



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 05:38 AM UTC

PDB ID : 4EGG / pdb_00004egg
Title : Computationally Designed Self-assembling tetrahedron protein, T310
Authors : Sawaya, M.R.; King, N.P.; Sheffler, W.; Baker, D.; Yeates, T.O.
Deposited on : 2012-03-30
Resolution : 2.21 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

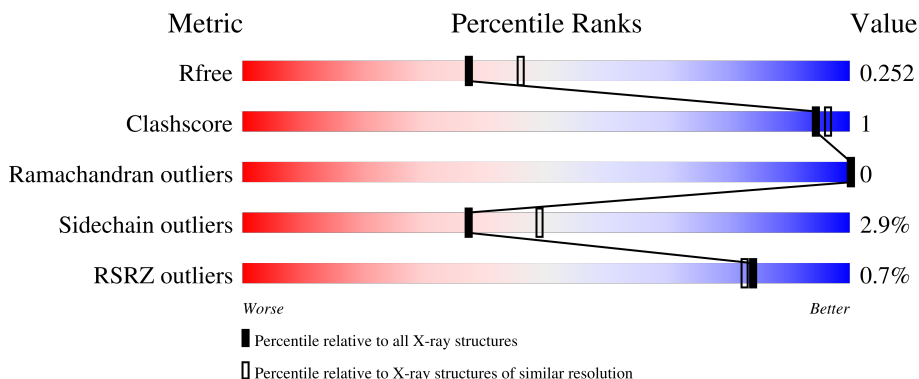
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.21 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	7682 (2.24-2.20)
Clashscore	190562	8402 (2.24-2.20)
Ramachandran outliers	187476	8303 (2.24-2.20)
Sidechain outliers	187428	8304 (2.24-2.20)
RSRZ outliers	180081	7683 (2.24-2.20)

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	207	83% 8% 9%
1	B	207	86% 5% 9%
1	C	207	84% 7% 10%
1	D	207	83% 7% 9%
1	E	207	84% 7% 9%

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Mol	Chain	Length	Quality of chain
1	F	207	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into three segments: a green segment labeled '84%', a yellow segment labeled '7%', and a grey segment labeled '9%'. A small red square is at the beginning of the bar, and a '%' symbol is above it.</p>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 9087 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 Putative acetyltransferase SACOL2570.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	188	1456	928	250	269	9	0	0	0
1	B	188	1456	928	250	269	9	0	0	0
1	C	187	1453	926	249	268	10	0	1	0
1	D	188	1461	932	250	269	10	0	1	0
1	E	188	1461	932	250	269	10	0	1	0
1	F	188	1456	928	250	269	9	0	0	0

There are 108 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	20	THR	TYR	engineered mutation	UNP Q5HCZ5
A	26	LEU	ALA	engineered mutation	UNP Q5HCZ5
A	30	VAL	ASP	engineered mutation	UNP Q5HCZ5
A	34	ALA	GLU	engineered mutation	UNP Q5HCZ5
A	39	ASN	ARG	engineered mutation	UNP Q5HCZ5
A	41	VAL	SER	engineered mutation	UNP Q5HCZ5
A	44	MET	ASN	engineered mutation	UNP Q5HCZ5
A	45	MET	LYS	engineered mutation	UNP Q5HCZ5
A	48	VAL	GLU	engineered mutation	UNP Q5HCZ5
A	52	ALA	GLN	engineered mutation	UNP Q5HCZ5
A	200	LEU	-	expression tag	UNP Q5HCZ5
A	201	GLU	-	expression tag	UNP Q5HCZ5
A	202	HIS	-	expression tag	UNP Q5HCZ5
A	203	HIS	-	expression tag	UNP Q5HCZ5
A	204	HIS	-	expression tag	UNP Q5HCZ5
A	205	HIS	-	expression tag	UNP Q5HCZ5
A	206	HIS	-	expression tag	UNP Q5HCZ5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	207	HIS	-	expression tag	UNP Q5HCZ5
B	20	THR	TYR	engineered mutation	UNP Q5HCZ5
B	26	LEU	ALA	engineered mutation	UNP Q5HCZ5
B	30	VAL	ASP	engineered mutation	UNP Q5HCZ5
B	34	ALA	GLU	engineered mutation	UNP Q5HCZ5
B	39	ASN	ARG	engineered mutation	UNP Q5HCZ5
B	41	VAL	SER	engineered mutation	UNP Q5HCZ5
B	44	MET	ASN	engineered mutation	UNP Q5HCZ5
B	45	MET	LYS	engineered mutation	UNP Q5HCZ5
B	48	VAL	GLU	engineered mutation	UNP Q5HCZ5
B	52	ALA	GLN	engineered mutation	UNP Q5HCZ5
B	200	LEU	-	expression tag	UNP Q5HCZ5
B	201	GLU	-	expression tag	UNP Q5HCZ5
B	202	HIS	-	expression tag	UNP Q5HCZ5
B	203	HIS	-	expression tag	UNP Q5HCZ5
B	204	HIS	-	expression tag	UNP Q5HCZ5
B	205	HIS	-	expression tag	UNP Q5HCZ5
B	206	HIS	-	expression tag	UNP Q5HCZ5
B	207	HIS	-	expression tag	UNP Q5HCZ5
C	20	THR	TYR	engineered mutation	UNP Q5HCZ5
C	26	LEU	ALA	engineered mutation	UNP Q5HCZ5
C	30	VAL	ASP	engineered mutation	UNP Q5HCZ5
C	34	ALA	GLU	engineered mutation	UNP Q5HCZ5
C	39	ASN	ARG	engineered mutation	UNP Q5HCZ5
C	41	VAL	SER	engineered mutation	UNP Q5HCZ5
C	44	MET	ASN	engineered mutation	UNP Q5HCZ5
C	45	MET	LYS	engineered mutation	UNP Q5HCZ5
C	48	VAL	GLU	engineered mutation	UNP Q5HCZ5
C	52	ALA	GLN	engineered mutation	UNP Q5HCZ5
C	200	LEU	-	expression tag	UNP Q5HCZ5
C	201	GLU	-	expression tag	UNP Q5HCZ5
C	202	HIS	-	expression tag	UNP Q5HCZ5
C	203	HIS	-	expression tag	UNP Q5HCZ5
C	204	HIS	-	expression tag	UNP Q5HCZ5
C	205	HIS	-	expression tag	UNP Q5HCZ5
C	206	HIS	-	expression tag	UNP Q5HCZ5
C	207	HIS	-	expression tag	UNP Q5HCZ5
D	20	THR	TYR	engineered mutation	UNP Q5HCZ5
D	26	LEU	ALA	engineered mutation	UNP Q5HCZ5
D	30	VAL	ASP	engineered mutation	UNP Q5HCZ5
D	34	ALA	GLU	engineered mutation	UNP Q5HCZ5
D	39	ASN	ARG	engineered mutation	UNP Q5HCZ5

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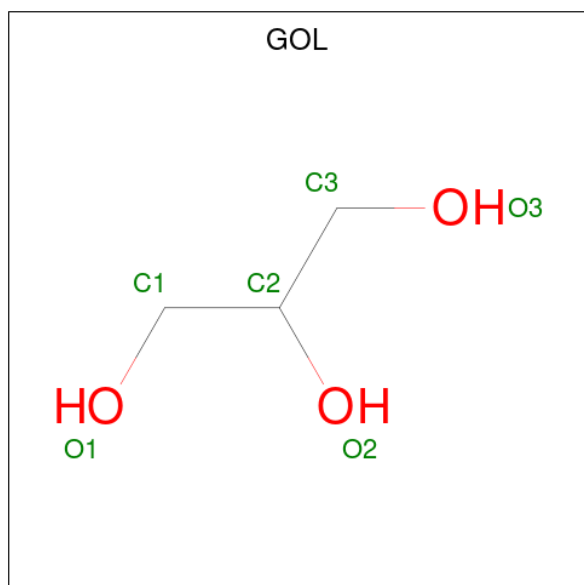
Chain	Residue	Modelled	Actual	Comment	Reference
D	41	VAL	SER	engineered mutation	UNP Q5HCZ5
D	44	MET	ASN	engineered mutation	UNP Q5HCZ5
D	45	MET	LYS	engineered mutation	UNP Q5HCZ5
D	48	VAL	GLU	engineered mutation	UNP Q5HCZ5
D	52	ALA	GLN	engineered mutation	UNP Q5HCZ5
D	200	LEU	-	expression tag	UNP Q5HCZ5
D	201	GLU	-	expression tag	UNP Q5HCZ5
D	202	HIS	-	expression tag	UNP Q5HCZ5
D	203	HIS	-	expression tag	UNP Q5HCZ5
D	204	HIS	-	expression tag	UNP Q5HCZ5
D	205	HIS	-	expression tag	UNP Q5HCZ5
D	206	HIS	-	expression tag	UNP Q5HCZ5
D	207	HIS	-	expression tag	UNP Q5HCZ5
E	20	THR	TYR	engineered mutation	UNP Q5HCZ5
E	26	LEU	ALA	engineered mutation	UNP Q5HCZ5
E	30	VAL	ASP	engineered mutation	UNP Q5HCZ5
E	34	ALA	GLU	engineered mutation	UNP Q5HCZ5
E	39	ASN	ARG	engineered mutation	UNP Q5HCZ5
E	41	VAL	SER	engineered mutation	UNP Q5HCZ5
E	44	MET	ASN	engineered mutation	UNP Q5HCZ5
E	45	MET	LYS	engineered mutation	UNP Q5HCZ5
E	48	VAL	GLU	engineered mutation	UNP Q5HCZ5
E	52	ALA	GLN	engineered mutation	UNP Q5HCZ5
E	200	LEU	-	expression tag	UNP Q5HCZ5
E	201	GLU	-	expression tag	UNP Q5HCZ5
E	202	HIS	-	expression tag	UNP Q5HCZ5
E	203	HIS	-	expression tag	UNP Q5HCZ5
E	204	HIS	-	expression tag	UNP Q5HCZ5
E	205	HIS	-	expression tag	UNP Q5HCZ5
E	206	HIS	-	expression tag	UNP Q5HCZ5
E	207	HIS	-	expression tag	UNP Q5HCZ5
F	20	THR	TYR	engineered mutation	UNP Q5HCZ5
F	26	LEU	ALA	engineered mutation	UNP Q5HCZ5
F	30	VAL	ASP	engineered mutation	UNP Q5HCZ5
F	34	ALA	GLU	engineered mutation	UNP Q5HCZ5
F	39	ASN	ARG	engineered mutation	UNP Q5HCZ5
F	41	VAL	SER	engineered mutation	UNP Q5HCZ5
F	44	MET	ASN	engineered mutation	UNP Q5HCZ5
F	45	MET	LYS	engineered mutation	UNP Q5HCZ5
F	48	VAL	GLU	engineered mutation	UNP Q5HCZ5
F	52	ALA	GLN	engineered mutation	UNP Q5HCZ5
F	200	LEU	-	expression tag	UNP Q5HCZ5

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Chain	Residue	Modelled	Actual	Comment	Reference
F	201	GLU	-	expression tag	UNP Q5HCZ5
F	202	HIS	-	expression tag	UNP Q5HCZ5
F	203	HIS	-	expression tag	UNP Q5HCZ5
F	204	HIS	-	expression tag	UNP Q5HCZ5
F	205	HIS	-	expression tag	UNP Q5HCZ5
F	206	HIS	-	expression tag	UNP Q5HCZ5
F	207	HIS	-	expression tag	UNP Q5HCZ5


- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	56	Total O 56 56	0	0
3	B	68	Total O 68 68	0	0
3	C	45	Total O 45 45	0	0
3	D	52	Total O 52 52	0	0
3	E	43	Total O 43 43	0	0
3	F	32	Total O 32 32	0	0

Chain F:  %
84% 7% 9%



4 Data and refinement statistics i

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	183.76Å 90.84Å 107.70Å 90.00° 125.30° 90.00°	Depositor
Resolution (Å)	22.28 – 2.21 22.28 – 2.24	Depositor EDS
% Data completeness (in resolution range)	92.6 (22.28-2.21) 94.9 (22.28-2.24)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.98 (at 2.24Å)	Xtrriage
Refinement program	BUSTER-TNT, BUSTER 2.10.0	Depositor
R, R_{free}	0.208 , 0.238 (Not available) , 0.252	Depositor DCC
R_{free} test set	3386 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	44.8	Xtrriage
Anisotropy	0.151	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 67.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.012 for -h-2*1,-k,l	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9087	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.24% 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: 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	0.90	0/1492	1.26	6/2029 (0.3%)
1	B	0.86	0/1492	1.22	4/2029 (0.2%)
1	C	0.82	0/1492	1.25	5/2028 (0.2%)
1	D	0.85	0/1500	1.22	4/2039 (0.2%)
1	E	0.87	0/1500	1.23	4/2039 (0.2%)
1	F	0.81	0/1492	1.24	4/2029 (0.2%)
All	All	0.85	0/8968	1.24	27/12193 (0.2%)

There are no bond length outliers.

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	91	ASP	N-CA-C	8.99	122.73	112.57
1	A	175	GLY	N-CA-C	8.80	121.01	112.04
1	D	91	ASP	N-CA-C	8.31	121.96	112.57
1	F	91	ASP	N-CA-C	8.30	121.95	112.57
1	E	91	ASP	N-CA-C	8.23	121.88	112.57
1	B	91	ASP	N-CA-C	8.08	121.70	112.57
1	E	175	GLY	N-CA-C	7.47	119.66	112.04
1	F	175	GLY	N-CA-C	7.42	119.61	112.04
1	C	175	GLY	N-CA-C	7.20	119.38	112.04
1	D	175	GLY	N-CA-C	6.93	119.11	112.04
1	A	91	ASP	N-CA-C	6.68	121.08	112.26
1	C	187	ASP	CA-CB-CG	6.63	119.23	112.60
1	B	42	ALA	CA-C-N	6.13	128.81	120.54
1	B	42	ALA	C-N-CA	6.13	128.81	120.54
1	C	42	ALA	CA-C-N	6.12	128.39	120.44
1	C	42	ALA	C-N-CA	6.12	128.39	120.44
1	D	42	ALA	CA-C-N	5.82	128.01	120.44
1	D	42	ALA	C-N-CA	5.82	128.01	120.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	175	GLY	N-CA-C	5.77	119.31	112.33
1	F	42	ALA	CA-C-N	5.71	127.87	120.44
1	F	42	ALA	C-N-CA	5.71	127.87	120.44
1	E	42	ALA	CA-C-N	5.48	127.56	120.44
1	E	42	ALA	C-N-CA	5.48	127.56	120.44
1	A	21	LEU	CA-C-N	5.26	127.19	120.56
1	A	21	LEU	C-N-CA	5.26	127.19	120.56
1	A	49	LEU	CA-C-N	5.05	126.92	120.56
1	A	49	LEU	C-N-CA	5.05	126.92	120.56

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	A	1456	0	1430	5	0
1	B	1456	0	1430	2	0
1	C	1453	0	1428	3	0
1	D	1461	0	1439	6	0
1	E	1461	0	1439	3	0
1	F	1456	0	1430	4	0
2	A	18	0	24	2	0
2	C	6	0	8	0	0
2	D	6	0	8	1	0
2	E	12	0	16	0	0
2	F	6	0	8	0	0
3	A	56	0	0	0	0
3	B	68	0	0	0	0
3	C	45	0	0	0	0
3	D	52	0	0	0	0
3	E	43	0	0	0	0
3	F	32	0	0	0	0
All	All	9087	0	8660	23	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 1.

All (23) 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:F:158:GLY:HA3	1:F:174:VAL:HG23	1.83	0.60
1:D:50:ILE:HG23	1:D:54:PHE:CE2	2.39	0.57
1:E:158:GLY:HA3	1:E:174:VAL:HG23	1.86	0.56
1:D:140:GLY:HA2	2:D:301:GOL:H12	1.88	0.54
1:D:50:ILE:HG23	1:D:54:PHE:HE2	1.73	0.53
1:C:158:GLY:HA3	1:C:174:VAL:HG23	1.90	0.53
1:A:111:THR:HG22	1:A:131:ILE:HG13	1.97	0.47
1:D:158:GLY:HA3	1:D:174:VAL:HG13	1.97	0.47
1:E:146:LEU:HD22	1:E:164:THR:HG22	2.00	0.43
1:A:141:GLY:H	2:A:302:GOL:H12	1.84	0.43
1:D:146:LEU:HD22	1:D:164:THR:HG22	2.01	0.43
1:F:146:LEU:HD22	1:F:164:THR:HG22	2.01	0.43
1:A:13:TYR:CE1	1:A:15:ALA:HB2	2.54	0.43
1:A:138:TRP:HE1	2:A:302:GOL:H32	1.82	0.43
1:C:146:LEU:HD22	1:C:164:THR:HG22	2.02	0.42
1:A:177:PRO:HG2	1:A:179:LYS:HE3	2.01	0.41
1:B:146:LEU:HD22	1:B:164:THR:HG22	2.02	0.41
1:D:177:PRO:HG2	1:D:179:LYS:HE3	2.01	0.41
1:E:177:PRO:HG2	1:E:179:LYS:HE3	2.02	0.41
1:B:158:GLY:HA3	1:B:174:VAL:HG12	2.03	0.41
1:C:177:PRO:HG2	1:C:179:LYS:HE3	2.03	0.41
1:F:149:VAL:HG11	1:F:163:VAL:HG12	2.03	0.40
1:F:177:PRO:HG2	1:F:179:LYS:HE3	2.04	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	186/207 (90%)	183 (98%)	3 (2%)	0	100	100
1	B	186/207 (90%)	183 (98%)	3 (2%)	0	100	100
1	C	186/207 (90%)	182 (98%)	4 (2%)	0	100	100
1	D	187/207 (90%)	184 (98%)	3 (2%)	0	100	100
1	E	187/207 (90%)	184 (98%)	3 (2%)	0	100	100
1	F	186/207 (90%)	182 (98%)	4 (2%)	0	100	100
All	All	1118/1242 (90%)	1098 (98%)	20 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	159/178 (89%)	154 (97%)	5 (3%)	35	46
1	B	159/178 (89%)	155 (98%)	4 (2%)	42	55
1	C	159/178 (89%)	155 (98%)	4 (2%)	42	55
1	D	160/178 (90%)	155 (97%)	5 (3%)	35	46
1	E	160/178 (90%)	154 (96%)	6 (4%)	29	38
1	F	159/178 (89%)	155 (98%)	4 (2%)	42	55
All	All	956/1068 (90%)	928 (97%)	28 (3%)	37	49

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

Mol	Chain	Res	Type
1	A	26	LEU
1	A	41	VAL
1	A	64	SER
1	A	146	LEU
1	A	151	ILE
1	B	26	LEU
1	B	41	VAL

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Mol	Chain	Res	Type
1	B	62	SER
1	B	64	SER
1	C	26	LEU
1	C	41	VAL
1	C	62	SER
1	C	64	SER
1	D	26	LEU
1	D	41	VAL
1	D	62	SER
1	D	64	SER
1	D	174	VAL
1	E	26	LEU
1	E	41	VAL
1	E	62	SER
1	E	64	SER
1	E	182	ARG
1	E	183	LYS
1	F	26	LEU
1	F	41	VAL
1	F	62	SER
1	F	64	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	GLN
1	B	19	GLN
1	B	60	ASN
1	C	60	ASN
1	E	60	ASN
1	F	19	GLN
1	F	60	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 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
2	GOL	A	303	-	5,5,5	0.13	0	5,5,5	0.16	0
2	GOL	A	301	-	5,5,5	0.10	0	5,5,5	0.27	0
2	GOL	F	301	-	5,5,5	0.08	0	5,5,5	0.30	0
2	GOL	D	301	-	5,5,5	0.15	0	5,5,5	0.44	0
2	GOL	E	301	-	5,5,5	0.10	0	5,5,5	0.34	0
2	GOL	C	301	-	5,5,5	0.06	0	5,5,5	0.21	0
2	GOL	E	302	-	5,5,5	0.11	0	5,5,5	0.40	0
2	GOL	A	302	-	5,5,5	0.14	0	5,5,5	0.20	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
2	GOL	A	303	-	-	0/4/4/4	-
2	GOL	A	301	-	-	3/4/4/4	-
2	GOL	F	301	-	-	4/4/4/4	-
2	GOL	D	301	-	-	1/4/4/4	-
2	GOL	E	301	-	-	2/4/4/4	-
2	GOL	C	301	-	-	2/4/4/4	-
2	GOL	E	302	-	-	1/4/4/4	-
2	GOL	A	302	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	301	GOL	O1-C1-C2-C3
2	F	301	GOL	C1-C2-C3-O3
2	F	301	GOL	O2-C2-C3-O3
2	A	301	GOL	O1-C1-C2-C3
2	A	301	GOL	C1-C2-C3-O3
2	F	301	GOL	O1-C1-C2-C3
2	A	301	GOL	O2-C2-C3-O3
2	C	301	GOL	O1-C1-C2-O2
2	D	301	GOL	O1-C1-C2-O2
2	E	302	GOL	O1-C1-C2-C3
2	F	301	GOL	O1-C1-C2-O2
2	E	301	GOL	C1-C2-C3-O3
2	E	301	GOL	O2-C2-C3-O3

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	301	GOL	1	0
2	A	302	GOL	2	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	188/207 (90%)	-0.03	1 (0%) 87 86	40, 60, 82, 118	0
1	B	188/207 (90%)	-0.09	1 (0%) 87 86	38, 55, 83, 102	0
1	C	187/207 (90%)	0.12	1 (0%) 87 86	35, 66, 97, 122	1 (0%)
1	D	188/207 (90%)	-0.00	1 (0%) 87 86	29, 55, 89, 110	1 (0%)
1	E	188/207 (90%)	0.16	2 (1%) 78 77	35, 63, 98, 135	1 (0%)
1	F	188/207 (90%)	0.43	2 (1%) 78 77	40, 80, 112, 144	0
All	All	1127/1242 (90%)	0.10	8 (0%) 84 83	29, 62, 100, 144	3 (0%)

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	188	LEU	5.2
1	E	188	LEU	3.7
1	A	188	LEU	3.5
1	C	187	ASP	2.9
1	B	188	LEU	2.3
1	D	188	LEU	2.3
1	E	184	ILE	2.2
1	F	109	PHE	2.1

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
2	GOL	A	302	6/6	0.83	0.12	64,65,66,66	0
2	GOL	F	301	6/6	0.85	0.14	79,81,82,82	0
2	GOL	E	302	6/6	0.86	0.14	67,70,72,74	0
2	GOL	A	301	6/6	0.89	0.15	68,69,69,69	0
2	GOL	D	301	6/6	0.90	0.09	56,58,58,59	0
2	GOL	E	301	6/6	0.90	0.10	63,63,65,67	0
2	GOL	A	303	6/6	0.91	0.10	58,58,59,60	0
2	GOL	C	301	6/6	0.91	0.10	59,59,60,60	0

6.5 Other polymers [i](#)

There are no such residues in this entry.