21	2:B:365:GLU:HA	2.00	0.44
1:A:981:ALA:CB	1:A:1000:LEU:HD11	2.47	0.44
1:A:414:TYR:OH	1:A:435:LYS:HG2	2.18	0.44
1:A:359:GLU:HG3	1:A:360:LEU:N	2.34	0.43
1:A:1000:LEU:HD23	1:A:1044:TYR:HD2	1.83	0.43
1:A:231:VAL:HG22	1:A:285:MET:CE	2.49	0.43
1:A:727:GLU:HG3	1:A:728:GLN:N	2.34	0.43
1:A:297:TYR:OH	3:A:1101:MES:O2S	2.33	0.43
1:A:298:ARG:HG2	2:B:332:LEU:HB2	2.00	0.42
1:A:1026:MET:HB2	1:A:1026:MET:HE3	1.94	0.42
1:A:183:VAL:HG21	1:A:226:LEU:HD12	2.00	0.42
1:A:906:LYS:O	1:A:910:ILE:HD13	2.19	0.42
2:B:333:ASP:HB3	2:B:336:THR:HG23	2.01	0.42
1:A:817:PRO:HB3	1:A:821:LEU:HD23	2.00	0.42
1:A:312:ILE:HA	1:A:315:TRP:CE3	2.55	0.42
1:A:930:MET:HG3	1:A:944:THR:HG21	2.01	0.42
1:A:281:ILE:HD13	1:A:284:MET:CE	2.49	0.42
1:A:957:LEU:H	1:A:957:LEU:HD12	1.83	0.42
1:A:1014:ASP:HA	1:A:1017:THR:OG1	2.20	0.42
1:A:281:ILE:HD13	1:A:284:MET:HE3	2.02	0.42
1:A:1010:LEU:HB3	1:A:1011:LEU:HB2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:778:ASN:O	1:A:784:LYS:HE3	2.19	0.41
2:B:394:THR:N	2:B:395:PRO:CD	2.84	0.41
1:A:529:ILE:HD13	1:A:591:LEU:CD2	2.50	0.41
2:B:393:LEU:O	2:B:395:PRO:HD2	2.21	0.41
1:A:735:GLN:O	1:A:738:HIS:HB3	2.21	0.41
1:A:329:LEU:HD13	1:A:367:PHE:CG	2.56	0.41
1:A:575:LEU:O	1:A:579:SER:HB3	2.21	0.41
1:A:715:LEU:HA	1:A:718:THR:HG22	2.03	0.41
1:A:861:ARG:HD2	1:A:896:TYR:OH	2.22	0.41
1:A:1029:GLN:O	1:A:1033:ARG:HG3	2.21	0.41
1:A:1000:LEU:N	1:A:1000:LEU:HD12	2.36	0.40
1:A:192:TYR:OH	1:A:237:LEU:HD11	2.22	0.40
1:A:697:PHE:HD1	1:A:701:HIS:CD2	2.39	0.40
1:A:908:ARG:HG2	1:A:912:LYS:HD2	2.03	0.40
1:A:240:ASN:O	1:A:244:THR:HG22	2.21	0.40
1:A:571:LEU:HB3	1:A:572:PRO:HD3	2.03	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:721:GLU:OE2	1:A:1028:PHE:H[3_545]	1.54	0.06

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	877/994 (88%)	841 (96%)	35 (4%)	1 (0%)	56	89
2	B	74/148 (50%)	70 (95%)	4 (5%)	0	100	100
All	All	951/1142 (83%)	911 (96%)	39 (4%)	1 (0%)	56	89

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	579	SER

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	819/891 (92%)	795 (97%)	24 (3%)	50	82
2	B	71/134 (53%)	67 (94%)	4 (6%)	26	63
All	All	890/1025 (87%)	862 (97%)	28 (3%)	47	81

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	153	ASP
1	A	225	LYS
1	A	296	ARG
1	A	319	TYR
1	A	404	VAL
1	A	424	VAL
1	A	474	HIS
1	A	535	CYS
1	A	548	LEU
1	A	601	THR
1	A	636	TYR
1	A	669	LEU
1	A	699	ASN
1	A	708	LEU
1	A	711	CYS
1	A	737	THR
1	A	803	MET
1	A	818	ASP
1	A	853	SER
1	A	910	ILE
1	A	943	SER
1	A	973	LEU

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Mol	Chain	Res	Type
1	A	1017	THR
1	A	1019	TYR
2	B	337	ILE
2	B	348	VAL
2	B	366	THR
2	B	396	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	744	GLN
1	A	764	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	MES	A	1101	-	12,12,12	1.82	1 (8%)	16,16,16	1.95	4 (25%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MES	A	1101	-	-	0/6/14/14	1/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1101	MES	C8-S	-4.61	1.69	1.78

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1101	MES	C6-C5-N4	-4.50	104.35	109.98
3	A	1101	MES	O2S-S-O1S	-3.08	106.06	112.48
3	A	1101	MES	C5-N4-C3	2.11	114.19	109.76
3	A	1101	MES	O1S-S-C8	2.43	112.18	106.41

There are no chirality outliers.

There are no torsion outliers.

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1101	MES	C2-C3-C5-C6-N4-O1

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1101	MES	1	0

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	903/994 (90%)	0.65	51 (5%) 28 15	25, 59, 105, 130	0
2	B	76/148 (51%)	0.53	0 100 100	30, 49, 85, 103	0
All	All	979/1142 (85%)	0.64	51 (5%) 31 17	25, 59, 104, 130	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1010	LEU	4.7
1	A	973	LEU	4.3
1	A	807	ARG	4.2
1	A	936	TYR	4.0
1	A	940	ARG	3.7
1	A	1038	TRP	3.7
1	A	982	PHE	3.7
1	A	938	PHE	3.6
1	A	1041	LEU	3.6
1	A	498	MET	3.5
1	A	90	MET	3.4
1	A	1025	PHE	3.4
1	A	1044	TYR	3.3
1	A	512	ALA	3.1
1	A	994	PRO	3.1
1	A	939	ASP	2.9
1	A	959	PHE	2.8
1	A	1011	LEU	2.8
1	A	995	LEU	2.7
1	A	945	PHE	2.7
1	A	937	ASN	2.7
1	A	1012	ARG	2.7
1	A	1042	MET	2.6
1	A	432	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	473	LEU	2.6
1	A	809	MET	2.6
1	A	927	PHE	2.5
1	A	1039	LEU	2.5
1	A	967	ARG	2.5
1	A	1030	MET	2.4
1	A	1040	PRO	2.4
1	A	492	LEU	2.4
1	A	970	ILE	2.4
1	A	166	PRO	2.3
1	A	1037	VAL	2.3
1	A	717	LYS	2.3
1	A	513	LEU	2.3
1	A	810	LEU	2.3
1	A	86	GLU	2.3
1	A	484	MET	2.3
1	A	1007	SER	2.3
1	A	1006	PHE	2.2
1	A	502	LEU	2.2
1	A	1018	VAL	2.1
1	A	713	TYR	2.1
1	A	501	LEU	2.1
1	A	503	LEU	2.1
1	A	521	LEU	2.1
1	A	461	VAL	2.1
1	A	1002	ILE	2.1
1	A	89	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

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(\AA^2)	Q<0.9
3	MES	A	1101	12/12	0.90	0.28	0.73	57,77,118,127	0

6.5 Other polymers [i](#)

There are no such residues in this entry.