



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 08:54 PM EDT

PDB ID : 3SF5 / pdb_00003sf5
Title : Crystal Structure of Helicobacter pylori Urease Accessory Protein UreF/H complex
Authors : Fong, Y.H.; Chen, Y.W.; Wong, K.B.
Deposited on : 2011-06-12
Resolution : 2.50 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

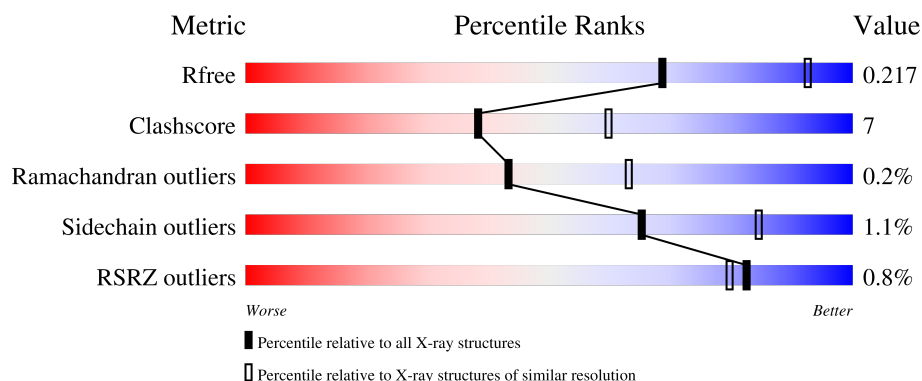
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	254	 76% 14% 10%
1	C	254	 76% 15% 9%
2	B	265	 86% 11% ..
2	D	265	 2% 80% 17% .

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	SO4	C	258	-	-	X	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 8053 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.

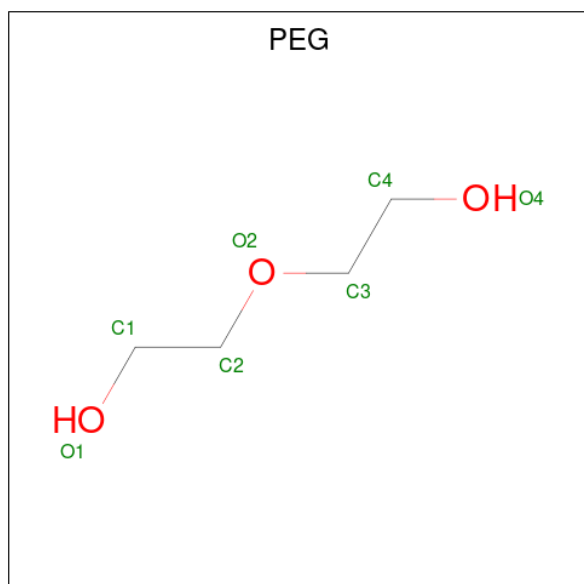
- Molecule 1 is a protein called Urease accessory protein ureF.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	229	Total	C	N	O	S	0	0	0
			1822	1159	300	353	10			
1	C	230	Total	C	N	O	S	0	0	0
			1830	1163	302	355	10			

- Molecule 2 is a protein called Urease accessory protein ureH.

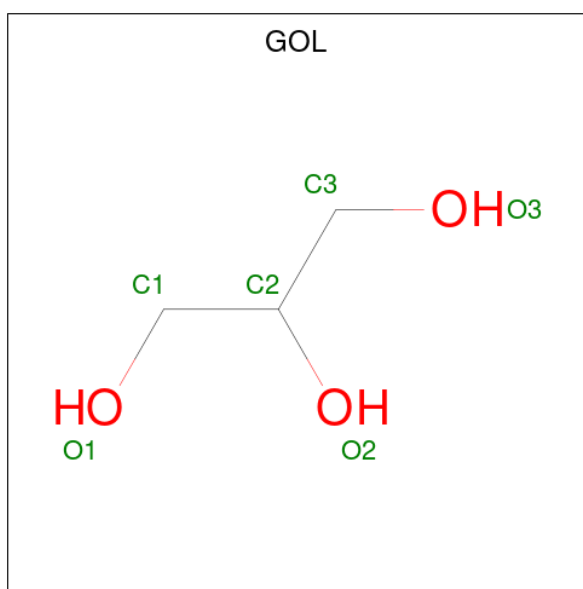
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	261	Total	C	N	O	S	0	0	0
			2050	1299	349	389	13			
2	D	260	Total	C	N	O	S	0	0	0
			2044	1296	347	388	13			

- 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
3	A	1	Total C O 7 4 3	0	0
3	A	1	Total C O 7 4 3	0	0
3	A	1	Total C O 7 4 3	0	0
3	B	1	Total C O 7 4 3	0	0
3	B	1	Total C O 7 4 3	0	0
3	C	1	Total C O 7 4 3	0	0
3	C	1	Total C O 7 4 3	0	0
3	D	1	Total C O 7 4 3	0	0

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0
4	C	1	Total C O 6 3 3	0	0

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		
5	C	1	Total	O	S	0	0
			5	4	1		
5	D	1	Total	O	S	0	0
			5	4	1		
5	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is water.

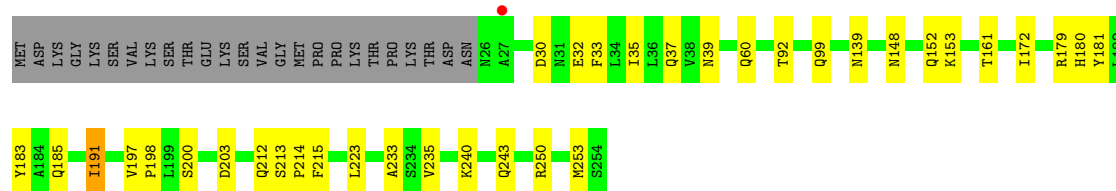
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	60	Total	O	0	0
			60	60		
6	B	53	Total	O	0	0
			53	53		
6	C	64	Total	O	0	0
			64	64		
6	D	30	Total	O	0	0
			30	30		

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.

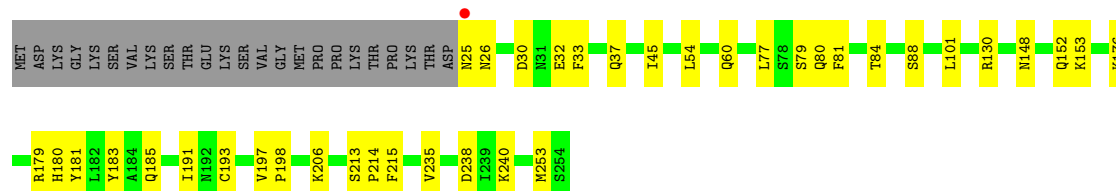
- Molecule 1: Urease accessory protein ureF

Chain A:



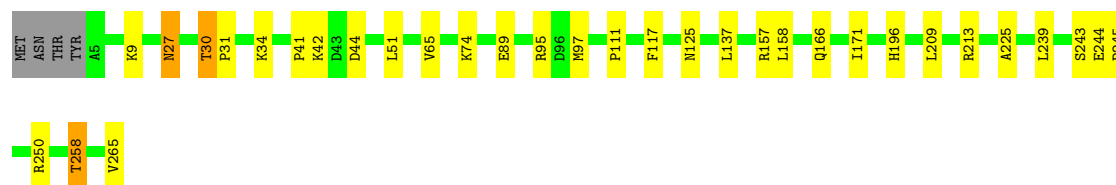
- Molecule 1: Urease accessory protein ureF

Chain C:



- Molecule 2: Urease accessory protein ureH

Chain B:



- Molecule 2: Urease accessory protein ureH

Chain D:





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	70.65Å 70.73Å 205.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.83 – 2.50 35.83 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.1 (35.83-2.50) 99.0 (35.83-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.72 (at 2.51Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.173 , 0.217 0.171 , 0.217	Depositor DCC
R_{free} test set	1820 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	30.0	Xtriage
Anisotropy	0.114	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 41.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.035 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8053	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.92% 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, 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	0.29	0/1852	0.64	0/2498
1	C	0.31	0/1860	0.65	0/2509
2	B	0.28	0/2089	0.69	1/2824 (0.0%)
2	D	0.27	0/2084	0.69	1/2820 (0.0%)
All	All	0.29	0/7885	0.67	2/10651 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	89	GLU	CB-CA-C	-5.86	109.26	117.23
2	D	89	GLU	CB-CA-C	-5.54	109.69	117.23

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	1822	0	1834	28	0
1	C	1830	0	1840	29	0
2	B	2050	0	2057	28	0
2	D	2044	0	2042	32	0
3	A	28	0	40	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	14	0	20	3	0
3	C	14	0	20	2	0
3	D	7	0	10	1	0
4	A	6	0	8	1	0
4	C	6	0	8	2	0
5	B	10	0	0	1	0
5	C	5	0	0	4	0
5	D	10	0	0	0	0
6	A	60	0	0	1	0
6	B	53	0	0	0	0
6	C	64	0	0	1	0
6	D	30	0	0	0	0
All	All	8053	0	7879	108	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 7.

All (108) 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)
2:B:243:SER:H	3:B:268:PEG:H12	1.34	0.93
2:D:85:ILE:HD11	2:D:114:LEU:HD22	1.68	0.76
2:B:95:ARG:HD2	2:B:97:MET:HE3	1.70	0.72
2:D:30:THR:HG23	2:D:31:PRO:HD2	1.71	0.72
2:B:34:LYS:HD3	2:B:51:LEU:HD11	1.75	0.68
1:A:39:ASN:OD1	3:A:258:PEG:H42	1.93	0.68
2:D:95:ARG:HD2	2:D:97:MET:HE3	1.74	0.68
1:C:25:ASN:O	1:C:26:ASN:HB2	1.93	0.68
2:B:30:THR:HG23	2:B:31:PRO:HD2	1.79	0.64
2:D:34:LYS:HD3	2:D:51:LEU:HD11	1.80	0.64
1:C:213:SER:HB3	1:C:214:PRO:HD3	1.80	0.63
2:D:44:ASP:OD2	2:D:74:LYS:HD2	1.97	0.63
1:A:179:ARG:HG3	1:C:33:PHE:CE1	2.33	0.62
2:B:97:MET:HE1	2:B:111:PRO:HB3	1.82	0.62
2:B:65:VAL:HB	2:B:97:MET:HG2	1.80	0.61
2:D:65:VAL:HB	2:D:97:MET:HG2	1.82	0.61
1:A:180:HIS:HE1	5:C:258:SO4:O2	1.84	0.60
1:A:37:GLN:HA	1:C:183:TYR:OH	2.01	0.60
1:A:183:TYR:OH	1:C:37:GLN:HA	2.04	0.58
1:A:235:VAL:HG11	2:B:239:LEU:HD21	1.86	0.58
2:B:209:LEU:HD21	2:B:213:ARG:CZ	2.34	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:213:SER:HB3	1:A:214:PRO:HD3	1.85	0.57
1:C:253:MET:HA	1:C:253:MET:HE2	1.85	0.57
1:C:176:LYS:HE3	5:C:258:SO4:O4	2.05	0.56
2:D:3:THR:HG23	2:D:4:TYR:CD2	2.40	0.56
1:C:206:LYS:NZ	3:C:255:PEG:H41	2.21	0.56
1:A:180:HIS:HD2	6:A:290:HOH:O	1.89	0.54
1:C:30:ASP:OD1	1:C:32:GLU:HG2	2.08	0.53
2:B:137:LEU:HD22	2:B:250:ARG:NH2	2.24	0.53
2:B:196:HIS:NE2	3:B:268:PEG:H41	2.24	0.53
2:D:209:LEU:HD21	2:D:213:ARG:CZ	2.40	0.52
1:C:60:GLN:OE1	1:C:240:LYS:HE3	2.09	0.52
1:A:180:HIS:CE1	5:C:258:SO4:O2	2.62	0.52
2:D:34:LYS:HB3	2:D:51:LEU:CD1	2.40	0.52
1:A:33:PHE:CE1	1:C:179:ARG:HG3	2.45	0.52
2:B:243:SER:N	3:B:268:PEG:H12	2.15	0.52
2:D:82:PHE:CD2	2:D:113:PRO:HB2	2.45	0.52
1:C:238:ASP:OD2	4:C:257:GOL:H12	2.10	0.51
2:B:265:VAL:O	2:B:265:VAL:HG13	2.11	0.51
1:A:92:THR:HG21	1:A:161:THR:HB	1.93	0.51
2:B:209:LEU:HD21	2:B:213:ARG:NH2	2.26	0.51
1:C:206:LYS:HZ1	3:C:255:PEG:H41	1.75	0.51
2:D:200:LEU:HD23	2:D:200:LEU:C	2.36	0.50
2:D:252:LYS:O	2:D:256:LEU:HD23	2.10	0.50
2:B:9:LYS:H	2:B:30:THR:HB	1.78	0.48
1:C:180:HIS:HD2	6:C:300:HOH:O	1.96	0.48
2:D:158:LEU:C	2:D:158:LEU:HD23	2.38	0.48
2:D:196:HIS:NE2	3:D:268:PEG:H11	2.29	0.48
1:A:39:ASN:ND2	1:A:180:HIS:HB3	2.29	0.47
2:B:117:PHE:CD1	2:B:117:PHE:N	2.83	0.47
1:A:33:PHE:CZ	1:C:215:PHE:HB3	2.50	0.46
1:A:191:ILE:HD13	1:A:191:ILE:HA	1.75	0.46
2:B:34:LYS:HB3	2:B:51:LEU:CD1	2.45	0.46
2:B:27:ASN:ND2	2:B:27:ASN:C	2.73	0.46
1:A:253:MET:HA	1:A:253:MET:HE2	1.97	0.46
2:D:85:ILE:HD13	2:D:122:PHE:HB2	1.98	0.46
2:B:157:ARG:NH2	5:B:267:SO4:O4	2.43	0.45
2:D:242:GLY:O	2:D:245:PRO:HD2	2.16	0.45
1:C:181:TYR:O	1:C:185:GLN:HG2	2.16	0.45
2:D:65:VAL:HG21	2:D:97:MET:HE2	1.98	0.45
1:C:79:SER:OG	1:C:80:GLN:N	2.49	0.45
2:D:167:ASP:O	2:D:168:GLU:HB2	2.17	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:34:LYS:HB3	2:D:51:LEU:HD11	1.99	0.45
1:C:197:VAL:N	1:C:198:PRO:HA	2.32	0.44
1:A:148:ASN:O	1:A:152:GLN:HG3	2.18	0.44
1:C:235:VAL:HG11	2:D:239:LEU:HD21	1.98	0.44
1:A:99:GLN:HE21	1:A:99:GLN:HB3	1.64	0.44
2:B:158:LEU:C	2:B:158:LEU:HD23	2.42	0.44
2:B:166:GLN:HB2	2:B:171:ILE:HD13	1.99	0.44
2:D:260:THR:HG22	2:D:261:THR:N	2.32	0.44
1:A:60:GLN:OE1	1:A:240:LYS:HE3	2.19	0.43
1:C:77:LEU:HA	1:C:81:PHE:HB3	2.01	0.43
1:A:181:TYR:O	1:A:185:GLN:HG2	2.19	0.43
1:C:180:HIS:CE1	5:C:258:SO4:O4	2.71	0.43
1:A:233:ALA:HA	4:A:259:GOL:O3	2.18	0.43
2:D:209:LEU:HD21	2:D:213:ARG:NH2	2.34	0.43
1:A:197:VAL:N	1:A:198:PRO:HA	2.34	0.43
2:D:97:MET:HE1	2:D:111:PRO:HB3	2.01	0.43
1:A:243:GLN:HG3	2:B:225:ALA:HB2	2.01	0.42
2:B:44:ASP:OD2	2:B:74:LYS:HD2	2.18	0.42
2:D:169:LYS:HA	2:D:170:PRO:HD3	1.90	0.42
2:B:34:LYS:HB3	2:B:51:LEU:HD11	2.01	0.42
1:C:84:THR:O	1:C:88:SER:HB3	2.20	0.42
2:D:49:MET:HE2	2:D:49:MET:HB3	1.97	0.42
1:A:179:ARG:HG3	1:C:33:PHE:CZ	2.54	0.42
1:C:80:GLN:OE1	4:C:257:GOL:H2	2.20	0.42
2:B:42:LYS:C	2:B:44:ASP:H	2.27	0.42
2:B:42:LYS:C	2:B:44:ASP:N	2.76	0.42
1:C:54:LEU:HD21	1:C:193:CYS:SG	2.60	0.42
2:D:32:PRO:HG3	2:D:54:SER:HB2	2.01	0.42
2:D:244:GLU:HB3	2:D:245:PRO:HD3	2.01	0.42
2:D:207:ILE:HD12	2:D:256:LEU:HB3	2.02	0.42
1:A:30:ASP:OD1	1:A:32:GLU:HG2	2.20	0.41
1:A:212:GLN:O	1:A:215:PHE:HB2	2.20	0.41
2:B:244:GLU:HB3	2:B:245:PRO:HD3	2.01	0.41
1:C:45:ILE:O	1:C:130:ARG:HD2	2.19	0.41
1:C:101:LEU:HD21	1:C:153:LYS:HD3	2.01	0.41
1:C:191:ILE:HD13	1:C:191:ILE:HA	1.85	0.41
1:C:148:ASN:O	1:C:152:GLN:HG3	2.21	0.41
2:D:72:ASN:HD22	2:D:104:ASN:HB3	1.85	0.41
2:D:108:ASP:OD1	2:D:108:ASP:C	2.63	0.41
1:A:35:ILE:HD13	1:A:172:ILE:HD13	2.02	0.41
1:A:153:LYS:HE2	1:A:153:LYS:HB3	1.97	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:124:GLY:O	2:D:160:THR:HA	2.21	0.41
1:A:200:SER:O	1:A:203:ASP:HB2	2.21	0.41
2:B:42:LYS:HE3	2:B:258:THR:CG2	2.52	0.40
2:B:117:PHE:N	2:B:117:PHE:HD1	2.18	0.40
2:D:248:HIS:CD2	2:D:252:LYS:HE3	2.56	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	227/254 (89%)	224 (99%)	3 (1%)	0	100	100
1	C	228/254 (90%)	222 (97%)	6 (3%)	0	100	100
2	B	259/265 (98%)	248 (96%)	10 (4%)	1 (0%)	30	49
2	D	258/265 (97%)	248 (96%)	9 (4%)	1 (0%)	30	49
All	All	972/1038 (94%)	942 (97%)	28 (3%)	2 (0%)	43	63

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	41	PRO
2	D	41	PRO

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	205/228 (90%)	201 (98%)	4 (2%)	48	75
1	C	206/228 (90%)	206 (100%)	0	100	100
2	B	230/234 (98%)	226 (98%)	4 (2%)	53	78
2	D	229/234 (98%)	227 (99%)	2 (1%)	70	87
All	All	870/924 (94%)	860 (99%)	10 (1%)	65	84

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	139	ASN
1	A	191	ILE
1	A	223	LEU
1	A	250	ARG
2	B	27	ASN
2	B	30	THR
2	B	125	ASN
2	B	258	THR
2	D	66	GLN
2	D	72	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	80	GLN
1	A	99	GLN
1	A	125	GLN
1	A	148	ASN
1	A	180	HIS
1	A	217	GLN
1	A	229	HIS
1	A	237	ASN
2	B	27	ASN
2	B	125	ASN
2	B	135	GLN
2	B	199	ASN
2	B	259	GLN
1	C	39	ASN
1	C	98	GLN
1	C	99	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	125	GLN
1	C	136	GLN
1	C	148	ASN
1	C	180	HIS
1	C	192	ASN
1	C	202	ASN
1	C	217	GLN
2	D	2	ASN
2	D	66	GLN
2	D	72	ASN
2	D	80	GLN
2	D	104	ASN
2	D	186	ASN
2	D	259	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](#)

16 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
5	SO4	D	266	-	4,4,4	0.23	0	6,6,6	0.06	0
3	PEG	A	255	-	6,6,6	0.65	0	5,5,5	1.43	0
5	SO4	B	266	-	4,4,4	0.24	0	6,6,6	0.10	0
4	GOL	C	257	-	5,5,5	0.37	0	5,5,5	0.31	0
3	PEG	A	258	-	6,6,6	0.64	0	5,5,5	1.40	0
3	PEG	C	255	-	6,6,6	0.65	0	5,5,5	1.28	0
3	PEG	A	257	-	6,6,6	0.64	0	5,5,5	1.39	0
3	PEG	B	269	-	6,6,6	0.65	0	5,5,5	1.35	0
3	PEG	D	268	-	6,6,6	0.66	0	5,5,5	1.39	0
5	SO4	B	267	-	4,4,4	0.23	0	6,6,6	0.09	0
3	PEG	B	268	-	6,6,6	0.63	0	5,5,5	1.49	0
5	SO4	C	258	-	4,4,4	0.23	0	6,6,6	0.12	0
4	GOL	A	259	-	5,5,5	0.35	0	5,5,5	0.39	0
3	PEG	A	256	-	6,6,6	0.62	0	5,5,5	1.47	0
3	PEG	C	256	-	6,6,6	0.65	0	5,5,5	1.38	0
5	SO4	D	267	-	4,4,4	0.24	0	6,6,6	0.09	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	255	-	-	1/4/4/4	-
4	GOL	C	257	-	-	2/4/4/4	-
3	PEG	A	258	-	-	2/4/4/4	-
3	PEG	C	255	-	-	2/4/4/4	-
3	PEG	A	257	-	-	0/4/4/4	-
3	PEG	B	269	-	-	1/4/4/4	-
3	PEG	D	268	-	-	1/4/4/4	-
3	PEG	B	268	-	-	2/4/4/4	-
4	GOL	A	259	-	-	4/4/4/4	-
3	PEG	A	256	-	-	3/4/4/4	-
3	PEG	C	256	-	-	1/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	259	GOL	C1-C2-C3-O3
4	C	257	GOL	O1-C1-C2-C3
4	C	257	GOL	O1-C1-C2-O2
3	C	256	PEG	O2-C3-C4-O4
4	A	259	GOL	O1-C1-C2-C3
3	A	258	PEG	O2-C3-C4-O4
4	A	259	GOL	O2-C2-C3-O3
4	A	259	GOL	O1-C1-C2-O2
3	A	255	PEG	O2-C3-C4-O4
3	C	255	PEG	O1-C1-C2-O2
3	A	256	PEG	C1-C2-O2-C3
3	B	269	PEG	C1-C2-O2-C3
3	A	256	PEG	O1-C1-C2-O2
3	A	256	PEG	C4-C3-O2-C2
3	D	268	PEG	C1-C2-O2-C3
3	B	268	PEG	O1-C1-C2-O2
3	C	255	PEG	O2-C3-C4-O4
3	B	268	PEG	C1-C2-O2-C3
3	A	258	PEG	C1-C2-O2-C3

There are no ring outliers.

8 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	257	GOL	2	0
3	A	258	PEG	1	0
3	C	255	PEG	2	0
3	D	268	PEG	1	0
5	B	267	SO4	1	0
3	B	268	PEG	3	0
5	C	258	SO4	4	0
4	A	259	GOL	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 [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	229/254 (90%)	-0.62	1 (0%) 88 86	17, 25, 43, 95	0
1	C	230/254 (90%)	-0.59	1 (0%) 88 86	16, 25, 45, 85	0
2	B	261/265 (98%)	-0.33	0 100 100	17, 30, 59, 83	0
2	D	260/265 (98%)	-0.26	6 (2%) 61 57	18, 32, 62, 110	0
All	All	980/1038 (94%)	-0.44	8 (0%) 82 80	16, 28, 54, 110	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	27	ALA	5.5
2	D	261	THR	4.0
2	D	3	THR	3.0
2	D	260	THR	2.8
2	D	4	TYR	2.4
1	C	25	ASN	2.4
2	D	2	ASN	2.4
2	D	44	ASP	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

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	PEG	A	257	7/7	0.78	0.16	39,53,60,63	0
3	PEG	A	256	7/7	0.79	0.15	42,45,50,54	0
3	PEG	B	268	7/7	0.79	0.18	36,42,50,50	0
5	SO4	C	258	5/5	0.79	0.16	54,65,85,88	0
3	PEG	A	258	7/7	0.83	0.17	29,35,47,64	0
3	PEG	B	269	7/7	0.85	0.12	41,47,55,59	0
3	PEG	D	268	7/7	0.86	0.15	41,46,55,56	0
3	PEG	C	255	7/7	0.87	0.14	21,39,45,65	0
4	GOL	C	257	6/6	0.90	0.11	28,29,43,46	0
3	PEG	C	256	7/7	0.91	0.09	39,45,57,61	0
3	PEG	A	255	7/7	0.92	0.10	38,43,51,57	0
4	GOL	A	259	6/6	0.92	0.10	25,32,35,38	0
5	SO4	D	267	5/5	0.96	0.10	41,47,53,61	0
5	SO4	B	266	5/5	0.98	0.04	27,41,44,50	0
5	SO4	B	267	5/5	0.98	0.06	36,39,43,53	0
5	SO4	D	266	5/5	0.99	0.05	28,31,42,46	0

6.5 Other polymers

There are no such residues in this entry.