



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 10:35 AM UTC

PDB ID : 8BW8 / pdb_00008bw8
Title : Crystal structure of the dCNK-SAM-CRIC-PDZ/dHYP-SAM complex
Authors : Maisonneuve, P.; Kurinov, I.; Sicheri, F.
Deposited on : 2022-12-06
Resolution : 2.10 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

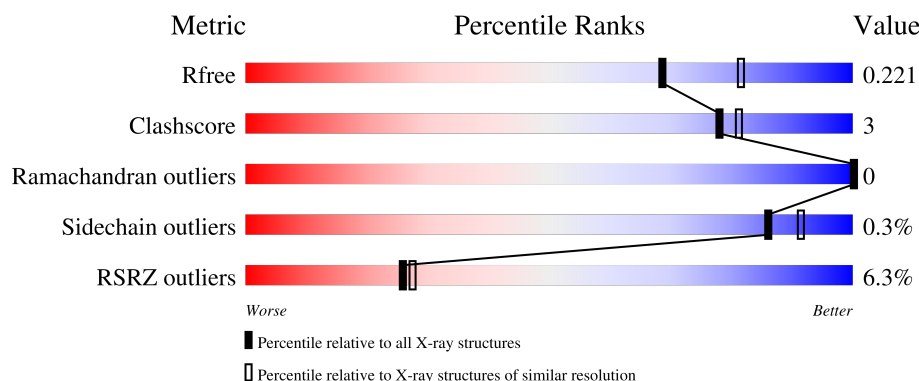
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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.



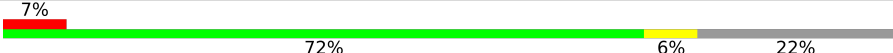
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	110	 2% 71% 8% 21%
1	C	110	 2% 76% 2% 22%
1	E	110	 5% 70% 9% 21%
2	B	335	 7% 73% 6% 21%
2	D	335	 3% 77% 5% 18%

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Mol	Chain	Length	Quality of chain
2	F	335	 A horizontal bar chart showing the quality of chain F. The bar is divided into four segments: a small red segment at the beginning labeled '7%', a large green segment labeled '72%', a small yellow segment labeled '6%', and a grey segment at the end labeled '22%'.

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8734 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 Protein aveugle.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	87	Total	C	N	O	S	0	0	0
			742	467	138	133	4			
1	C	86	Total	C	N	O	S	0	0	0
			713	444	135	130	4			
1	E	87	Total	C	N	O	S	0	0	0
			723	454	131	134	4			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	expression tag	UNP Q8ML92
A	-3	ALA	-	expression tag	UNP Q8ML92
A	-2	MET	-	expression tag	UNP Q8ML92
A	-1	ASP	-	expression tag	UNP Q8ML92
A	0	PRO	-	expression tag	UNP Q8ML92
C	-3	GLY	-	expression tag	UNP Q8ML92
C	-2	ALA	-	expression tag	UNP Q8ML92
C	-1	MET	-	expression tag	UNP Q8ML92
C	0	ASP	-	expression tag	UNP Q8ML92
C	1	PRO	-	expression tag	UNP Q8ML92
E	-4	GLY	-	expression tag	UNP Q8ML92
E	-3	ALA	-	expression tag	UNP Q8ML92
E	-2	MET	-	expression tag	UNP Q8ML92
E	-1	ASP	-	expression tag	UNP Q8ML92
E	0	PRO	-	expression tag	UNP Q8ML92

- Molecule 2 is a protein called Connector enhancer of KSR protein CNK.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	264	Total	C	N	O	S	0	0	0
			2044	1293	365	379	7			

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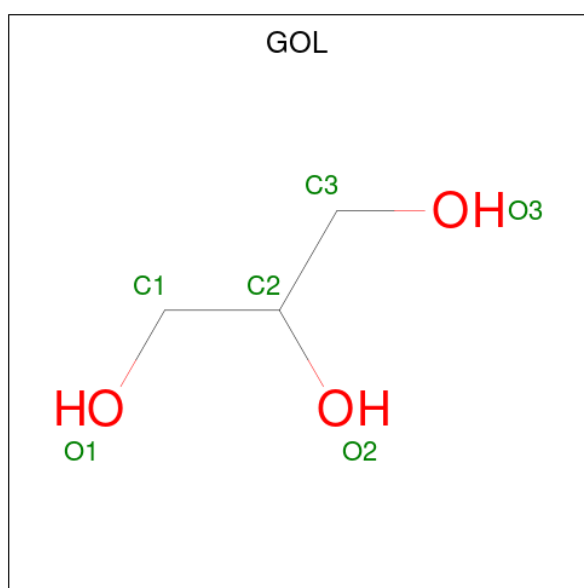
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	275	Total	C	N	O	S	0	0	0
			2137	1354	378	398	7			
2	F	262	Total	C	N	O	S	0	0	0
			2038	1290	363	378	7			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	GLY	-	expression tag	UNP Q7KNQ9
B	-3	ALA	-	expression tag	UNP Q7KNQ9
B	-2	MET	-	expression tag	UNP Q7KNQ9
B	-1	ASP	-	expression tag	UNP Q7KNQ9
B	0	PRO	-	expression tag	UNP Q7KNQ9
D	-4	GLY	-	expression tag	UNP Q7KNQ9
D	-3	ALA	-	expression tag	UNP Q7KNQ9
D	-2	MET	-	expression tag	UNP Q7KNQ9
D	-1	ASP	-	expression tag	UNP Q7KNQ9
D	0	PRO	-	expression tag	UNP Q7KNQ9
F	-4	GLY	-	expression tag	UNP Q7KNQ9
F	-3	ALA	-	expression tag	UNP Q7KNQ9
F	-2	MET	-	expression tag	UNP Q7KNQ9
F	-1	ASP	-	expression tag	UNP Q7KNQ9
F	0	PRO	-	expression tag	UNP Q7KNQ9

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).

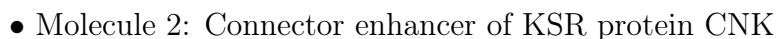


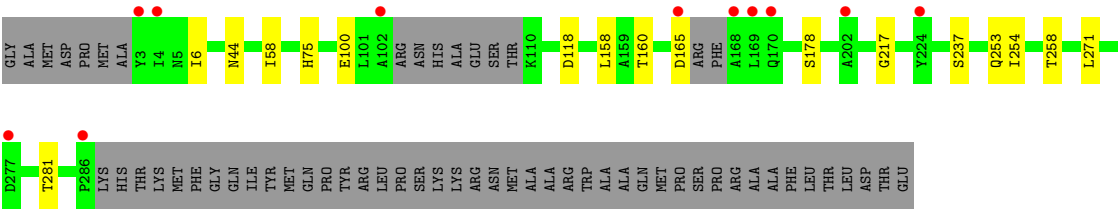
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 6	C 3	O 3	0	0
3	B	1	Total 6	C 3	O 3	0	0
3	B	1	Total 6	C 3	O 3	0	0
3	C	1	Total 6	C 3	O 3	0	0
3	D	1	Total 6	C 3	O 3	0	0
3	E	1	Total 6	C 3	O 3	0	0
3	E	1	Total 6	C 3	O 3	0	0
3	F	1	Total 6	C 3	O 3	0	0
3	F	1	Total 6	C 3	O 3	0	0

- Molecule 4 is water.

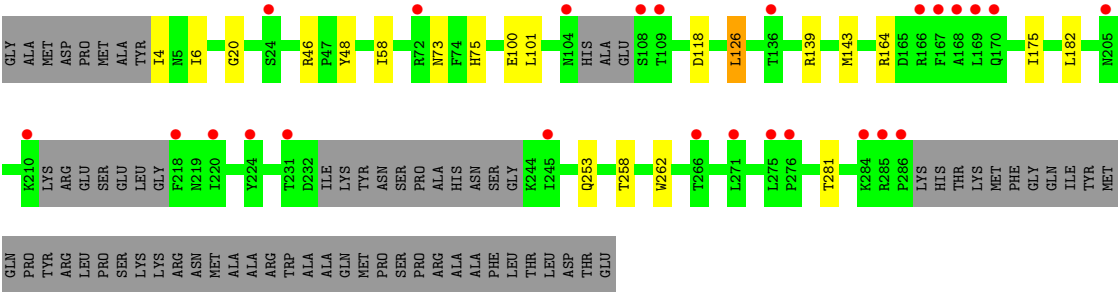
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	43	Total 43	O 43	0	0
4	B	77	Total 77	O 77	0	0
4	C	17	Total 17	O 17	0	0
4	D	52	Total 52	O 52	0	0
4	E	29	Total 29	O 29	0	0
4	F	65	Total 65	O 65	0	0

- Molecule 1: Protein aveugle





● Molecule 2: Connector enhancer of KSR protein CNK



4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	131.91Å 131.91Å 71.47Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	65.95 – 2.10 65.95 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (65.95-2.10) 92.6 (65.95-2.10)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.86 (at 2.10Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.188 , 0.219 0.189 , 0.221	Depositor DCC
R_{free} test set	4137 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	44.4	Xtriage
Anisotropy	0.141	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 55.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.002 for -h,-k,l 0.019 for h,-h-k,-l 0.000 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	8734	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 23.17 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.9194e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: GOL

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	0.08	0/756	0.25	0/1017
1	C	0.08	0/724	0.23	0/976
1	E	0.08	0/736	0.27	0/993
2	B	0.09	0/2077	0.27	0/2820
2	D	0.09	0/2176	0.27	0/2958
2	F	0.09	0/2074	0.27	0/2820
All	All	0.09	0/8543	0.27	0/11584

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 [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	742	0	740	9	0
1	C	713	0	696	2	0
1	E	723	0	704	8	0
2	B	2044	0	2003	14	0
2	D	2137	0	2092	10	0
2	F	2038	0	1977	14	0
3	A	6	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	12	0	16	0	0
3	C	6	0	8	0	0
3	D	6	0	8	0	0
3	E	12	0	16	2	0
3	F	12	0	16	0	0
4	A	43	0	0	1	0
4	B	77	0	0	2	0
4	C	17	0	0	1	0
4	D	52	0	0	1	0
4	E	29	0	0	1	0
4	F	65	0	0	0	0
All	All	8734	0	8284	47	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 3.

All (47) 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:103:ASN:ND2	2:B:134:GLU:OE2	2.20	0.72
1:A:61:ILE:O	1:A:88:ARG:NH2	2.25	0.69
1:A:69:MET:HG3	2:B:58:ILE:HD12	1.74	0.69
1:C:70:MET:HG3	2:D:58:ILE:HD12	1.76	0.67
2:D:6:ILE:HD12	2:D:75:HIS:HB2	1.75	0.67
2:F:126:LEU:HD11	2:F:182:LEU:HD21	1.75	0.66
2:D:254:ILE:HD13	2:D:271:LEU:HG	1.80	0.62
2:B:6:ILE:HD12	2:B:75:HIS:HB2	1.79	0.62
1:A:56:ARG:NH1	2:B:224:TYR:O	2.36	0.58
2:B:4:ILE:HD11	2:B:281:THR:HG21	1.85	0.58
2:F:253:GLN:HG2	2:F:258:THR:HA	1.87	0.57
1:A:105:TYR:CE2	2:F:143:MET:HE1	2.41	0.56
1:E:36:ARG:HH22	3:E:202:GOL:H12	1.72	0.54
1:C:69:ARG:NH2	4:C:301:HOH:O	2.31	0.53
2:D:44:ASN:ND2	4:D:501:HOH:O	2.36	0.52
2:D:253:GLN:HG2	2:D:258:THR:HA	1.92	0.52
1:A:98:ASP:OD1	1:A:101:ARG:NH2	2.44	0.51
2:F:100:GLU:HG3	2:F:118:ASP:OD2	2.11	0.51
2:F:4:ILE:HD11	2:F:281:THR:HG21	1.93	0.51
1:A:56:ARG:NH2	2:B:66:GLU:OE1	2.44	0.50
2:F:6:ILE:HD12	2:F:75:HIS:HB2	1.92	0.50
2:B:253:GLN:HG2	2:B:258:THR:HA	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:61:ILE:O	1:E:88:ARG:NH2	2.42	0.50
2:B:270:HIS:ND1	4:B:503:HOH:O	2.34	0.50
2:B:253:GLN:HB2	2:B:281:THR:HB	1.95	0.49
1:E:68:ARG:NH2	4:E:301:HOH:O	2.37	0.48
2:B:163:HIS:C	2:B:165:ASP:H	2.23	0.47
1:A:86:LYS:NZ	4:A:302:HOH:O	2.43	0.46
2:B:284:LYS:O	4:B:501:HOH:O	2.21	0.46
1:E:25:TRP:CZ2	3:E:202:GOL:H11	2.51	0.46
1:A:105:TYR:HE2	2:F:143:MET:HE1	1.81	0.45
2:B:101:LEU:HD11	2:B:175:ILE:HG22	1.98	0.45
2:D:217:GLY:HA3	2:D:237:SER:HB2	1.99	0.45
1:E:105:TYR:OXT	2:F:139:ARG:NH2	2.50	0.45
2:F:253:GLN:HB2	2:F:281:THR:HB	2.00	0.44
2:B:209:LEU:HB2	2:B:278:VAL:HG13	2.00	0.44
2:F:46:ARG:NH2	2:F:48:TYR:OH	2.52	0.43
2:D:253:GLN:HB2	2:D:281:THR:HB	2.00	0.43
2:D:160:THR:O	2:D:165:ASP:N	2.51	0.43
1:E:51:HIS:CE1	2:F:58:ILE:HD13	2.54	0.42
2:B:100:GLU:HG3	2:B:118:ASP:OD2	2.19	0.42
2:D:100:GLU:HG3	2:D:118:ASP:OD2	2.18	0.42
2:F:20:GLY:HA3	2:F:262:TRP:CE2	2.56	0.41
1:E:82:ARG:NH2	2:F:164:ARG:HH22	2.19	0.41
2:D:158:LEU:HG	2:D:178:SER:HB3	2.01	0.41
1:E:22:VAL:O	1:E:55:GLY:HA3	2.19	0.41
2:F:101:LEU:HD11	2:F:175:ILE:HG22	2.02	0.41

There are no symmetry-related clashes.

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	85/110 (77%)	83 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	84/110 (76%)	82 (98%)	2 (2%)	0	100	100
1	E	85/110 (77%)	83 (98%)	2 (2%)	0	100	100
2	B	254/335 (76%)	247 (97%)	7 (3%)	0	100	100
2	D	269/335 (80%)	265 (98%)	4 (2%)	0	100	100
2	F	254/335 (76%)	249 (98%)	5 (2%)	0	100	100
All	All	1031/1335 (77%)	1009 (98%)	22 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	79/100 (79%)	79 (100%)	0	100	100
1	C	74/100 (74%)	74 (100%)	0	100	100
1	E	76/100 (76%)	76 (100%)	0	100	100
2	B	214/292 (73%)	213 (100%)	1 (0%)	81	88
2	D	225/292 (77%)	225 (100%)	0	100	100
2	F	212/292 (73%)	210 (99%)	2 (1%)	70	78
All	All	880/1176 (75%)	877 (100%)	3 (0%)	86	91

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	73	ASN
2	F	73	ASN
2	F	126	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	257	GLN
2	F	75	HIS
2	F	257	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](#)

9 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	GOL	E	201	-	5,5,5	0.91	0	5,5,5	1.10	0
3	GOL	E	202	-	5,5,5	0.92	0	5,5,5	1.09	0
3	GOL	A	201	-	5,5,5	0.95	0	5,5,5	1.07	0
3	GOL	B	401	-	5,5,5	0.93	0	5,5,5	1.11	0
3	GOL	B	402	-	5,5,5	0.93	0	5,5,5	1.10	0
3	GOL	F	401	-	5,5,5	0.96	0	5,5,5	1.01	0
3	GOL	F	402	-	5,5,5	0.93	0	5,5,5	1.09	0
3	GOL	D	401	-	5,5,5	0.93	0	5,5,5	1.08	0
3	GOL	C	201	-	5,5,5	0.92	0	5,5,5	1.10	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	GOL	E	201	-	-	0/4/4/4	-
3	GOL	E	202	-	-	0/4/4/4	-
3	GOL	A	201	-	-	2/4/4/4	-
3	GOL	B	401	-	-	2/4/4/4	-
3	GOL	B	402	-	-	1/4/4/4	-
3	GOL	F	401	-	-	2/4/4/4	-
3	GOL	F	402	-	-	2/4/4/4	-
3	GOL	D	401	-	-	0/4/4/4	-
3	GOL	C	201	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	401	GOL	O1-C1-C2-C3
3	F	402	GOL	O1-C1-C2-C3
3	A	201	GOL	C1-C2-C3-O3
3	F	401	GOL	O1-C1-C2-C3
3	B	401	GOL	O1-C1-C2-O2
3	F	402	GOL	O1-C1-C2-O2
3	F	401	GOL	O1-C1-C2-O2
3	B	402	GOL	O2-C2-C3-O3
3	A	201	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	202	GOL	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	87/110 (79%)	0.15	2 (2%) 61 64	39, 52, 69, 105	0
1	C	86/110 (78%)	0.43	2 (2%) 61 64	50, 68, 90, 103	0
1	E	87/110 (79%)	0.20	5 (5%) 29 31	41, 59, 83, 114	0
2	B	264/335 (78%)	0.46	22 (8%) 17 18	36, 55, 107, 142	0
2	D	275/335 (82%)	0.47	11 (4%) 42 44	40, 63, 95, 134	0
2	F	262/335 (78%)	0.53	25 (9%) 14 14	37, 60, 111, 133	0
All	All	1061/1335 (79%)	0.43	67 (6%) 26 27	36, 60, 103, 142	0

All (67) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	245	ILE	4.8
2	B	286	PRO	4.7
2	B	243	GLY	4.4
2	D	202	ALA	4.3
2	F	104	ASN	4.2
2	B	3	TYR	4.2
2	D	3	TYR	4.0
1	A	19	PRO	4.0
2	B	4	ILE	3.9
2	F	169	LEU	3.9
2	F	285	ARG	3.8
2	D	168	ALA	3.8
1	E	19	PRO	3.8
2	F	109	THR	3.6
2	F	168	ALA	3.6
1	C	106	TYR	3.6
1	E	105	TYR	3.6
2	B	218	PHE	3.5
2	F	167	PHE	3.5

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Mol	Chain	Res	Type	RSRZ
2	F	170	GLN	3.5
2	B	211	LYS	3.2
2	B	165	ASP	3.1
2	F	224	TYR	3.1
2	D	286	PRO	3.1
2	F	72	ARG	3.0
2	B	109	THR	3.0
2	B	224	TYR	2.9
2	B	216	LEU	2.8
2	F	275	LEU	2.8
2	B	245	ILE	2.8
2	F	210	LYS	2.8
2	B	162	ALA	2.8
2	D	4	ILE	2.8
2	B	163	HIS	2.7
2	D	224	TYR	2.7
2	B	169	LEU	2.6
2	F	108	SER	2.6
2	F	220	ILE	2.5
2	F	286	PRO	2.5
2	D	165	ASP	2.5
2	F	284	LYS	2.5
2	F	166	ARG	2.5
2	B	108	SER	2.4
2	F	276	PRO	2.4
1	E	104	ILE	2.4
2	B	233	ILE	2.4
2	D	169	LEU	2.4
2	B	209	LEU	2.3
2	D	277	ASP	2.3
2	F	218	PHE	2.3
2	B	164	ARG	2.2
2	F	136	THR	2.2
2	F	231	THR	2.2
2	F	266	THR	2.2
2	D	102	ALA	2.2
2	D	170	GLN	2.2
2	B	217	GLY	2.2
2	F	205	ASN	2.2
1	C	105	ILE	2.1
1	E	61	ILE	2.1
2	F	271	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	23	TYR	2.1
2	B	101	LEU	2.1
2	B	285	ARG	2.1
2	B	244	LYS	2.1
2	F	24	SER	2.0
1	E	23	TYR	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(Å ²)	Q<0.9
3	GOL	E	201	6/6	0.71	0.19	73,85,91,96	0
3	GOL	A	201	6/6	0.85	0.18	71,76,79,82	0
3	GOL	C	201	6/6	0.86	0.15	79,85,88,97	0
3	GOL	E	202	6/6	0.87	0.14	72,86,88,92	0
3	GOL	D	401	6/6	0.88	0.12	79,87,95,98	0
3	GOL	F	401	6/6	0.89	0.16	59,65,77,78	0
3	GOL	B	401	6/6	0.90	0.13	62,71,78,86	0
3	GOL	F	402	6/6	0.90	0.10	72,83,88,89	0
3	GOL	B	402	6/6	0.91	0.13	66,78,84,88	0

6.5 Other polymers [i](#)

There are no such residues in this entry.