



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:49 AM UTC

PDB ID : 6EI6 / pdb_00006ei6
Title : CC2D1B coordinates ESRICT-III activity during the mitotic reformation of the nuclear envelope
Authors : Ventimiglia, L.N.; Cuesta-Geijo, M.A.; Martinelli, N.; Caballe, A.; Macheboeuf, P.; Miguët, N.; Parnham, I.M.; Olmos, Y.; Carlton, J.G.; Weis-sehorn, W.; martin-Serrano, J.
Deposited on : 2017-09-18
Resolution : 2.46 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

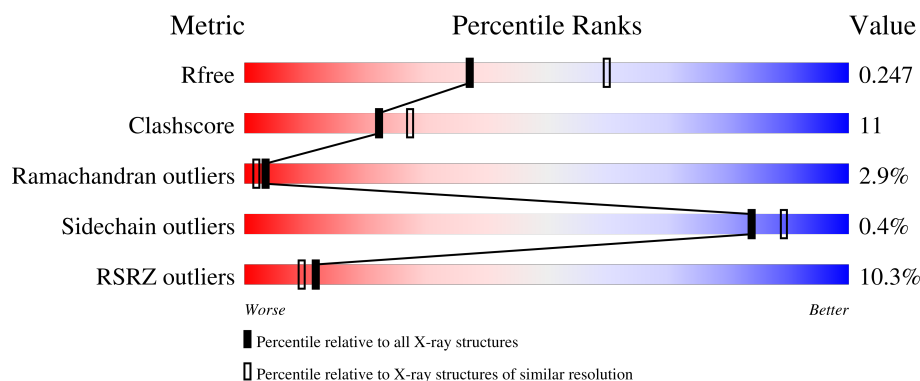
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.46 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	1190 (2.46-2.46)
Clashscore	190562	1229 (2.46-2.46)
Ramachandran outliers	187476	1218 (2.46-2.46)
Sidechain outliers	187428	1218 (2.46-2.46)
RSRZ outliers	180081	1190 (2.46-2.46)

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	270	13% 66% 21% • 10%
1	B	270	6% 73% 15% • 10%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4169 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 Coiled-coil and C2 domain-containing protein 1-like.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	242	Total	C	N	O	S	0	0	0
			1983	1242	357	372	12			
1	B	242	Total	C	N	O	S	0	0	0
			1980	1239	357	372	12			

There are 6 discrepancies between the modelled and reference sequences:

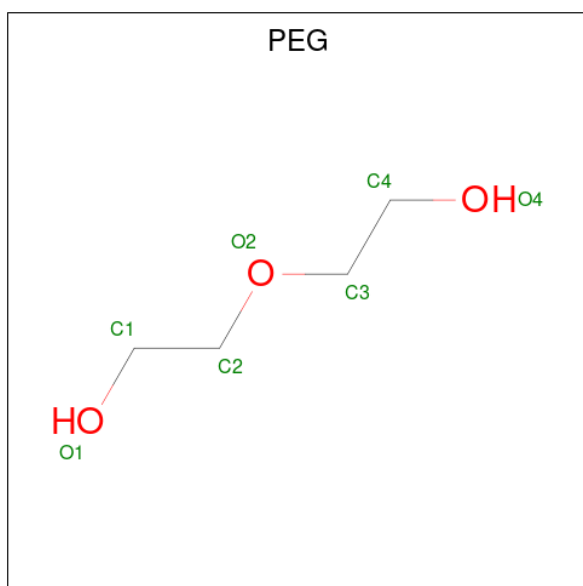
Chain	Residue	Modelled	Actual	Comment	Reference
A	547	GLY	-	expression tag	UNP Q9VKJ9
A	548	ALA	-	expression tag	UNP Q9VKJ9
A	549	MET	-	expression tag	UNP Q9VKJ9
B	547	GLY	-	expression tag	UNP Q9VKJ9
B	548	ALA	-	expression tag	UNP Q9VKJ9
B	549	MET	-	expression tag	UNP Q9VKJ9

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0

- Molecule 3 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 7 4 3	0	0

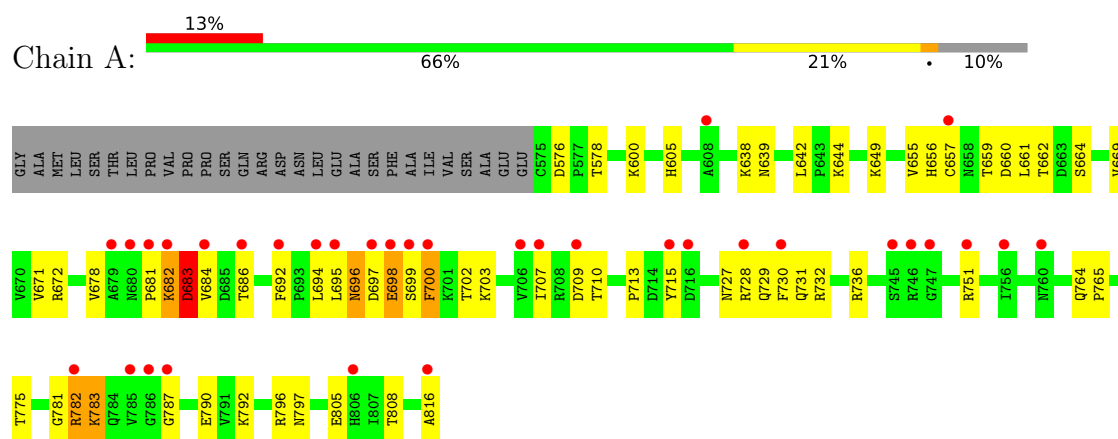
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	54	Total O 54 54	0	0
4	B	110	Total O 110 110	0	0

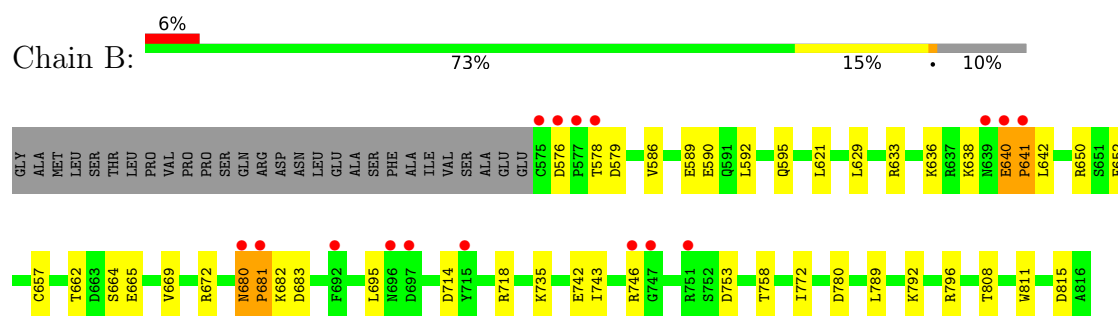
3 Residue-property plots [i](#)

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: Coiled-coil and C2 domain-containing protein 1-like



- Molecule 1: Coiled-coil and C2 domain-containing protein 1-like



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	87.41Å 54.05Å 97.90Å 90.00° 99.52° 90.00°	Depositor
Resolution (Å)	59.59 – 2.46 59.59 – 2.46	Depositor EDS
% Data completeness (in resolution range)	99.3 (59.59-2.46) 99.3 (59.59-2.46)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.18 (at 2.45Å)	Xtriage
Refinement program	PHENIX (1.12_2829: ???)	Depositor
R, R_{free}	0.205 , 0.247 0.207 , 0.247	Depositor DCC
R_{free} test set	1613 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	42.6	Xtriage
Anisotropy	0.166	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 38.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4169	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.07% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, PEG

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	0.43	0/2016	0.68	0/2713
1	B	0.49	0/2012	0.74	4/2706 (0.1%)
All	All	0.46	0/4028	0.71	4/5419 (0.1%)

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

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

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	652	PHE	CA-C-N	-6.87	108.43	121.54
1	B	652	PHE	C-N-CA	-6.87	108.43	121.54
1	B	640	GLU	CA-C-N	5.38	139.91	127.00
1	B	640	GLU	C-N-CA	5.38	139.91	127.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	683	ASP	Peptide
1	A	698	GLU	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1983	0	1992	57	0
1	B	1980	0	1983	29	0
2	A	15	0	0	0	0
2	B	20	0	0	0	0
3	A	7	0	10	3	0
4	A	54	0	0	3	0
4	B	110	0	0	3	0
All	All	4169	0	3985	85	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 11.

All (85) 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:662:THR:HG22	1:A:664:SER:H	1.38	0.89
1:A:781:GLY:HA3	1:A:782:ARG:HG3	1.55	0.88
1:B:589:GLU:OE1	1:B:636:LYS:NZ	2.10	0.85
1:A:695:LEU:HD12	1:A:729:GLN:HE21	1.44	0.81
1:B:662:THR:HG22	1:B:664:SER:H	1.46	0.79
1:A:816:ALA:O	4:A:1001:HOH:O	2.00	0.79
1:B:650:ARG:O	1:B:808:THR:HG23	1.83	0.78
1:A:682:LYS:HG2	1:A:683:ASP:H	1.48	0.77
1:A:649:LYS:HB2	3:A:904:PEG:H41	1.66	0.76
1:A:660:ASP:OD1	1:A:661:LEU:HD13	1.90	0.71
1:B:669:VAL:HB	1:B:792:LYS:HB2	1.72	0.70
1:A:707:ILE:HG12	1:A:713:PRO:HB3	1.75	0.69
1:A:764:GLN:HG3	1:A:765:PRO:HD3	1.76	0.68
1:B:718:ARG:NH1	4:B:1004:HOH:O	2.29	0.66
1:A:659:THR:HA	1:A:796:ARG:HH21	1.62	0.65
1:B:592:LEU:HB2	1:B:629:LEU:HD13	1.80	0.64
1:B:808:THR:HG21	4:B:1068:HOH:O	1.96	0.64
1:A:732:ARG:HE	1:A:736:ARG:HE	1.46	0.63
1:A:605:HIS:NE2	1:A:657:CYS:HB2	2.15	0.61
1:A:805:GLU:O	1:A:808:THR:HG22	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:683:ASP:HA	1:A:709:ASP:HA	1.83	0.59
1:A:732:ARG:HG3	1:A:736:ARG:HH21	1.69	0.57
1:B:680:ASN:HB2	1:B:683:ASP:HB2	1.87	0.56
1:B:595:GLN:HG2	1:B:811:TRP:CZ3	2.41	0.56
1:B:657:CYS:O	1:B:796:ARG:O	2.23	0.56
1:B:743:ILE:HD11	1:B:789:LEU:HD22	1.87	0.56
1:B:662:THR:HB	1:B:665:GLU:HG3	1.88	0.55
1:B:592:LEU:CB	1:B:629:LEU:HD13	2.37	0.54
1:A:644:LYS:NZ	1:B:815:ASP:OD2	2.42	0.54
1:A:605:HIS:CE1	1:A:657:CYS:HB2	2.44	0.52
1:B:579:ASP:OD1	4:B:1001:HOH:O	2.18	0.52
1:A:657:CYS:O	1:A:796:ARG:O	2.28	0.51
1:A:707:ILE:CD1	1:A:713:PRO:HB3	2.40	0.51
1:B:638:LYS:O	1:B:640:GLU:HG2	2.11	0.51
1:A:682:LYS:HG2	1:A:683:ASP:N	2.22	0.50
1:A:707:ILE:CG1	1:A:713:PRO:HB3	2.41	0.50
1:A:707:ILE:HG12	1:A:713:PRO:CB	2.42	0.49
1:A:669:VAL:HB	1:A:792:LYS:HB2	1.93	0.49
1:A:682:LYS:HG2	1:A:709:ASP:HB3	1.95	0.49
1:A:686:THR:OG1	1:A:707:ILE:HD11	2.13	0.48
1:B:672:ARG:HG2	1:B:714:ASP:OD1	2.13	0.48
1:A:692:PHE:HB3	1:A:700:PHE:HD2	1.77	0.48
1:B:772:ILE:O	1:B:792:LYS:HA	2.13	0.48
1:A:576:ASP:OD2	1:A:578:THR:OG1	2.26	0.48
1:A:644:LYS:HB3	1:A:644:LYS:HE2	1.53	0.48
1:B:629:LEU:O	1:B:633:ARG:HG3	2.13	0.47
1:A:682:LYS:O	1:A:684:VAL:N	2.48	0.47
1:A:655:VAL:HG12	1:A:656:HIS:CE1	2.50	0.47
1:A:697:ASP:HB2	1:A:698:GLU:HG3	1.96	0.47
1:A:775:THR:HG22	1:A:790:GLU:HB2	1.97	0.47
1:A:671:VAL:O	1:A:715:TYR:O	2.33	0.47
1:A:695:LEU:HD21	1:A:730:PHE:CE2	2.50	0.47
1:A:707:ILE:HD13	1:A:710:THR:HG23	1.97	0.47
1:A:751:ARG:HD2	4:A:1031:HOH:O	2.15	0.46
1:B:746:ARG:HA	1:B:753:ASP:OD1	2.16	0.45
1:A:702:THR:OG1	1:A:703:LYS:N	2.50	0.45
1:A:728:ARG:HA	1:A:731:GLN:CD	2.42	0.45
1:B:735:LYS:HE2	1:B:735:LYS:HB2	1.82	0.45
1:A:694:LEU:HD11	1:A:700:PHE:HB2	1.99	0.44
1:A:707:ILE:C	1:A:707:ILE:HD12	2.43	0.44
1:A:682:LYS:CG	1:A:709:ASP:HB3	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:680:ASN:O	1:B:681:PRO:C	2.61	0.44
1:A:732:ARG:CG	1:A:736:ARG:HH21	2.29	0.43
1:B:742:GLU:HG2	1:B:758:THR:HG22	2.01	0.43
1:A:600:LYS:NZ	4:A:1007:HOH:O	2.52	0.43
1:A:696:ASN:H	1:A:729:GLN:HE22	1.66	0.43
1:A:796:ARG:HG2	1:A:797:ASN:OD1	2.19	0.42
1:B:682:LYS:HE2	1:B:682:LYS:HB2	1.88	0.42
1:A:649:LYS:HB2	3:A:904:PEG:C4	2.45	0.42
1:A:707:ILE:HD13	1:A:710:THR:CG2	2.50	0.42
1:A:782:ARG:O	1:A:783:LYS:CB	2.68	0.42
1:B:621:LEU:HA	1:B:621:LEU:HD12	1.82	0.42
1:A:655:VAL:HG12	1:A:656:HIS:ND1	2.35	0.42
1:A:727:ASN:HD22	1:A:728:ARG:N	2.18	0.42
1:B:695:LEU:HD23	1:B:695:LEU:HA	1.77	0.41
1:A:678:VAL:HG11	1:A:684:VAL:HG21	2.03	0.41
1:B:641:PRO:HB2	1:B:642:LEU:H	1.60	0.41
1:A:659:THR:CA	1:A:796:ARG:HH21	2.32	0.41
1:A:695:LEU:HD21	1:A:730:PHE:HE2	1.85	0.41
1:A:671:VAL:O	1:A:672:ARG:HB3	2.20	0.41
1:A:649:LYS:CB	3:A:904:PEG:H41	2.45	0.41
1:B:586:VAL:O	1:B:590:GLU:HG2	2.21	0.41
1:A:695:LEU:HD11	1:A:730:PHE:CD2	2.55	0.41
1:A:736:ARG:HH11	1:A:736:ARG:HD3	1.75	0.40
1:B:576:ASP:OD1	1:B:578:THR:HG22	2.22	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	240/270 (89%)	209 (87%)	21 (9%)	10 (4%)	2 0

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	240/270 (89%)	219 (91%)	17 (7%)	4 (2%)	7	6
All	All	480/540 (89%)	428 (89%)	38 (8%)	14 (3%)	3	2

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	683	ASP
1	A	699	SER
1	A	700	PHE
1	A	783	LYS
1	B	641	PRO
1	B	680	ASN
1	A	681	PRO
1	A	682	LYS
1	A	696	ASN
1	B	780	ASP
1	A	638	LYS
1	A	782	ARG
1	B	681	PRO
1	A	787	GLY

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	225/248 (91%)	223 (99%)	2 (1%)	70	81
1	B	224/248 (90%)	224 (100%)	0	100	100
All	All	449/496 (90%)	447 (100%)	2 (0%)	84	89

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	639	ASN
1	A	642	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	727	ASN
1	A	729	GLN
1	A	760	ASN
1	A	784	GLN
1	B	724	GLN
1	B	737	HIS

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](#)

8 ligands are 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	PEG	A	904	-	6,6,6	0.45	0	5,5,5	0.66	0
2	SO4	A	902	-	4,4,4	0.30	0	6,6,6	0.06	0
2	SO4	B	902	-	4,4,4	0.35	0	6,6,6	0.31	0
2	SO4	B	904	-	4,4,4	0.32	0	6,6,6	0.10	0
2	SO4	B	901	-	4,4,4	0.33	0	6,6,6	0.08	0
2	SO4	A	903	-	4,4,4	0.30	0	6,6,6	0.17	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SO4	B	903	-	4,4,4	0.28	0	6,6,6	0.28	0
2	SO4	A	901	-	4,4,4	0.34	0	6,6,6	0.23	0

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	PEG	A	904	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	904	PEG	O1-C1-C2-O2
3	A	904	PEG	O2-C3-C4-O4
3	A	904	PEG	C4-C3-O2-C2
3	A	904	PEG	C1-C2-O2-C3

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	904	PEG	3	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	242/270 (89%)	0.73	34 (14%) 6 5	28, 51, 76, 99	0
1	B	242/270 (89%)	0.26	16 (6%) 24 22	26, 40, 63, 82	0
All	All	484/540 (89%)	0.49	50 (10%) 12 9	26, 46, 72, 99	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	681	PRO	4.5
1	A	816	ALA	4.5
1	B	640	GLU	4.0
1	A	707	ILE	3.9
1	A	698	GLU	3.8
1	B	578	THR	3.6
1	A	697	ASP	3.5
1	B	641	PRO	3.5
1	A	682	LYS	3.5
1	A	679	ALA	3.4
1	A	680	ASN	3.3
1	A	786	GLY	3.3
1	A	706	VAL	3.2
1	B	747	GLY	3.2
1	A	699	SER	3.2
1	A	715	TYR	3.0
1	A	728	ARG	2.8
1	A	747	GLY	2.8
1	B	715	TYR	2.8
1	A	686	THR	2.8
1	A	751	ARG	2.7
1	A	782	ARG	2.7
1	B	680	ASN	2.7
1	B	697	ASP	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	692	PHE	2.6
1	A	746	ARG	2.5
1	A	716	ASP	2.5
1	B	576	ASP	2.5
1	A	760	ASN	2.5
1	B	681	PRO	2.5
1	B	692	PHE	2.5
1	A	730	PHE	2.4
1	A	684	VAL	2.4
1	B	577	PRO	2.3
1	A	745	SER	2.3
1	B	746	ARG	2.3
1	B	575	CYS	2.3
1	A	785	VAL	2.3
1	A	806	HIS	2.3
1	A	694	LEU	2.3
1	A	657	CYS	2.2
1	B	696	ASN	2.1
1	A	709	ASP	2.1
1	A	700	PHE	2.0
1	A	608	ALA	2.0
1	B	751	ARG	2.0
1	A	695	LEU	2.0
1	A	787	GLY	2.0
1	B	639	ASN	2.0
1	A	756	ILE	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](#)

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	SO4	B	904	5/5	0.69	0.12	82,83,90,104	0
2	SO4	A	902	5/5	0.72	0.11	93,103,109,118	0
2	SO4	B	902	5/5	0.87	0.14	74,78,87,91	0
3	PEG	A	904	7/7	0.88	0.23	32,42,45,53	0
2	SO4	A	901	5/5	0.89	0.16	70,74,87,94	0
2	SO4	A	903	5/5	0.90	0.15	62,72,89,95	0
2	SO4	B	901	5/5	0.91	0.15	61,71,85,88	0
2	SO4	B	903	5/5	0.93	0.14	60,65,73,86	0

6.5 Other polymers [i](#)

There are no such residues in this entry.