



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 16, 2024 – 02:38 am GMT

PDB ID : 6I7S
Title : Microsomal triglyceride transfer protein
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Deposited on : 2018-11-17
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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

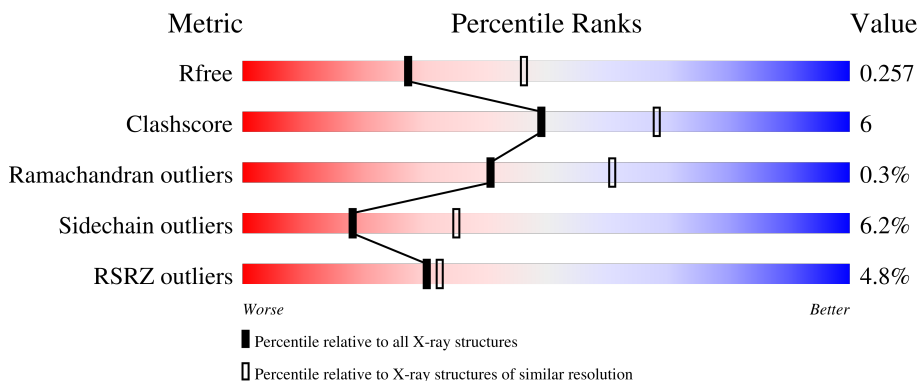
1 Overall quality at a glance

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}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (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	492	
1	B	492	
2	G	884	
2	H	884	

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	PGE	B	602	-	-	-	X
5	PGE	B	603	-	-	-	X
7	PEG	B	609	-	-	-	X
7	PEG	H	916	-	-	-	X
7	PEG	H	917	-	-	X	-
7	PEG	H	918	-	-	-	X
8	PE5	G	901	-	-	-	X
8	PE5	H	901	-	-	-	X

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 21452 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 disulfide-isomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	461	Total	C	N	O	S	0	1	0
			3668	2351	602	706	9			
1	B	462	Total	C	N	O	S	0	1	0
			3676	2354	600	713	9			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	17	MET	-	initiating methionine	UNP P07237
B	17	MET	-	initiating methionine	UNP P07237

- Molecule 2 is a protein called Microsomal triglyceride transfer protein large subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	G	863	Total	C	N	O	S	0	4	0
			6787	4299	1164	1296	28			
2	H	862	Total	C	N	O	S	0	2	0
			6757	4277	1162	1290	28			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	11	MET	-	initiating methionine	UNP P55157
G	12	HIS	-	expression tag	UNP P55157
G	13	HIS	-	expression tag	UNP P55157
G	14	HIS	-	expression tag	UNP P55157
G	15	HIS	-	expression tag	UNP P55157
G	16	HIS	-	expression tag	UNP P55157
G	17	HIS	-	expression tag	UNP P55157
G	18	MET	-	expression tag	UNP P55157
H	11	MET	-	initiating methionine	UNP P55157
H	12	HIS	-	expression tag	UNP P55157

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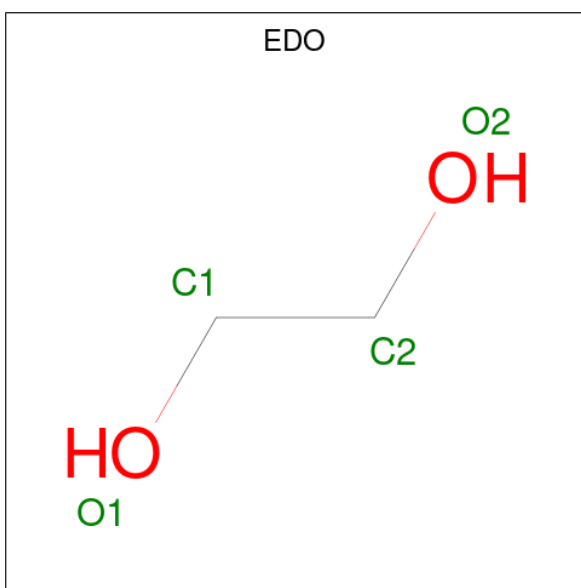
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Chain	Residue	Modelled	Actual	Comment	Reference
H	13	HIS	-	expression tag	UNP P55157
H	14	HIS	-	expression tag	UNP P55157
H	15	HIS	-	expression tag	UNP P55157
H	16	HIS	-	expression tag	UNP P55157
H	17	HIS	-	expression tag	UNP P55157
H	18	MET	-	expression tag	UNP P55157

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Ca 1 1	0	0
3	B	1	Total Ca 1 1	0	0

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0
4	G	1	Total 4	C 2	O 2	0	0
4	G	1	Total 4	C 2	O 2	0	0
4	G	1	Total 4	C 2	O 2	0	0
4	G	1	Total 4	C 2	O 2	0	0
4	G	1	Total 4	C 2	O 2	0	0
4	G	1	Total 4	C 2	O 2	0	0
4	H	1	Total 4	C 2	O 2	0	0
4	H	1	Total 4	C 2	O 2	0	0
4	H	1	Total 4	C 2	O 2	0	0
4	H	1	Total 4	C 2	O 2	0	0
4	H	1	Total 4	C 2	O 2	0	0

- Molecule 5 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: C₆H₁₄O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			10	6	4		
5	B	1	Total	C	O	0	0
			10	6	4		
5	G	1	Total	C	O	0	0
			10	6	4		
5	H	1	Total	C	O	0	0
			10	6	4		
5	H	1	Total	C	O	0	0
			10	6	4		

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



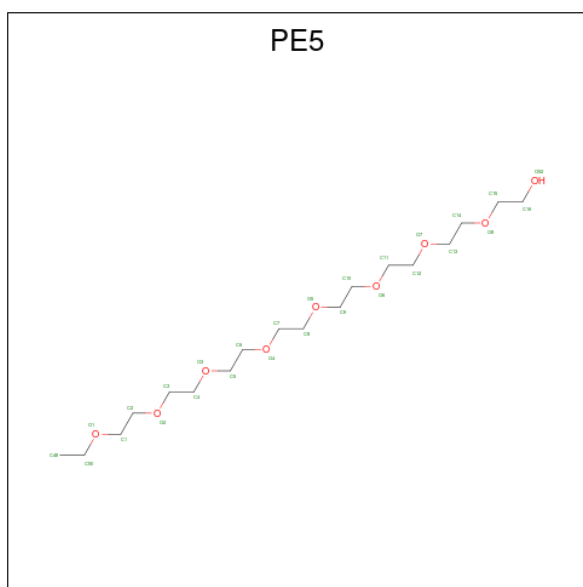
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	O	S	0	0
			5	4	1		
6	G	1	Total	O	S	0	0
			5	4	1		
6	G	1	Total	O	S	0	0
			5	4	1		
6	G	1	Total	O	S	0	0
			5	4	1		
6	G	1	Total	O	S	0	0
			5	4	1		
6	G	1	Total	O	S	0	0
			5	4	1		
6	G	1	Total	O	S	0	0
			5	4	1		
6	H	1	Total	O	S	0	0
			5	4	1		
6	H	1	Total	O	S	0	0
			5	4	1		
6	H	1	Total	O	S	0	0
			5	4	1		

- Molecule 7 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



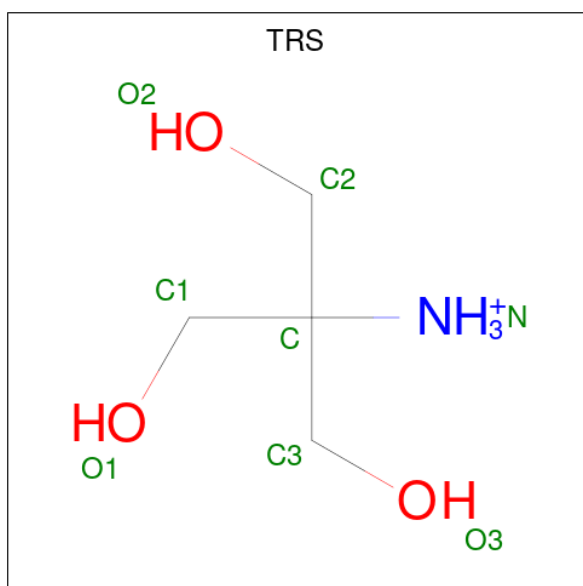
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	B	1	Total C O 7 4 3	0	0
7	B	1	Total C O 7 4 3	0	0
7	G	1	Total C O 7 4 3	0	0
7	G	1	Total C O 7 4 3	0	0
7	H	1	Total C O 7 4 3	0	0
7	H	1	Total C O 7 4 3	0	0
7	H	1	Total C O 7 4 3	0	0
7	H	1	Total C O 7 4 3	0	0
7	H	1	Total C O 7 4 3	0	0

- Molecule 8 is 3,6,9,12,15,18,21,24-OCTAOXAHEXACOSAN-1-OL (three-letter code: PE5) (formula: C₁₈H₃₈O₉).



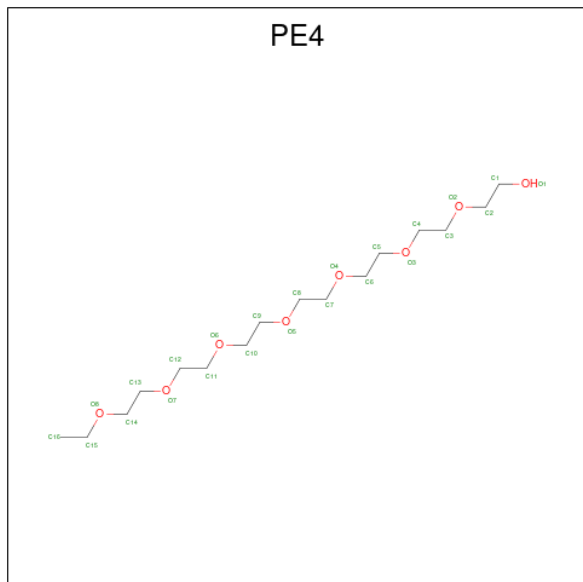
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	G	1	Total	C	O	0	0
			27	18	9		
8	H	1	Total	C	O	0	0
			27	18	9		

- Molecule 9 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: C₄H₁₂NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	G	1	Total	C	N	O	0	0
			8	4	1	3		

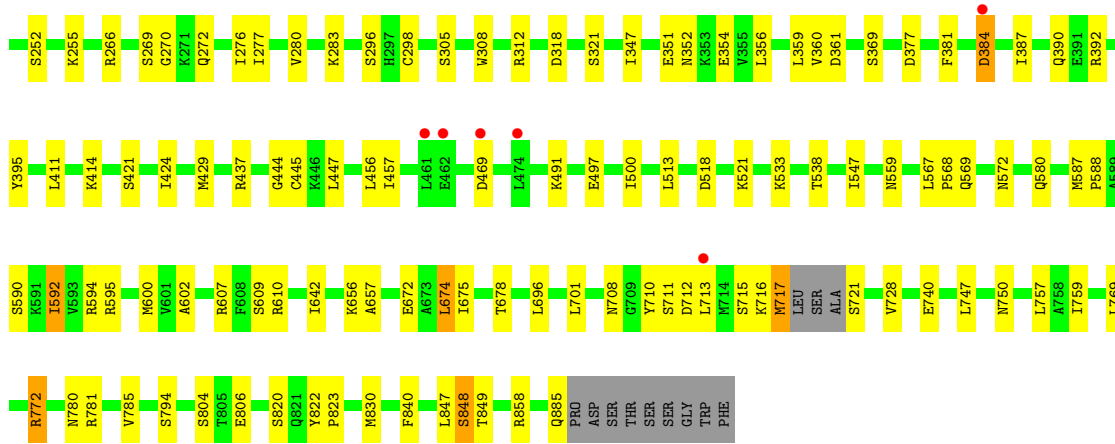
- Molecule 10 is 2-{2-[2-(2-{2-[2-(2-ETHOXY-ETHOXY)-ETHOXY]-ETHOXY}-ETHOXY)-ETHOXY]-ETHOXY}-ETHANOL (three-letter code: PE4) (formula: C₁₆H₃₄O₈).



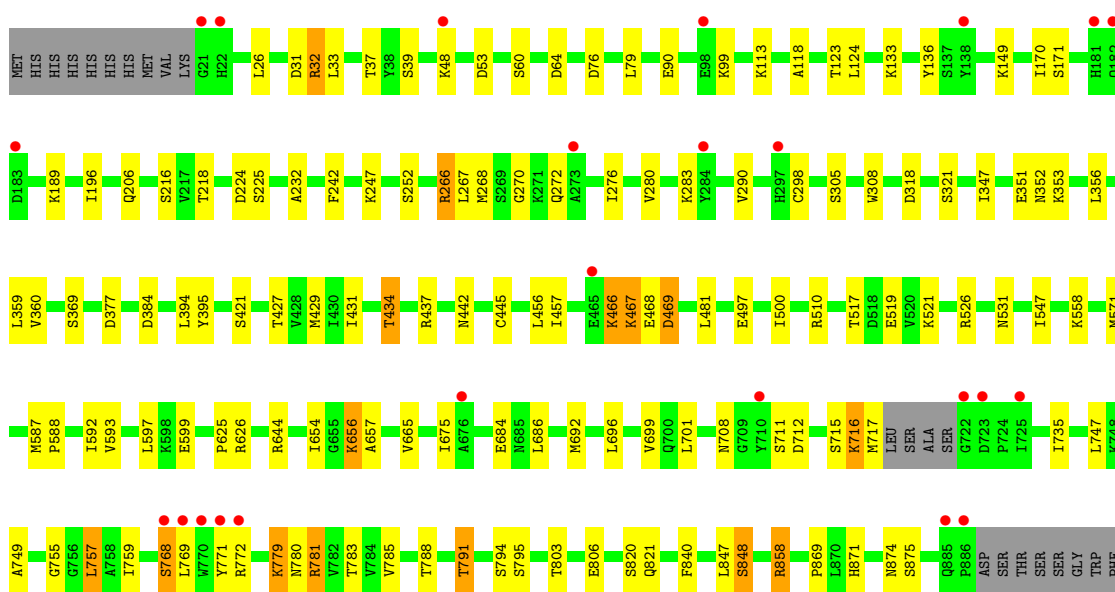
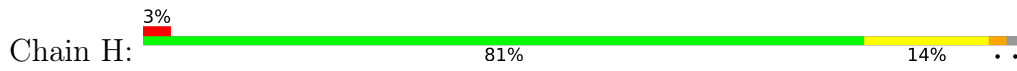
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	C O		
10	H	1	24	16 8	0	0

- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	22	Total	O	0	0
			22	22		
11	B	32	Total	O	0	0
			32	32		
11	G	81	Total	O	0	0
			81	81		
11	H	87	Total	O	0	0
			87	87		



• Molecule 2: Microsomal triglyceride transfer protein large subunit



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	77.54Å 105.59Å 112.27Å 89.81° 76.95° 74.24°	Depositor
Resolution (Å)	49.35 – 2.50 49.35 – 2.50	Depositor EDS
% Data completeness (in resolution range)	93.8 (49.35-2.50) 93.8 (49.35-2.50)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.07 (at 2.51Å)	Xtrriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.204 , 0.257 0.204 , 0.257	Depositor DCC
R_{free} test set	5414 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	65.6	Xtrriage
Anisotropy	0.143	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 50.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	21452	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.33% 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, PGE, PE5, EDO, PE4, TRS, PEG, CA

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	0.34	0/3756	0.68	0/5071
1	B	0.35	0/3764	0.68	0/5082
2	G	0.40	0/6897	0.71	0/9297
2	H	0.39	0/6868	0.72	0/9258
All	All	0.38	0/21285	0.70	0/28708

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	3668	0	3593	35	0
1	B	3676	0	3588	41	0
2	G	6787	0	6921	89	0
2	H	6757	0	6899	90	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	20	0	30	4	0
4	B	12	0	18	0	0
4	G	24	0	36	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	H	20	0	30	0	0
5	B	20	0	28	1	0
5	G	10	0	14	5	0
5	H	30	0	42	2	0
6	B	5	0	0	0	0
6	G	35	0	0	2	0
6	H	15	0	0	1	0
7	B	14	0	20	0	0
7	G	14	0	20	0	0
7	H	35	0	50	7	0
8	G	27	0	38	1	0
8	H	27	0	38	6	0
9	G	8	0	12	1	0
10	H	24	0	34	3	0
11	A	22	0	0	0	0
11	B	32	0	0	1	0
11	G	81	0	0	4	0
11	H	87	0	0	3	0
All	All	21452	0	21411	252	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 6.

All (252) 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:G:717:MET:CE	2:G:721:SER:CB	2.12	1.28
2:G:717:MET:CE	2:G:721:SER:HB3	1.69	1.19
2:H:79:LEU:CD2	2:H:276:ILE:HD11	1.72	1.18
2:G:717:MET:HE2	2:G:721:SER:CB	1.73	1.15
2:G:395:TYR:CE2	5:G:902:PGE:H22	1.92	1.04
2:H:780:ASN:ND2	8:H:901:PE5:H142	1.76	1.01
2:H:780:ASN:HD22	8:H:901:PE5:H142	1.21	1.00
2:G:717:MET:CE	2:G:721:SER:HB2	1.94	0.97
2:G:717:MET:HE2	2:G:721:SER:HB3	1.29	0.96
2:G:717:MET:HE3	2:G:721:SER:HB3	1.49	0.91
2:G:717:MET:HE2	2:G:721:SER:HB2	1.48	0.91
2:H:79:LEU:HD23	2:H:276:ILE:HD11	1.48	0.90
2:G:587:MET:HB3	2:G:588:PRO:HD2	1.53	0.90
2:G:717:MET:HE3	2:G:721:SER:CB	2.02	0.89
2:H:656:LYS:HE2	2:H:656:LYS:H	1.39	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:822[B]:TYR:CD1	2:G:823[B]:PRO:HA	2.11	0.84
2:H:780:ASN:ND2	8:H:901:PE5:H151	1.93	0.84
2:H:587:MET:HB3	2:H:588:PRO:HD2	1.60	0.82
2:G:569:GLN:O	11:G:1001:HOH:O	1.99	0.80
2:G:429:MET:HE2	2:G:457:ILE:HG12	1.62	0.80
1:A:20:PRO:HG2	1:A:27:LEU:HD22	1.66	0.77
2:H:79:LEU:HD22	2:H:276:ILE:HD11	1.64	0.76
1:B:163:ASP:HB3	1:B:166:SER:HB2	1.69	0.74
2:H:79:LEU:CD2	2:H:276:ILE:CD1	2.60	0.74
2:H:79:LEU:HD23	2:H:276:ILE:CD1	2.17	0.74
2:H:429:MET:HE2	2:H:457:ILE:HG12	1.69	0.73
1:A:163:ASP:HB3	1:A:166:SER:HB2	1.71	0.72
1:A:19:ALA:N	1:A:20:PRO:CD	2.54	0.71
2:H:466:LYS:HB2	2:H:469:ASP:HB2	1.71	0.71
1:B:41:HIS:CE1	1:B:78:ARG:HG3	2.26	0.70
2:G:270:GLY:HA3	2:G:276:ILE:HD11	1.71	0.70
2:H:352:ASN:O	2:H:356:LEU:HB2	1.90	0.70
2:G:352:ASN:O	2:G:356:LEU:HB2	1.92	0.70
2:G:444:GLY:HA2	2:G:447:LEU:HD13	1.74	0.69
1:B:22:GLU:HG2	1:B:25:HIS:HA	1.72	0.69
2:G:717:MET:CE	2:G:721:SER:CA	2.71	0.68
2:H:526:ARG:HA	2:H:531:ASN:HD22	1.58	0.68
2:H:356:LEU:O	2:H:360:VAL:HG23	1.93	0.68
2:G:356:LEU:O	2:G:360:VAL:HG23	1.94	0.68
2:G:717:MET:HE3	2:G:721:SER:CA	2.24	0.67
1:A:262:PRO:HG2	1:A:265:VAL:HB	1.75	0.67
1:B:458:ASN:HB2	1:B:479:GLY:H	1.60	0.67
1:B:262:PRO:HG2	1:B:265:VAL:HB	1.76	0.66
2:G:847:LEU:O	2:G:848:SER:HB3	1.96	0.66
2:H:429:MET:CE	2:H:457:ILE:HG12	2.24	0.66
2:H:847:LEU:O	2:H:848:SER:HB3	1.96	0.66
2:H:517:THR:HB	6:H:906:SO4:O4	1.96	0.65
2:G:429:MET:CE	2:G:457:ILE:HG12	2.27	0.65
2:G:227:VAL:O	9:G:903:TRS:H11	1.97	0.64
1:B:174:GLN:HB3	1:B:222:LYS:HD2	1.78	0.64
2:H:780:ASN:HD22	8:H:901:PE5:C14	2.05	0.63
2:G:602:ALA:O	2:G:607:ARG:HD2	1.99	0.62
2:H:701:LEU:HD13	7:H:914:PEG:H42	1.82	0.62
1:A:150:VAL:HG13	4:A:603:EDO:H22	1.82	0.61
1:B:230:LYS:HA	1:B:233:GLN:HE21	1.64	0.61
1:B:458:ASN:H	1:B:478:ALA:HA	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:444:GLY:CA	2:G:447:LEU:HD13	2.31	0.61
1:A:276:LYS:HE2	4:A:604:EDO:O1	2.00	0.61
2:G:36:LEU:HD12	2:G:36:LEU:N	2.16	0.61
2:H:60:SER:HB2	7:H:917:PEG:H21	1.82	0.61
2:H:434:THR:HG21	2:H:699:VAL:HG22	1.83	0.61
2:H:768:SER:HB2	2:H:771:TYR:HB2	1.83	0.60
2:H:99:LYS:NZ	10:H:902:PE4:H81	2.17	0.60
2:G:390:GLN:NE2	2:G:424:ILE:HD13	2.18	0.59
1:B:242:GLU:N	1:B:242:GLU:OE1	2.35	0.59
2:H:779:LYS:HE2	2:H:781:ARG:HD2	1.84	0.58
1:A:208:LYS:HG2	4:A:603:EDO:H12	1.86	0.58
2:H:276:ILE:O	2:H:280:VAL:HG23	2.03	0.58
2:G:381:PHE:CD1	2:G:414:LYS:HE3	2.39	0.58
1:A:387:ASN:HD22	1:A:419:ASN:ND2	2.02	0.57
2:G:255:LYS:HE2	6:G:907:SO4:O1	2.04	0.57
2:G:780:ASN:HD22	8:G:901:PE5:H72	1.69	0.57
2:H:840[A]:PHE:CD1	2:H:858:ARG:HG2	2.39	0.57
2:G:717:MET:CE	2:G:721:SER:HA	2.34	0.57
2:G:822[B]:TYR:CG	2:G:823[B]:PRO:HA	2.39	0.57
2:H:124:LEU:HB2	2:H:136:TYR:HB2	1.87	0.55
1:A:47:GLU:HG3	1:A:102:ILE:HD13	1.87	0.55
2:H:466:LYS:O	2:H:469:ASP:N	2.37	0.55
1:A:121:GLU:O	1:A:125:ILE:HD13	2.07	0.55
2:G:33:LEU:HD11	2:G:64:ASP:HB3	1.89	0.55
2:H:840[A]:PHE:HD1	2:H:858:ARG:HG2	1.72	0.55
1:B:245:ALA:HB3	1:B:246:PRO:HD3	1.89	0.55
1:A:245:ALA:HB3	1:A:246:PRO:HD3	1.89	0.55
2:G:390:GLN:HE21	2:G:424:ILE:HG21	1.72	0.54
2:G:840[A]:PHE:HD1	2:G:858:ARG:HG2	1.73	0.54
1:B:239:GLU:HB2	1:B:290:PHE:CZ	2.43	0.54
2:G:276:ILE:O	2:G:280:VAL:HG23	2.07	0.54
2:H:37:THR:HB	7:H:917:PEG:H31	1.90	0.54
2:H:196:ILE:HD13	2:H:290:VAL:CG1	2.38	0.54
2:H:429:MET:CE	2:H:457:ILE:CG1	2.85	0.54
2:G:587:MET:HB3	2:G:588:PRO:CD	2.33	0.54
2:G:717:MET:HE3	2:G:721:SER:HA	1.89	0.54
1:B:282:PHE:CZ	1:B:343:CYS:HB2	2.43	0.54
1:B:70:LEU:HD23	1:B:75:SER:HB3	1.89	0.53
2:H:48:LYS:HB2	2:H:247:LYS:NZ	2.24	0.53
2:H:780:ASN:HD22	8:H:901:PE5:H151	1.67	0.53
1:B:174:GLN:O	1:B:177:GLU:HG3	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:121:GLU:O	1:B:125:ILE:HD13	2.08	0.53
2:G:429:MET:CE	2:G:457:ILE:CG1	2.87	0.53
2:H:196:ILE:HD13	2:H:290:VAL:HG11	1.90	0.53
2:G:124:LEU:HB2	2:G:136:TYR:HB2	1.92	0.52
1:A:184:PHE:HZ	1:A:229:ILE:HD13	1.73	0.52
1:A:282:PHE:CZ	1:A:343:CYS:HB2	2.44	0.52
1:A:239:GLU:HB2	1:A:290:PHE:CZ	2.45	0.52
1:A:30:ARG:HB3	1:A:33:ASN:HD21	1.75	0.52
2:G:580:GLN:HG2	11:G:1033:HOH:O	2.08	0.52
2:G:717:MET:HE1	2:G:721:SER:CB	2.31	0.52
2:H:847:LEU:O	2:H:848:SER:CB	2.56	0.52
2:G:31:ASP:OD1	2:G:266:ARG:HA	2.10	0.52
2:H:558:LYS:NZ	2:H:599:GLU:OE2	2.43	0.52
1:A:19:ALA:N	1:A:20:PRO:HD2	2.24	0.51
1:B:458:ASN:HB2	1:B:479:GLY:N	2.24	0.51
2:H:788:THR:HG1	2:H:803:THR:HG1	1.56	0.51
2:H:394:LEU:HB3	2:H:431:ILE:HD13	1.93	0.51
2:H:171:SER:O	2:H:196:ILE:HG21	2.11	0.51
2:H:283:LYS:HB3	11:H:1022:HOH:O	2.10	0.51
1:B:59:LEU:HD13	1:B:120:ARG:HD3	1.93	0.51
2:G:840[A]:PHE:CD1	2:G:858:ARG:HG2	2.45	0.51
1:B:184:PHE:HZ	1:B:229:ILE:HD13	1.76	0.50
2:H:785:VAL:HG22	2:H:806:GLU:HB3	1.93	0.50
2:H:26:LEU:HA	5:H:905:PGE:H1	1.93	0.50
1:A:77:ILE:HD11	1:A:132:ARG:NH1	2.27	0.50
2:G:717:MET:HE1	2:G:721:SER:HB2	1.86	0.50
2:H:33:LEU:HD11	2:H:64:ASP:HB3	1.94	0.49
1:A:304:PHE:HB2	2:G:609:SER:OG	2.12	0.49
2:G:592:ILE:HD12	2:G:595:ARG:NH1	2.28	0.49
1:A:190:SER:HB3	4:A:602:EDO:H22	1.93	0.48
1:A:378:GLU:CD	1:A:452:ARG:HH22	2.15	0.48
1:B:97:ARG:NH2	1:B:250:GLY:O	2.46	0.48
2:G:701:LEU:HD13	5:G:902:PGE:H2	1.94	0.48
2:H:189:LYS:HB3	2:H:216:SER:HB3	1.95	0.48
2:G:572:ASN:HB3	2:G:610:ARG:CD	2.44	0.48
2:G:747:LEU:HD22	2:G:794:SER:HB3	1.95	0.48
1:A:475:GLN:HE21	1:A:475:GLN:N	2.12	0.48
2:G:572:ASN:HB3	2:G:610:ARG:HD3	1.95	0.48
2:H:48:LYS:HB2	2:H:247:LYS:HZ2	1.79	0.48
2:G:189:LYS:HB3	2:G:216:SER:HB3	1.96	0.48
2:H:39:SER:HB2	7:H:917:PEG:H42	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:429:MET:HE1	2:H:457:ILE:CG1	2.44	0.48
2:H:266:ARG:H	2:H:266:ARG:HD3	1.78	0.47
2:G:308:TRP:CD1	2:G:347:ILE:HG23	2.49	0.47
2:G:769:LEU:O	2:G:772:ARG:HD3	2.15	0.47
2:G:123:THR:HG21	11:G:1040:HOH:O	2.13	0.47
2:G:296:SER:HB2	11:G:1077:HOH:O	2.12	0.47
2:G:674:LEU:HD11	2:G:713:LEU:HD21	1.95	0.47
2:H:308:TRP:CD1	2:H:347:ILE:HG23	2.49	0.47
2:G:847:LEU:O	2:G:848:SER:CB	2.56	0.47
1:A:42:LYS:O	1:A:106:ARG:O	2.32	0.47
1:A:94:TYR:O	1:A:103:LYS:HE3	2.15	0.47
2:G:351:GLU:HB3	2:G:356:LEU:HD13	1.97	0.47
2:G:124:LEU:HD23	2:G:277:ILE:HG12	1.97	0.47
2:H:395:TYR:CD2	7:H:914:PEG:H41	2.49	0.47
2:H:429:MET:HE1	2:H:457:ILE:HG13	1.97	0.47
2:H:521:LYS:HG2	2:H:547:ILE:HG12	1.97	0.47
1:B:82:VAL:HA	11:B:704:HOH:O	2.14	0.46
2:G:384:ASP:OD1	2:G:387:ILE:HD11	2.15	0.46
2:H:32:ARG:HD3	11:H:1028:HOH:O	2.15	0.46
2:H:99:LYS:HD2	2:H:99:LYS:HA	1.77	0.46
2:H:206:GLN:HB2	2:H:657:ALA:CB	2.45	0.46
2:H:747:LEU:HD22	2:H:794:SER:HB3	1.97	0.46
1:B:335:THR:OG1	1:B:337:GLU:HG2	2.15	0.46
2:H:242:PHE:HA	2:H:654:ILE:HD11	1.98	0.46
2:H:593:VAL:O	2:H:597:LEU:HG	2.16	0.46
2:H:171:SER:O	2:H:196:ILE:CG2	2.63	0.45
1:B:154:GLU:O	1:B:207:LYS:HA	2.16	0.45
2:G:312:ARG:HH22	4:G:915:EDO:H21	1.80	0.45
2:H:625:PRO:HG2	11:H:1048:HOH:O	2.16	0.45
2:G:785:VAL:HG22	2:G:806:GLU:HB3	1.98	0.45
2:G:51:LEU:HD11	2:G:249:LYS:HD2	1.99	0.45
1:A:30:ARG:HB3	1:A:33:ASN:ND2	2.32	0.45
2:G:521:LYS:HG2	2:G:547:ILE:HG12	1.99	0.45
2:H:467:LYS:HE2	2:H:467:LYS:HB3	1.60	0.45
2:G:696:LEU:HD23	2:G:696:LEU:HA	1.87	0.44
2:H:467:LYS:HG2	2:H:468:GLU:OE2	2.17	0.44
1:A:336:ALA:O	1:A:340:THR:OG1	2.33	0.44
2:G:347:ILE:HG22	2:G:359:LEU:HD21	1.99	0.44
1:A:154:GLU:O	1:A:207:LYS:HA	2.17	0.44
1:B:230:LYS:HA	1:B:233:GLN:NE2	2.30	0.44
2:G:136:TYR:CZ	2:G:277:ILE:HD13	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:395:TYR:HE2	5:G:902:PGE:H22	1.71	0.44
2:G:708:ASN:O	2:G:712:ASP:HB3	2.17	0.44
2:H:749:ALA:HA	2:H:791:THR:O	2.18	0.44
2:G:538:THR:HG23	6:G:906:SO4:O2	2.18	0.44
1:B:363:ASP:HB2	1:B:366:LYS:HB2	1.99	0.43
2:G:769:LEU:O	2:G:772:ARG:CD	2.66	0.43
1:B:396:TRP:CH2	2:H:875:SER:HB3	2.53	0.43
2:H:769:LEU:C	2:H:769:LEU:HD13	2.39	0.43
2:H:587:MET:HB3	2:H:588:PRO:CD	2.42	0.43
1:A:39:ALA:HA	1:A:107:ASN:ND2	2.33	0.43
1:B:116:TYR:CZ	1:B:118:ALA:HB3	2.53	0.43
2:H:31:ASP:OD1	2:H:266:ARG:HA	2.19	0.43
2:G:138:TYR:HE1	2:G:283:LYS:HB2	1.84	0.43
2:H:37:THR:HG22	7:H:917:PEG:H12	2.00	0.43
2:H:351:GLU:HB3	2:H:356:LEU:HD13	2.01	0.43
2:H:37:THR:CG2	7:H:917:PEG:H12	2.49	0.43
1:A:139:THR:O	1:A:141:PRO:HD3	2.19	0.43
2:H:526:ARG:HA	2:H:531:ASN:ND2	2.30	0.43
1:A:24:ASP:O	1:A:25:HIS:HB2	2.18	0.43
5:G:902:PGE:H2	5:G:902:PGE:H4	1.77	0.42
2:H:696:LEU:HD23	2:H:696:LEU:HA	1.88	0.42
2:G:381:PHE:CE1	2:G:414:LYS:HE3	2.54	0.42
1:A:116:TYR:CZ	1:A:118:ALA:HB3	2.54	0.42
2:H:99:LYS:HZ2	10:H:902:PE4:H81	1.84	0.42
2:H:735:ILE:HB	2:H:755:GLY:HA3	2.00	0.42
1:B:336:ALA:O	1:B:340:THR:OG1	2.35	0.42
2:G:361:ASP:OD2	2:G:392:ARG:NH1	2.52	0.42
2:G:51:LEU:HD11	2:G:249:LYS:CD	2.49	0.42
2:G:182:GLN:OE1	2:G:182:GLN:HA	2.19	0.42
2:G:772:ARG:HG2	2:G:820:SER:HA	2.01	0.42
2:H:347:ILE:HG22	2:H:359:LEU:HD21	2.01	0.42
2:H:481:LEU:HD21	2:H:510:ARG:HB2	2.01	0.42
1:B:367:GLN:HE21	1:B:367:GLN:HB2	1.69	0.42
2:H:780:ASN:HD21	8:H:901:PE5:H151	1.77	0.42
1:B:333:GLU:HB2	1:B:338:ARG:HG3	2.02	0.42
2:G:642:ILE:HD12	2:G:672:GLU:HG3	2.02	0.42
1:A:19:ALA:N	1:A:20:PRO:HD3	2.33	0.41
2:G:206:GLN:HB2	2:G:657:ALA:CB	2.49	0.41
1:A:47:GLU:HG3	1:A:102:ILE:CD1	2.48	0.41
1:B:139:THR:O	1:B:141:PRO:HD3	2.20	0.41
2:H:218:THR:HG23	2:H:232:ALA:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:24:ASP:O	1:B:25:HIS:HB2	2.20	0.41
2:G:740:GLU:HG3	2:G:750:ASN:HD21	1.85	0.41
2:G:567:LEU:HB3	2:G:568:PRO:HD2	2.01	0.41
1:B:403:LEU:HD21	1:B:443:LEU:HD21	2.02	0.41
2:G:218:THR:HG23	2:G:232:ALA:HB2	2.03	0.41
2:G:352:ASN:OD1	2:G:354:GLU:HG2	2.21	0.41
1:A:129:LEU:O	1:A:132:ARG:HD3	2.19	0.41
1:A:256:HIS:CE1	2:G:600:MET:HE3	2.55	0.41
2:G:456:LEU:HD12	2:G:456:LEU:HA	1.94	0.41
2:G:559:ASN:HD22	2:G:559:ASN:HA	1.67	0.41
2:G:590:SER:HB3	2:G:594:ARG:NH2	2.35	0.41
2:H:708:ASN:O	2:H:712:ASP:HB3	2.20	0.41
2:H:757:LEU:HA	2:H:783:THR:O	2.20	0.41
1:A:154:GLU:HA	1:A:208:LYS:HG3	2.03	0.41
2:G:69:TRP:CD1	2:G:276:ILE:HG13	2.56	0.41
2:H:99:LYS:HZ1	10:H:902:PE4:H81	1.83	0.41
2:H:427:THR:O	2:H:431:ILE:HD12	2.21	0.41
1:B:69:LYS:O	1:B:73:GLU:HB2	2.21	0.40
1:B:132:ARG:HD3	1:B:132:ARG:HA	1.76	0.40
1:B:349:GLY:HA2	5:B:603:PGE:H1	2.01	0.40
1:B:396:TRP:HH2	2:H:875:SER:HB3	1.85	0.40
2:G:728:VAL:HG13	5:G:902:PGE:H5	2.02	0.40
2:H:456:LEU:HD12	2:H:456:LEU:HA	1.96	0.40
1:B:160:PHE:CD1	1:B:198:LEU:CD1	3.05	0.40
2:H:118:ALA:O	2:H:149:LYS:HE2	2.20	0.40
2:H:665:VAL:O	2:H:692:MET:HA	2.21	0.40
1:B:199:ASP:OD1	1:B:199:ASP:N	2.54	0.40
1:B:440:PHE:CE2	2:H:869:PRO:HB3	2.56	0.40
2:H:871:HIS:CE1	2:H:874:ASN:HB2	2.56	0.40
1:B:116:TYR:OH	1:B:119:GLY:O	2.26	0.40
5:H:903:PGE:H32	5:H:903:PGE:H52	1.54	0.40

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	460/492 (94%)	436 (95%)	22 (5%)	2 (0%)	34	54
1	B	461/492 (94%)	440 (95%)	19 (4%)	2 (0%)	34	54
2	G	863/884 (98%)	831 (96%)	31 (4%)	1 (0%)	51	73
2	H	860/884 (97%)	828 (96%)	28 (3%)	4 (0%)	29	48
All	All	2644/2752 (96%)	2535 (96%)	100 (4%)	9 (0%)	41	61

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	23	GLU
1	A	166	SER
1	B	23	GLU
1	B	166	SER
2	H	716	LYS
2	G	76	ASP
2	H	76	ASP
2	H	795	SER
2	H	270	GLY

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	391/419 (93%)	368 (94%)	23 (6%)	19	37
1	B	393/419 (94%)	376 (96%)	17 (4%)	29	53
2	G	753/768 (98%)	708 (94%)	45 (6%)	19	37
2	H	750/768 (98%)	694 (92%)	56 (8%)	13	26
All	All	2287/2374 (96%)	2146 (94%)	141 (6%)	18	35

All (141) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	73	GLU
1	A	93	GLN
1	A	102	ILE
1	A	117	THR
1	A	121	GLU
1	A	132	ARG
1	A	148	SER
1	A	151	GLU
1	A	167	ASP
1	A	200	LYS
1	A	221	THR
1	A	233	GLN
1	A	243	GLN
1	A	247	LYS
1	A	273	SER
1	A	340	THR
1	A	367	GLN
1	A	379	ASP
1	A	402	GLN
1	A	419	ASN
1	A	433	GLU
1	A	451	ASP
1	A	475	GLN
1	B	42	LYS
1	B	71	LYS
1	B	93	GLN
1	B	112	SER
1	B	117	THR
1	B	130	LYS
1	B	131	LYS
1	B	132	ARG
1	B	199	ASP
1	B	221	THR
1	B	273	SER
1	B	332	GLU
1	B	337	GLU
1	B	340	THR
1	B	362	GLU
1	B	367	GLN
1	B	375	LYS
2	G	46	ARG
2	G	90	GLU
2	G	113	LYS

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Mol	Chain	Res	Type
2	G	123	THR
2	G	170	ILE
2	G	252	SER
2	G	269	SER
2	G	272	GLN
2	G	298	CYS
2	G	305	SER
2	G	318	ASP
2	G	321	SER
2	G	369	SER
2	G	377	ASP
2	G	384	ASP
2	G	411	LEU
2	G	421	SER
2	G	437	ARG
2	G	445	CYS
2	G	469	ASP
2	G	491	LYS
2	G	497	GLU
2	G	500	ILE
2	G	513	LEU
2	G	518	ASP
2	G	533	LYS
2	G	592	ILE
2	G	656	LYS
2	G	674	LEU
2	G	675	ILE
2	G	678	THR
2	G	710	TYR
2	G	711	SER
2	G	715	SER
2	G	716	LYS
2	G	717	MET
2	G	757	LEU
2	G	759	ILE
2	G	772	ARG
2	G	781	ARG
2	G	804	SER
2	G	830	MET
2	G	848	SER
2	G	849	THR
2	G	885	GLN

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Mol	Chain	Res	Type
2	H	32	ARG
2	H	53	ASP
2	H	90	GLU
2	H	113	LYS
2	H	123	THR
2	H	133	LYS
2	H	170	ILE
2	H	224	ASP
2	H	225	SER
2	H	252	SER
2	H	266	ARG
2	H	267	LEU
2	H	268	MET
2	H	272	GLN
2	H	298	CYS
2	H	305	SER
2	H	318	ASP
2	H	321	SER
2	H	353	LYS
2	H	369	SER
2	H	377	ASP
2	H	384	ASP
2	H	421	SER
2	H	434	THR
2	H	437	ARG
2	H	442	ASN
2	H	445	CYS
2	H	466	LYS
2	H	467	LYS
2	H	469	ASP
2	H	497	GLU
2	H	500	ILE
2	H	519	GLU
2	H	571	MET
2	H	592	ILE
2	H	626	ARG
2	H	644	ARG
2	H	656	LYS
2	H	675	ILE
2	H	684	GLU
2	H	686	LEU
2	H	711	SER

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Mol	Chain	Res	Type
2	H	715	SER
2	H	716	LYS
2	H	717	MET
2	H	757	LEU
2	H	759	ILE
2	H	768	SER
2	H	772	ARG
2	H	779	LYS
2	H	781	ARG
2	H	791	THR
2	H	820	SER
2	H	821	GLN
2	H	848	SER
2	H	858	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	224	ASN
1	A	243	GLN
1	A	367	GLN
1	A	419	ASN
1	A	475	GLN
1	B	41	HIS
1	B	224	ASN
1	B	233	GLN
1	B	367	GLN
1	B	402	GLN
2	G	334	GLN
2	G	390	GLN
2	G	559	ASN
2	G	569	GLN
2	G	685	ASN
2	G	744	GLN
2	G	780	ASN
2	H	272	GLN
2	H	334	GLN
2	H	442	ASN
2	H	531	ASN
2	H	780	ASN
2	H	821	GLN
2	H	856	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 51 ligands modelled in this entry, 2 are monoatomic - leaving 49 for Mogul analysis.

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	$\# Z > 2$
4	EDO	A	604	-	3,3,3	0.22	0	2,2,2	0.43	0
7	PEG	H	914	-	6,6,6	0.10	0	5,5,5	0.13	0
4	EDO	H	910	-	3,3,3	0.04	0	2,2,2	0.21	0
4	EDO	G	914	-	3,3,3	0.13	0	2,2,2	0.18	0
5	PGE	H	904	-	9,9,9	0.18	0	8,8,8	0.17	0
6	SO4	G	904	-	4,4,4	0.32	0	6,6,6	0.08	0
6	SO4	G	909	-	4,4,4	0.41	0	6,6,6	0.10	0
7	PEG	B	608	-	6,6,6	0.17	0	5,5,5	0.06	0
6	SO4	G	907	-	4,4,4	0.33	0	6,6,6	0.06	0
6	SO4	G	908	-	4,4,4	0.51	0	6,6,6	0.27	0
4	EDO	H	912	-	3,3,3	0.12	0	2,2,2	0.12	0
5	PGE	B	602	-	9,9,9	0.20	0	8,8,8	0.13	0
9	TRS	G	903	-	7,7,7	0.13	0	9,9,9	0.36	0
7	PEG	H	916	-	6,6,6	0.14	0	5,5,5	0.08	0
4	EDO	A	605	-	3,3,3	0.07	0	2,2,2	0.10	0
7	PEG	G	918	-	6,6,6	0.16	0	5,5,5	0.07	0
6	SO4	G	905	-	4,4,4	0.43	0	6,6,6	0.15	0
7	PEG	H	915	-	6,6,6	0.13	0	5,5,5	0.09	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	EDO	H	913	-	3,3,3	0.10	0	2,2,2	0.20	0
4	EDO	B	607	-	3,3,3	0.08	0	2,2,2	0.41	0
4	EDO	H	909	-	3,3,3	0.13	0	2,2,2	0.35	0
4	EDO	H	911	-	3,3,3	0.09	0	2,2,2	0.25	0
6	SO4	G	910	-	4,4,4	0.36	0	6,6,6	0.06	0
7	PEG	G	917	-	6,6,6	0.21	0	5,5,5	0.14	0
5	PGE	B	603	-	9,9,9	0.16	0	8,8,8	0.14	0
4	EDO	B	606	-	3,3,3	0.18	0	2,2,2	0.56	0
4	EDO	G	912	-	3,3,3	0.07	0	2,2,2	0.16	0
8	PE5	H	901	-	26,26,26	0.29	0	25,25,25	0.14	0
6	SO4	H	906	-	4,4,4	0.45	0	6,6,6	0.32	0
7	PEG	H	917	-	6,6,6	0.29	0	5,5,5	0.24	0
6	SO4	B	604	-	4,4,4	0.37	0	6,6,6	0.13	0
7	PEG	H	918	-	6,6,6	0.16	0	5,5,5	0.04	0
4	EDO	A	603	-	3,3,3	0.30	0	2,2,2	0.92	0
4	EDO	G	911	-	3,3,3	0.26	0	2,2,2	0.45	0
4	EDO	G	913	-	3,3,3	0.10	0	2,2,2	0.13	0
6	SO4	H	907	-	4,4,4	0.37	0	6,6,6	0.22	0
4	EDO	G	916	-	3,3,3	0.29	0	2,2,2	0.66	0
5	PGE	G	902	-	9,9,9	0.23	0	8,8,8	0.22	0
8	PE5	G	901	-	26,26,26	0.34	0	25,25,25	0.16	0
6	SO4	G	906	-	4,4,4	0.29	0	6,6,6	0.21	0
10	PE4	H	902	-	23,23,23	0.23	0	22,22,22	0.16	0
4	EDO	A	602	-	3,3,3	0.06	0	2,2,2	0.07	0
5	PGE	H	905	-	9,9,9	0.23	0	8,8,8	0.13	0
6	SO4	H	908	-	4,4,4	0.35	0	6,6,6	0.08	0
4	EDO	A	606	-	3,3,3	0.09	0	2,2,2	0.19	0
7	PEG	B	609	-	6,6,6	0.19	0	5,5,5	0.14	0
5	PGE	H	903	-	9,9,9	0.18	0	8,8,8	0.27	0
4	EDO	G	915	-	3,3,3	0.04	0	2,2,2	0.16	0
4	EDO	B	605	-	3,3,3	0.25	0	2,2,2	0.41	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
4	EDO	A	604	-	-	0/1/1/1	-
7	PEG	H	914	-	-	2/4/4/4	-
4	EDO	H	910	-	-	1/1/1/1	-
4	EDO	G	914	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PGE	H	904	-	-	5/7/7/7	-
7	PEG	B	608	-	-	2/4/4/4	-
4	EDO	H	912	-	-	1/1/1/1	-
5	PGE	B	602	-	-	5/7/7/7	-
9	TRS	G	903	-	-	0/9/9/9	-
7	PEG	H	916	-	-	2/4/4/4	-
4	EDO	A	605	-	-	1/1/1/1	-
7	PEG	G	918	-	-	0/4/4/4	-
7	PEG	H	915	-	-	1/4/4/4	-
4	EDO	H	913	-	-	0/1/1/1	-
4	EDO	B	607	-	-	1/1/1/1	-
4	EDO	H	909	-	-	1/1/1/1	-
4	EDO	H	911	-	-	1/1/1/1	-
7	PEG	G	917	-	-	3/4/4/4	-
5	PGE	B	603	-	-	7/7/7/7	-
4	EDO	B	606	-	-	1/1/1/1	-
4	EDO	G	912	-	-	0/1/1/1	-
8	PE5	H	901	-	-	15/24/24/24	-
7	PEG	H	917	-	-	2/4/4/4	-
7	PEG	H	918	-	-	4/4/4/4	-
4	EDO	A	603	-	-	0/1/1/1	-
4	EDO	G	911	-	-	1/1/1/1	-
4	EDO	G	913	-	-	1/1/1/1	-
4	EDO	G	916	-	-	1/1/1/1	-
5	PGE	G	902	-	-	5/7/7/7	-
8	PE5	G	901	-	-	15/24/24/24	-
10	PE4	H	902	-	-	14/21/21/21	-
4	EDO	A	602	-	-	1/1/1/1	-
5	PGE	H	905	-	-	3/7/7/7	-
4	EDO	A	606	-	-	0/1/1/1	-
7	PEG	B	609	-	-	2/4/4/4	-
5	PGE	H	903	-	-	5/7/7/7	-
4	EDO	G	915	-	-	0/1/1/1	-
4	EDO	B	605	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (104) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	H	902	PE4	C3-C4-O3-C5
5	G	902	PGE	C3-C4-O3-C5
7	G	917	PEG	O1-C1-C2-O2
5	G	902	PGE	O2-C3-C4-O3
8	G	901	PE5	O3-C5-C6-O4
8	H	901	PE5	O2-C3-C4-O3
8	G	901	PE5	O6-C10-C9-O5
10	H	902	PE4	O6-C10-C9-O5
5	H	904	PGE	O2-C3-C4-O3
8	G	901	PE5	O6-C11-C12-O7
7	H	917	PEG	O2-C3-C4-O4
8	G	901	PE5	O1-C1-C2-O2
8	H	901	PE5	O3-C5-C6-O4
5	H	903	PGE	O2-C3-C4-O3
4	H	909	EDO	O1-C1-C2-O2
4	H	912	EDO	O1-C1-C2-O2
5	B	603	PGE	O2-C3-C4-O3
8	G	901	PE5	O2-C3-C4-O3
10	H	902	PE4	O4-C7-C8-O5
8	G	901	PE5	O4-C7-C8-O5
5	B	603	PGE	O1-C1-C2-O2
5	G	902	PGE	O3-C5-C6-O4
7	H	914	PEG	O1-C1-C2-O2
8	G	901	PE5	O8-C15-C16-O52
5	B	603	PGE	O3-C5-C6-O4
5	G	902	PGE	C4-C3-O2-C2
5	H	903	PGE	C3-C4-O3-C5
5	B	602	PGE	O1-C1-C2-O2
4	A	602	EDO	O1-C1-C2-O2
4	G	913	EDO	O1-C1-C2-O2
4	G	916	EDO	O1-C1-C2-O2
10	H	902	PE4	O7-C13-C14-O8
5	H	903	PGE	O3-C5-C6-O4
8	G	901	PE5	O7-C13-C14-O8
7	H	915	PEG	O2-C3-C4-O4
8	H	901	PE5	O8-C15-C16-O52
8	G	901	PE5	C9-C10-O6-C11
5	H	905	PGE	O3-C5-C6-O4
4	B	607	EDO	O1-C1-C2-O2
4	H	910	EDO	O1-C1-C2-O2
10	H	902	PE4	O1-C1-C2-O2
8	H	901	PE5	C48-C50-O1-C1

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Mol	Chain	Res	Type	Atoms
8	G	901	PE5	C48-C50-O1-C1
10	H	902	PE4	O6-C11-C12-O7
7	H	918	PEG	O1-C1-C2-O2
7	B	609	PEG	C4-C3-O2-C2
10	H	902	PE4	C8-C7-O4-C6
10	H	902	PE4	C12-C11-O6-C10
7	B	609	PEG	C1-C2-O2-C3
7	H	918	PEG	C1-C2-O2-C3
8	G	901	PE5	C13-C14-O8-C15
8	H	901	PE5	C6-C5-O3-C4
5	H	904	PGE	C6-C5-O3-C4
7	H	916	PEG	C1-C2-O2-C3
5	B	603	PGE	C1-C2-O2-C3
8	H	901	PE5	C9-C10-O6-C11
8	H	901	PE5	C11-C12-O7-C13
5	G	902	PGE	C6-C5-O3-C4
7	B	608	PEG	C4-C3-O2-C2
8	G	901	PE5	C4-C3-O2-C2
10	H	902	PE4	C13-C14-O8-C15
5	H	904	PGE	C3-C4-O3-C5
4	A	605	EDO	O1-C1-C2-O2
5	H	905	PGE	C4-C3-O2-C2
7	H	918	PEG	C4-C3-O2-C2
8	H	901	PE5	C13-C14-O8-C15
8	G	901	PE5	C12-C11-O6-C10
7	H	916	PEG	C4-C3-O2-C2
5	B	602	PGE	C1-C2-O2-C3
5	B	603	PGE	C6-C5-O3-C4
5	B	602	PGE	C6-C5-O3-C4
8	G	901	PE5	C7-C8-O5-C9
7	G	917	PEG	C4-C3-O2-C2
5	H	904	PGE	O1-C1-C2-O2
7	G	917	PEG	C1-C2-O2-C3
8	H	901	PE5	C2-C1-O1-C50
5	B	602	PGE	C3-C4-O3-C5
8	G	901	PE5	C10-C9-O5-C8
4	G	914	EDO	O1-C1-C2-O2
10	H	902	PE4	O3-C5-C6-O4
8	H	901	PE5	O6-C10-C9-O5
8	H	901	PE5	C16-C15-O8-C14
5	B	603	PGE	C4-C3-O2-C2
10	H	902	PE4	C16-C15-O8-C14

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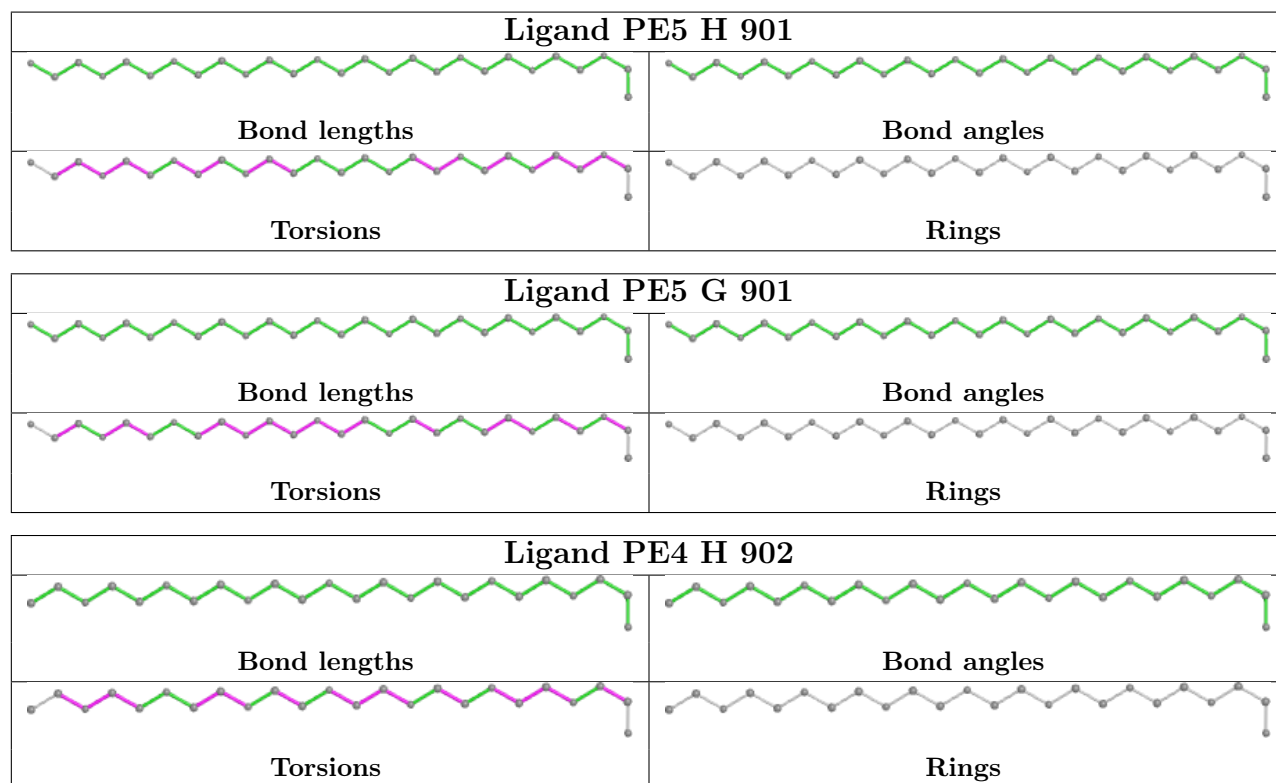
Mol	Chain	Res	Type	Atoms
8	H	901	PE5	O1-C1-C2-O2
5	H	904	PGE	O3-C5-C6-O4
7	B	608	PEG	C1-C2-O2-C3
7	H	917	PEG	C4-C3-O2-C2
5	B	602	PGE	C4-C3-O2-C2
5	H	903	PGE	C4-C3-O2-C2
7	H	914	PEG	C4-C3-O2-C2
10	H	902	PE4	O2-C3-C4-O3
5	B	603	PGE	C3-C4-O3-C5
10	H	902	PE4	C4-C3-O2-C2
8	H	901	PE5	O6-C11-C12-O7
4	B	606	EDO	O1-C1-C2-O2
4	H	911	EDO	O1-C1-C2-O2
5	H	905	PGE	C6-C5-O3-C4
5	H	903	PGE	O1-C1-C2-O2
7	H	918	PEG	O2-C3-C4-O4
4	G	911	EDO	O1-C1-C2-O2
8	H	901	PE5	C1-C2-O2-C3
10	H	902	PE4	C7-C8-O5-C9
8	H	901	PE5	O7-C13-C14-O8

There are no ring outliers.

17 monomers are involved in 34 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	604	EDO	1	0
7	H	914	PEG	2	0
6	G	907	SO4	1	0
9	G	903	TRS	1	0
5	B	603	PGE	1	0
8	H	901	PE5	6	0
6	H	906	SO4	1	0
7	H	917	PEG	5	0
4	A	603	EDO	2	0
5	G	902	PGE	5	0
8	G	901	PE5	1	0
6	G	906	SO4	1	0
10	H	902	PE4	3	0
4	A	602	EDO	1	0
5	H	905	PGE	1	0
5	H	903	PGE	1	0
4	G	915	EDO	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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	461/492 (93%)	0.58	68 (14%) 2 2	38, 76, 149, 188	0
1	B	462/492 (93%)	0.16	23 (4%) 28 30	39, 72, 120, 167	0
2	G	863/884 (97%)	0.03	11 (1%) 77 79	34, 61, 107, 150	0
2	H	862/884 (97%)	0.18	24 (2%) 53 56	35, 64, 122, 167	0
All	All	2648/2752 (96%)	0.20	126 (4%) 30 32	34, 66, 127, 188	0

All (126) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	77	ILE	11.4
1	B	72	ALA	7.6
1	A	79	LEU	7.2
1	A	72	ALA	6.7
1	A	111	ALA	6.7
1	A	104	PHE	6.5
1	A	78	ARG	6.3
1	A	20	PRO	6.2
1	A	45	LEU	6.1
1	A	76	GLU	6.0
1	B	479	GLY	5.8
1	A	43	TYR	5.7
2	H	770	TRP	5.6
1	A	19	ALA	5.6
1	B	140	LEU	5.5
1	A	105	PHE	5.5
1	A	80	ALA	5.3
1	A	479	GLY	5.3
1	A	103	LYS	5.2
1	A	29	LEU	5.1
1	A	113	PRO	5.1

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Mol	Chain	Res	Type	RSRZ
1	A	26	VAL	5.1
1	A	126	VAL	5.1
1	A	108	GLY	5.0
2	H	885	GLN	4.8
1	A	67	ALA	4.7
1	A	63	TYR	4.6
2	H	182	GLN	4.5
1	A	121	GLU	4.4
2	G	462	GLU	4.4
2	H	297	HIS	4.4
1	A	122	ALA	4.3
1	A	75	SER	4.2
1	B	187	THR	4.1
1	A	25	HIS	4.1
1	A	478	ALA	4.1
2	G	461	LEU	4.1
1	B	144	ALA	4.1
1	A	44	LEU	4.0
1	A	74	GLY	4.0
1	A	120	ARG	4.0
1	A	125	ILE	3.9
1	B	143	GLY	3.9
1	A	46	VAL	3.9
1	A	27	LEU	3.8
1	A	112	SER	3.8
1	B	480	ASP	3.8
1	B	202	GLY	3.7
1	B	164	VAL	3.7
2	H	886	PRO	3.7
2	H	676	ALA	3.7
1	A	106	ARG	3.7
2	G	49	GLY	3.6
2	H	722	GLY	3.6
2	G	21	GLY	3.6
1	A	28	VAL	3.6
1	A	129	LEU	3.5
1	A	132	ARG	3.5
1	B	173	LEU	3.5
1	A	23	GLU	3.4
2	H	98	GLU	3.3
1	A	123	ASP	3.3
1	A	66	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	102	ILE	3.2
2	H	710	TYR	3.2
1	A	70	LEU	3.2
2	H	48	LYS	3.2
2	G	713	LEU	3.1
1	A	21	GLU	3.0
1	A	24	ASP	3.0
1	B	71	LYS	3.0
1	A	22	GLU	3.0
1	A	124	ASP	3.0
2	H	181	HIS	2.9
2	H	465	GLU	2.9
1	A	71	LYS	2.9
1	A	34	PHE	2.8
1	A	107	ASN	2.8
1	A	133	THR	2.8
2	H	138	TYR	2.8
1	A	59	LEU	2.8
1	A	41	HIS	2.7
1	B	21	GLU	2.6
1	A	127	ASN	2.6
1	A	65	LYS	2.6
1	A	130	LYS	2.6
2	H	772	ARG	2.6
1	A	47	GLU	2.6
1	A	40	ALA	2.6
1	A	110	THR	2.6
2	H	768	SER	2.6
2	G	20	LYS	2.5
1	B	141	PRO	2.5
2	G	474	LEU	2.5
2	H	22	HIS	2.4
1	A	69	LYS	2.4
1	B	186	ILE	2.3
1	A	450	ALA	2.3
1	A	73	GLU	2.3
2	H	273	ALA	2.3
2	H	723	ASP	2.3
2	G	22	HIS	2.3
1	A	42	LYS	2.3
1	B	169	ALA	2.2
2	H	769	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	476	ASP	2.2
1	B	43	TYR	2.2
2	H	183	ASP	2.2
2	H	21	GLY	2.2
1	A	38	LEU	2.2
2	H	771	TYR	2.2
1	B	138	THR	2.2
2	G	47	GLY	2.2
2	H	725	ILE	2.1
1	B	265	VAL	2.1
1	B	25	HIS	2.1
1	A	64	ALA	2.1
1	B	146	ALA	2.1
1	B	196	TYR	2.1
2	G	469	ASP	2.1
1	A	62	GLU	2.1
1	B	74	GLY	2.1
1	B	183	PRO	2.0
2	G	384	ASP	2.0
1	A	39	ALA	2.0
2	H	284	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 monosaccharides 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
4	EDO	G	913	4/4	0.54	0.28	90,96,103,106	0
4	EDO	G	912	4/4	0.55	0.21	72,78,81,83	4

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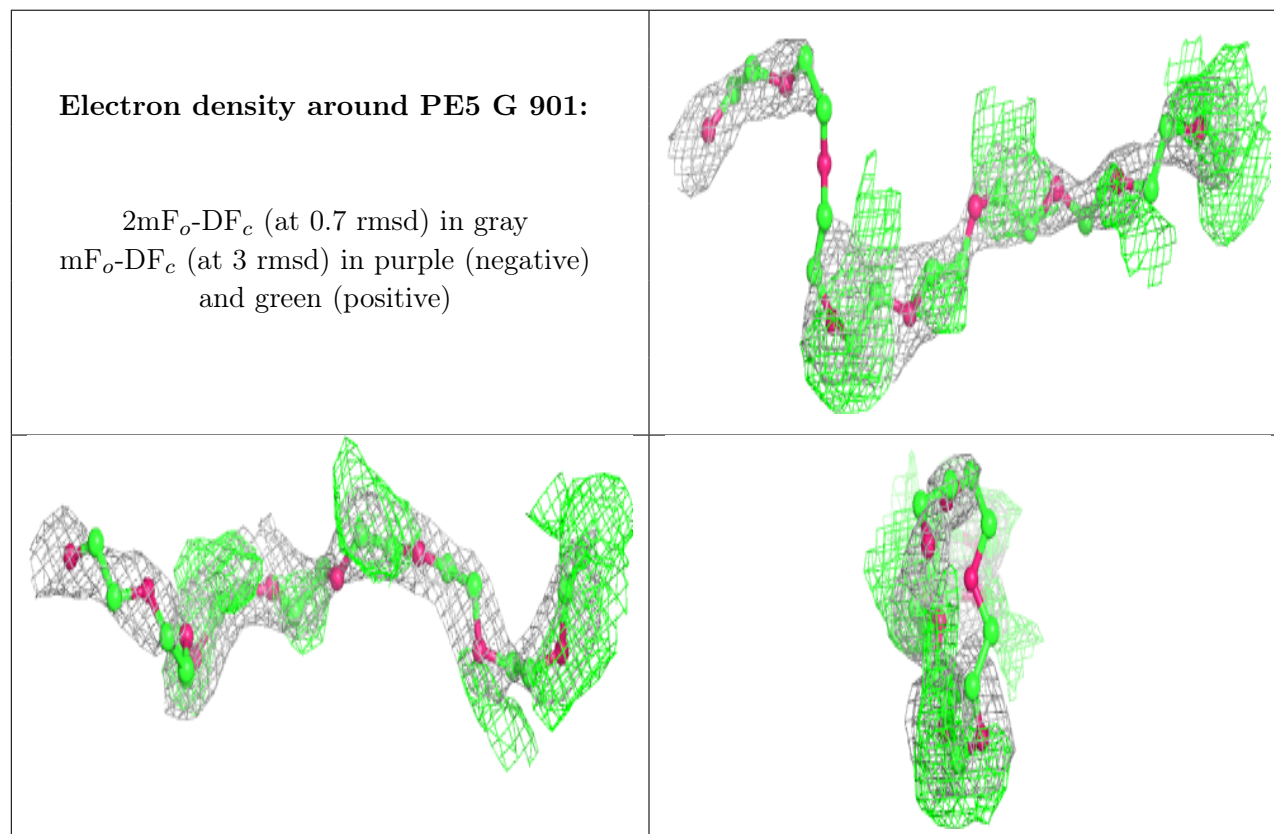
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
7	PEG	B	608	7/7	0.55	0.34	65,74,81,82	7
8	PE5	G	901	27/27	0.55	0.75	85,106,117,126	27
4	EDO	H	910	4/4	0.62	0.21	94,98,102,104	0
4	EDO	G	914	4/4	0.63	0.39	101,104,110,113	0
8	PE5	H	901	27/27	0.64	0.59	70,98,130,142	27
7	PEG	H	916	7/7	0.66	0.51	89,101,106,106	7
4	EDO	H	913	4/4	0.67	0.19	78,81,82,85	4
7	PEG	H	918	7/7	0.69	0.40	71,78,87,95	7
4	EDO	H	911	4/4	0.70	0.34	81,88,93,94	0
4	EDO	A	604	4/4	0.71	0.20	71,84,84,92	0
4	EDO	H	909	4/4	0.72	0.30	75,82,91,91	0
7	PEG	B	609	7/7	0.72	0.77	60,69,80,81	7
4	EDO	B	606	4/4	0.72	0.28	88,90,96,96	0
4	EDO	H	912	4/4	0.73	0.34	98,103,111,115	0
10	PE4	H	902	24/24	0.73	0.24	84,109,117,122	24
5	PGE	B	602	10/10	0.76	0.59	67,76,90,93	10
4	EDO	A	606	4/4	0.76	0.21	96,106,110,114	0
5	PGE	B	603	10/10	0.79	0.43	92,98,103,105	10
7	PEG	H	917	7/7	0.80	0.24	66,71,78,78	7
4	EDO	A	602	4/4	0.82	0.17	68,71,73,75	0
4	EDO	G	911	4/4	0.82	0.14	64,79,85,91	0
7	PEG	G	918	7/7	0.82	0.31	62,79,88,89	7
5	PGE	G	902	10/10	0.83	0.42	65,69,88,88	10
5	PGE	H	903	10/10	0.83	0.38	64,73,81,85	10
5	PGE	H	904	10/10	0.83	0.32	67,78,96,99	10
4	EDO	A	605	4/4	0.84	0.21	62,72,73,76	0
7	PEG	H	915	7/7	0.84	0.26	76,77,81,82	7
4	EDO	A	603	4/4	0.85	0.54	64,66,67,68	0
6	SO4	G	906	5/5	0.85	0.25	64,65,74,75	5
4	EDO	B	605	4/4	0.85	0.17	79,89,90,92	0
4	EDO	G	916	4/4	0.86	0.22	64,69,71,75	0
5	PGE	H	905	10/10	0.87	0.33	83,89,102,103	0
7	PEG	H	914	7/7	0.87	0.23	77,89,90,91	0
6	SO4	G	909	5/5	0.87	0.36	78,81,86,89	5
6	SO4	G	910	5/5	0.88	0.32	87,87,90,91	5
9	TRS	G	903	8/8	0.88	0.27	51,62,66,74	0
4	EDO	G	915	4/4	0.88	0.25	57,60,63,65	4
6	SO4	B	604	5/5	0.89	0.29	63,65,73,76	5
4	EDO	B	607	4/4	0.90	0.18	69,72,76,78	4
6	SO4	G	907	5/5	0.91	0.18	76,78,85,87	5
7	PEG	G	917	7/7	0.91	0.38	67,83,95,102	0
6	SO4	G	905	5/5	0.92	0.29	66,68,72,74	5

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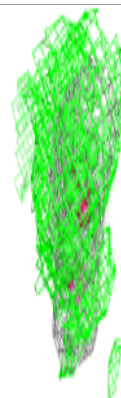
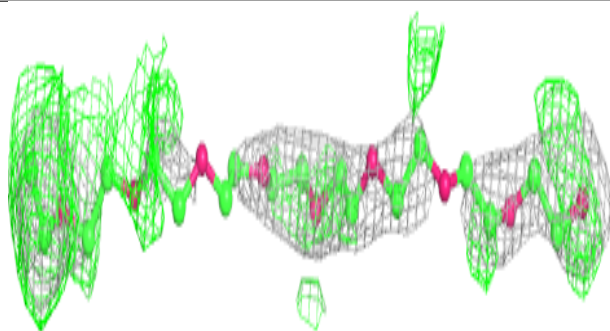
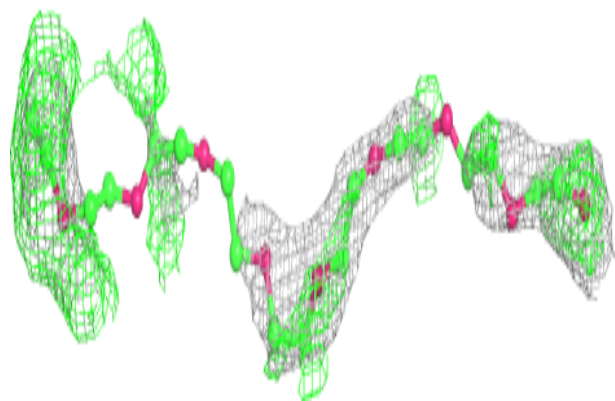
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
6	SO4	G	904	5/5	0.93	0.23	77,78,83,88	5
6	SO4	H	908	5/5	0.95	0.25	66,69,74,76	5
6	SO4	G	908	5/5	0.95	0.21	47,48,54,57	0
3	CA	B	601	1/1	0.96	0.09	60,60,60,60	0
3	CA	A	601	1/1	0.96	0.06	57,57,57,57	0
6	SO4	H	907	5/5	0.97	0.19	63,65,72,72	5
6	SO4	H	906	5/5	0.98	0.12	66,68,80,80	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

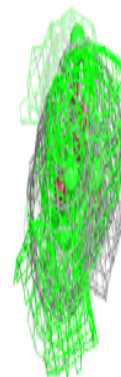
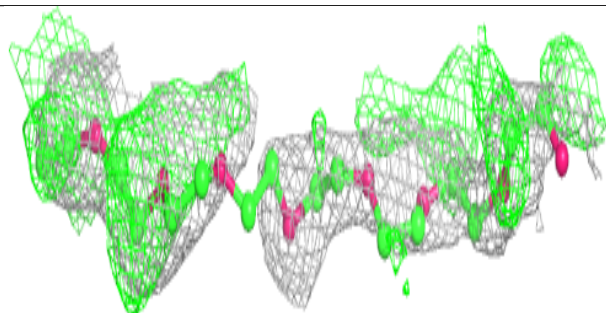
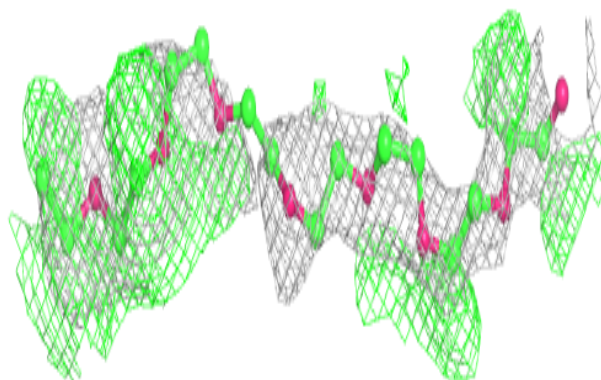


Electron density around PE5 H 901:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around PE4 H 902:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.