



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 7, 2020 – 01:53 am BST

PDB ID : 6H2Y
Title : human Fab 1E6 bound to fHbp variant 3 from Neisseria meningitidis serogroup B
Authors : Veggi, D.; Bianchi, F.; Cozzi, R.; Malito, E.; Bottomley, M.J.
Deposited on : 2018-07-17
Resolution : 2.65 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

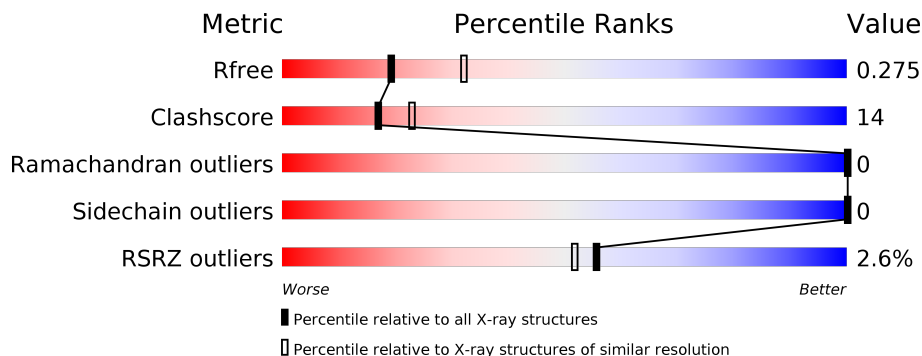
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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	1332 (2.68-2.64)
Clashscore	141614	1374 (2.68-2.64)
Ramachandran outliers	138981	1349 (2.68-2.64)
Sidechain outliers	138945	1349 (2.68-2.64)
RSRZ outliers	127900	1318 (2.68-2.64)

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 on 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	D	275	 6% 56% 28% 16%
2	H	224	 79% 19%
3	L	216	 78% 20%

2 Entry composition i

There are 8 unique types of molecules in this entry. The entry contains 5135 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 Lipoprotein GNA1870.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
1	D	231	1751	1099	306	346	7	0	0

There are 25 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	0	MET	-	initiating methionine	UNP Q19KF7
D	1	GLY	-	expression tag	UNP Q19KF7
D	2	PRO	-	expression tag	UNP Q19KF7
D	3	ASP	-	expression tag	UNP Q19KF7
D	4	SER	-	expression tag	UNP Q19KF7
D	5	ASP	-	expression tag	UNP Q19KF7
D	6	ARG	-	expression tag	UNP Q19KF7
D	7	LEU	-	expression tag	UNP Q19KF7
D	8	GLN	-	expression tag	UNP Q19KF7
D	9	GLN	-	expression tag	UNP Q19KF7
D	10	ARG	-	expression tag	UNP Q19KF7
D	11	ARG	-	expression tag	UNP Q19KF7
D	262	LYS	-	expression tag	UNP Q19KF7
D	263	LEU	-	expression tag	UNP Q19KF7
D	264	ALA	-	expression tag	UNP Q19KF7
D	265	ALA	-	expression tag	UNP Q19KF7
D	266	ALA	-	expression tag	UNP Q19KF7
D	267	LEU	-	expression tag	UNP Q19KF7
D	268	GLU	-	expression tag	UNP Q19KF7
D	269	HIS	-	expression tag	UNP Q19KF7
D	270	HIS	-	expression tag	UNP Q19KF7
D	271	HIS	-	expression tag	UNP Q19KF7
D	272	HIS	-	expression tag	UNP Q19KF7
D	273	HIS	-	expression tag	UNP Q19KF7
D	274	HIS	-	expression tag	UNP Q19KF7

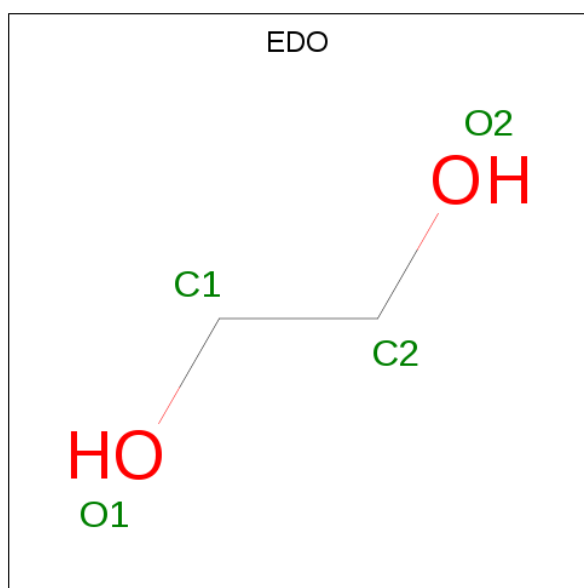
- Molecule 2 is a protein called Heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	219	Total	C	N	O	S	0	1	0
			1623	1023	270	323	7			

- Molecule 3 is a protein called Light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	212	Total	C	N	O	S	0	0	0
			1597	1000	271	322	4			

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



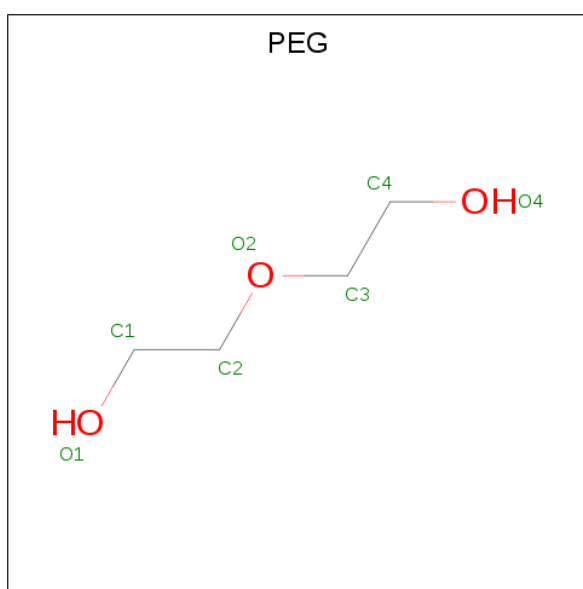
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	H	1	Total	C	O	0	0
			4	2	2		
4	H	1	Total	C	O	0	0
			4	2	2		
4	H	1	Total	C	O	0	0
			4	2	2		
4	H	1	Total	C	O	0	0
			4	2	2		
4	H	1	Total	C	O	0	0
			4	2	2		
4	H	1	Total	C	O	0	0
			4	2	2		

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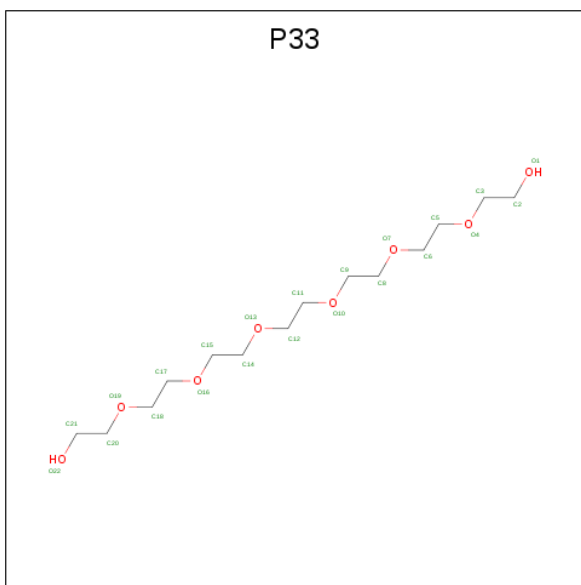
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	L	1	Total	C	O	0	0
			4	2	2		
4	L	1	Total	C	O	0	0
			4	2	2		
4	L	1	Total	C	O	0	0
			4	2	2		
4	L	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



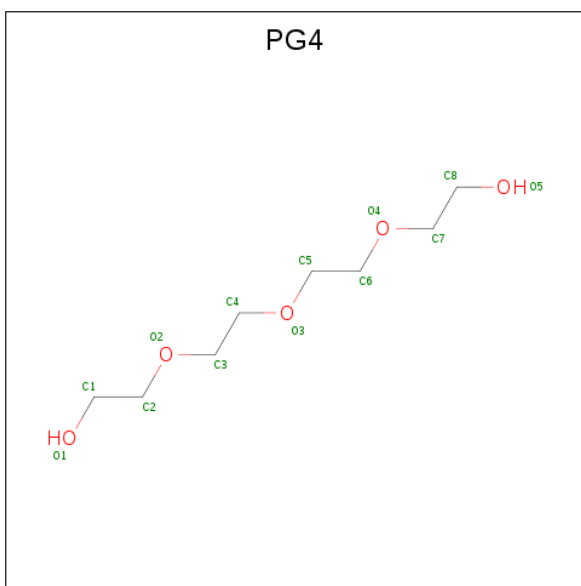
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	H	1	Total	C	O	0	0
			7	4	3		

- Molecule 6 is 3,6,9,12,15,18-HEXA-OXAICOSANE-1,20-DIOL (three-letter code: P33) (formula: C₁₄H₃₀O₈).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	L	1	Total	C	O	0	0
			22	14	8		

- Molecule 7 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	L	1	Total	C	O	0	0
			13	8	5		

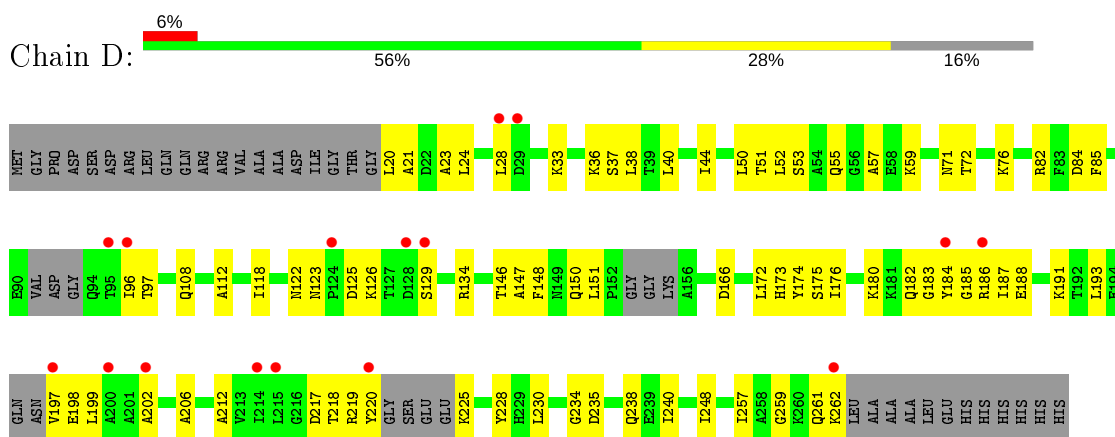
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	D	16	Total 16	O 16	0	0
8	H	28	Total 28	O 28	0	0
8	L	30	Total 30	O 30	0	0

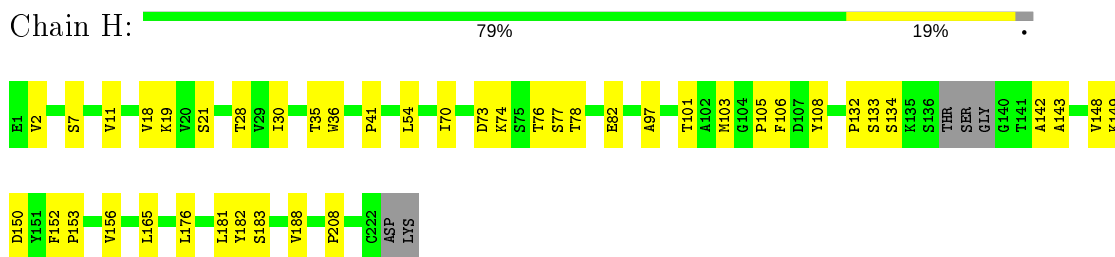
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

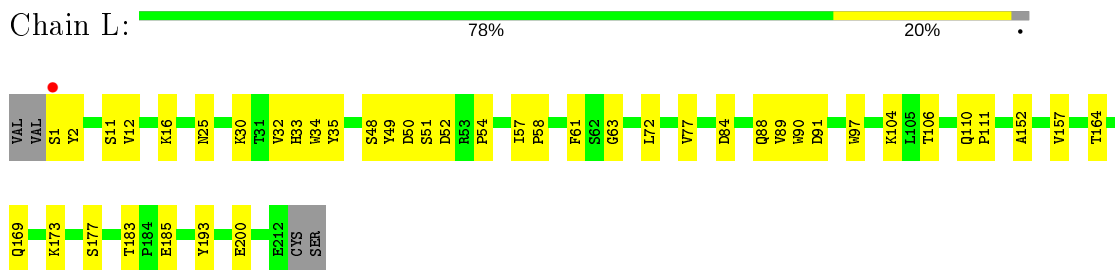
- Molecule 1: Lipoprotein GNA1870



- Molecule 2: Heavy chain



- Molecule 3: Light chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants a, b, c, α , β , γ	42.98Å 65.28Å 278.83Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	63.56 – 2.65 63.56 – 2.65	Depositor EDS
% Data completeness (in resolution range)	96.8 (63.56-2.65) 96.8 (63.56-2.65)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.04 (at 2.65Å)	Xtrriage
Refinement program	PHENIX (1.13_2998: 000)	Depositor
R, R_{free}	0.205 , 0.275 0.213 , 0.275	Depositor DCC
R_{free} test set	1139 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	37.9	Xtrriage
Anisotropy	0.332	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 61.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	5135	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.08% 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: P33, PG4, PEG, EDO

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	D	0.44	0/1774	0.63	0/2385
2	H	0.54	0/1662	0.68	0/2263
3	L	0.71	0/1639	0.68	0/2245
All	All	0.57	0/5075	0.67	0/6893

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	D	1751	0	1716	73	1
2	H	1623	0	1604	35	1
3	L	1597	0	1536	39	0
4	H	32	0	48	2	0
4	L	16	0	24	1	0
5	H	7	0	10	1	0
6	L	22	0	30	3	0
7	L	13	0	18	1	0
8	D	16	0	0	0	0
8	H	28	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	L	30	0	0	1	0
All	All	5135	0	4986	140	1

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 14.

All (140) 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:D:198:GLU:HB3	1:D:219:ARG:O	1.43	1.17
3:L:51:SER:HB3	3:L:63:GLY:O	1.52	1.08
1:D:176:ILE:HD11	1:D:183:GLY:HA2	1.45	0.97
1:D:176:ILE:CD1	1:D:183:GLY:HA2	1.94	0.97
1:D:198:GLU:CB	1:D:219:ARG:O	2.20	0.89
2:H:7:SER:HB3	2:H:21:SER:H	1.41	0.84
3:L:32:VAL:HG13	3:L:88:GLN:O	1.81	0.80
3:L:164:THR:HG22	3:L:177:SER:H	1.46	0.80
3:L:104:LYS:HB3	6:L:305:P33:H201	1.67	0.76
1:D:186:ARG:HH12	1:D:188:GLU:HB3	1.49	0.76
1:D:219:ARG:NH2	1:D:220:TYR:HD2	1.84	0.75
1:D:172:LEU:HD22	1:D:257:ILE:HB	1.69	0.75
1:D:187:ILE:HB	1:D:197:VAL:HG12	1.71	0.72
1:D:33:LYS:HE3	1:D:76:LYS:HA	1.72	0.71
1:D:53:SER:HB3	2:H:54:LEU:CD1	2.21	0.70
1:D:28:LEU:HD11	1:D:36:LYS:HB3	1.74	0.69
1:D:187:ILE:HD12	1:D:197:VAL:CG1	2.24	0.67
3:L:157:VAL:HG22	7:L:306:PG4:H22	1.75	0.67
1:D:21:ALA:HB1	1:D:57:ALA:HB3	1.77	0.67
1:D:217:ASP:O	1:D:218:THR:CG2	2.43	0.66
2:H:101:THR:HG22	2:H:103:MET:H	1.61	0.66
1:D:219:ARG:HH21	1:D:220:TYR:HD2	1.42	0.66
1:D:219:ARG:NH2	1:D:220:TYR:CD2	2.64	0.65
1:D:53:SER:HB3	2:H:54:LEU:HD11	1.79	0.65
3:L:32:VAL:HG22	3:L:89:VAL:CG1	2.28	0.63
3:L:32:VAL:HG22	3:L:89:VAL:HG12	1.79	0.63
1:D:146:THR:HG22	1:D:234:GLY:O	1.99	0.63
1:D:82:ARG:HD2	3:L:49:TYR:OH	1.98	0.62
1:D:123:ASN:HB3	1:D:126:LYS:O	1.99	0.62
2:H:36:TRP:HD1	2:H:70:ILE:HD13	1.65	0.61
1:D:24:LEU:HD22	1:D:59:LYS:HB3	1.82	0.61
1:D:217:ASP:O	1:D:218:THR:HG23	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:12:VAL:HG13	3:L:77:VAL:HG21	1.83	0.61
1:D:175:SER:O	1:D:176:ILE:HG13	2.02	0.60
1:D:174:TYR:CE2	1:D:176:ILE:HD12	2.39	0.58
2:H:176:LEU:HD13	2:H:182:TYR:CE1	2.38	0.58
3:L:58:PRO:HG2	3:L:61:PHE:CD2	2.39	0.57
1:D:52:LEU:HD23	1:D:85:PHE:HB2	1.87	0.57
1:D:218:THR:HG23	1:D:228:TYR:HD2	1.69	0.57
2:H:105:PRO:HB3	3:L:33:HIS:CG	2.41	0.56
1:D:217:ASP:C	1:D:218:THR:HG23	2.25	0.56
2:H:97:ALA:HB1	2:H:106:PHE:HB3	1.87	0.55
1:D:174:TYR:CD1	1:D:185:GLY:HA3	2.41	0.55
1:D:219:ARG:O	1:D:220:TYR:C	2.44	0.55
2:H:35:THR:HG21	2:H:106:PHE:CZ	2.42	0.54
1:D:82:ARG:CZ	3:L:49:TYR:CE1	2.90	0.54
1:D:186:ARG:NH1	1:D:188:GLU:HB3	2.21	0.54
2:H:41:PRO:HA	4:H:305:EDO:H21	1.90	0.54
1:D:218:THR:CG2	1:D:228:TYR:CD2	2.90	0.54
3:L:51:SER:CB	3:L:63:GLY:O	2.41	0.54
2:H:36:TRP:CD1	2:H:70:ILE:HD13	2.44	0.53
1:D:21:ALA:HB2	1:D:55:GLN:HB2	1.90	0.53
1:D:261:GLN:O	1:D:262:LYS:HB2	2.09	0.53
1:D:96:ILE:HD12	1:D:97:THR:H	1.74	0.52
2:H:132:PRO:HA	2:H:143:ALA:O	2.08	0.52
2:H:73:ASP:OD1	2:H:76:THR:HG23	2.10	0.52
1:D:148:PHE:CG	1:D:206:ALA:HB2	2.45	0.52
1:D:40:LEU:O	1:D:44:ILE:HG13	2.10	0.52
2:H:76:THR:O	2:H:78:THR:HG23	2.10	0.51
1:D:174:TYR:HD1	1:D:185:GLY:HA3	1.74	0.51
2:H:106:PHE:CD1	2:H:106:PHE:N	2.75	0.51
1:D:118:ILE:O	1:D:134:ARG:HA	2.10	0.51
3:L:16:LYS:O	3:L:77:VAL:HG13	2.11	0.51
1:D:20:LEU:HA	1:D:55:GLN:OE1	2.11	0.50
1:D:82:ARG:CD	3:L:49:TYR:OH	2.59	0.50
1:D:235:ASP:HB3	1:D:238:GLN:HE22	1.77	0.50
3:L:84:ASP:OD2	3:L:104:LYS:HG2	2.12	0.50
3:L:48:SER:O	3:L:52:ASP:HB3	2.11	0.50
3:L:32:VAL:CG1	3:L:88:GLN:O	2.56	0.50
3:L:34:TRP:CD2	3:L:72:LEU:HB2	2.47	0.49
3:L:88:GLN:NE2	3:L:97:TRP:CE3	2.79	0.49
2:H:2:VAL:HB	2:H:108:TYR:CE2	2.47	0.49
1:D:50:LEU:HD21	1:D:52:LEU:HD21	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:164:THR:CG2	3:L:177:SER:H	2.23	0.49
3:L:49:TYR:O	3:L:50:ASP:HB2	2.13	0.49
1:D:82:ARG:NE	3:L:49:TYR:CZ	2.79	0.49
1:D:230:LEU:HD22	1:D:240:ILE:HB	1.95	0.49
3:L:48:SER:O	3:L:52:ASP:CB	2.61	0.49
3:L:169:GLN:HG2	3:L:173:LYS:O	2.13	0.49
1:D:184:TYR:HA	1:D:199:LEU:O	2.13	0.48
1:D:51:THR:O	1:D:85:PHE:HA	2.13	0.48
3:L:2:TYR:CD1	3:L:91:ASP:OD2	2.66	0.48
1:D:166:ASP:O	1:D:191:LYS:NZ	2.39	0.48
1:D:108:GLN:HE22	1:D:259:GLY:N	2.12	0.48
1:D:151:LEU:HD21	1:D:212:ALA:HB2	1.95	0.47
2:H:134:SER:HA	2:H:142:ALA:HA	1.95	0.47
2:H:11:VAL:HG21	2:H:208:PRO:HB3	1.97	0.47
1:D:126:LYS:O	1:D:129:SER:HB3	2.15	0.47
1:D:176:ILE:HD11	1:D:184:TYR:H	1.80	0.47
1:D:28:LEU:CD1	1:D:36:LYS:HB3	2.42	0.46
1:D:52:LEU:HA	1:D:84:ASP:O	2.16	0.46
1:D:38:LEU:HD12	1:D:38:LEU:HA	1.75	0.46
3:L:32:VAL:HG12	3:L:33:HIS:N	2.31	0.45
1:D:96:ILE:HD11	1:D:122:ASN:ND2	2.32	0.45
3:L:54:PRO:HD2	3:L:57:ILE:HD13	1.99	0.45
2:H:19:LYS:HE2	4:H:304:EDO:O1	2.16	0.45
2:H:176:LEU:HD13	2:H:182:TYR:CD1	2.52	0.45
1:D:173:HIS:NE2	1:D:186:ARG:HD3	2.32	0.45
2:H:105:PRO:HG3	3:L:48:SER:HB2	1.99	0.45
2:H:165:LEU:HD21	2:H:188:VAL:HG11	1.98	0.44
1:D:147:ALA:HB3	1:D:150:GLN:HB2	1.99	0.44
1:D:218:THR:CG2	1:D:228:TYR:HD2	2.27	0.44
3:L:104:LYS:CE	6:L:305:P33:H112	2.47	0.44
3:L:200:GLU:HA	4:L:303:EDO:H21	1.99	0.44
1:D:176:ILE:HD13	1:D:183:GLY:HA2	1.93	0.44
2:H:176:LEU:HD13	2:H:182:TYR:CZ	2.53	0.44
2:H:18:VAL:O	2:H:82:GLU:HA	2.17	0.44
3:L:11:SER:HA	3:L:106:THR:O	2.18	0.44
2:H:150:ASP:HB3	2:H:181:LEU:HD13	2.00	0.44
3:L:110:GLN:HA	3:L:111:PRO:HD3	1.88	0.44
1:D:38:LEU:HD22	1:D:112:ALA:HB3	2.00	0.44
3:L:30:LYS:HE2	3:L:91:ASP:HA	2.00	0.43
2:H:28:THR:HG23	2:H:30:ILE:H	1.83	0.43
1:D:217:ASP:C	1:D:218:THR:CG2	2.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:148:VAL:HG11	2:H:156:VAL:HG11	2.00	0.43
2:H:152:PHE:HA	2:H:153:PRO:HA	1.79	0.43
2:H:7:SER:HB3	2:H:21:SER:N	2.22	0.43
2:H:103:MET:HG2	3:L:90:TRP:CD1	2.54	0.42
2:H:149:LYS:HG2	8:L:416:HOH:O	2.18	0.42
5:H:309:PEG:H11	8:H:413:HOH:O	2.20	0.42
3:L:35:TYR:CE2	3:L:88:GLN:OE1	2.72	0.42
1:D:176:ILE:HG21	1:D:182:GLN:O	2.20	0.42
1:D:180:LYS:HB3	1:D:182:GLN:HG2	2.01	0.42
1:D:176:ILE:HD11	1:D:183:GLY:CA	2.31	0.42
1:D:225:LYS:HD2	1:D:248:ILE:HD13	2.01	0.42
1:D:38:LEU:CD2	1:D:112:ALA:HB3	2.50	0.42
1:D:183:GLY:HA3	1:D:202:ALA:HB3	2.01	0.42
1:D:52:LEU:HD23	1:D:85:PHE:CB	2.48	0.41
2:H:77:SER:O	2:H:78:THR:CG2	2.69	0.41
3:L:152:ALA:HB2	3:L:193:TYR:CE2	2.56	0.41
1:D:23:ALA:HA	1:D:71:ASN:HB3	2.01	0.41
1:D:176:ILE:CG1	1:D:183:GLY:HA2	2.46	0.41
6:L:305:P33:H181	6:L:305:P33:H152	1.71	0.41
2:H:133:SER:O	2:H:134:SER:HB3	2.21	0.41
1:D:37:SER:HA	1:D:72:THR:H	1.87	0.40
2:H:152:PHE:CE2	2:H:153:PRO:HB3	2.56	0.40
2:H:149:LYS:HD2	2:H:183:SER:OG	2.21	0.40
3:L:183:THR:HG22	3:L:185:GLU:N	2.36	0.40
3:L:1:SER:HB3	3:L:25:ASN:O	2.21	0.40
1:D:193:LEU:HA	1:D:193:LEU:HD12	1.84	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:125:ASP:OD2	2:H:74:LYS:O[1_655]	2.19	0.01

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	D	221/275 (80%)	194 (88%)	27 (12%)	0	100	100
2	H	215/224 (96%)	202 (94%)	13 (6%)	0	100	100
3	L	210/216 (97%)	195 (93%)	15 (7%)	0	100	100
All	All	646/715 (90%)	591 (92%)	55 (8%)	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	D	181/221 (82%)	181 (100%)	0	100	100
2	H	185/188 (98%)	185 (100%)	0	100	100
3	L	177/182 (97%)	177 (100%)	0	100	100
All	All	543/591 (92%)	543 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

15 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
4	EDO	L	304	-	3,3,3	0.43	0	2,2,2	0.33	0
4	EDO	H	304	-	3,3,3	0.48	0	2,2,2	0.11	0
4	EDO	H	303	-	3,3,3	0.50	0	2,2,2	0.26	0
4	EDO	L	303	-	3,3,3	0.52	0	2,2,2	0.19	0
6	P33	L	305	-	21,21,21	0.57	0	20,20,20	0.49	0
4	EDO	H	302	-	3,3,3	0.50	0	2,2,2	0.04	0
4	EDO	H	307	-	3,3,3	0.47	0	2,2,2	0.40	0
4	EDO	H	306	-	3,3,3	0.47	0	2,2,2	0.26	0
7	PG4	L	306	-	12,12,12	0.55	0	11,11,11	0.40	0
5	PEG	H	309	-	6,6,6	0.51	0	5,5,5	0.34	0
4	EDO	H	301	-	3,3,3	0.50	0	2,2,2	0.03	0
4	EDO	H	308	-	3,3,3	0.51	0	2,2,2	0.35	0
4	EDO	H	305	-	3,3,3	0.42	0	2,2,2	0.33	0
4	EDO	L	302	-	3,3,3	0.48	0	2,2,2	0.42	0
4	EDO	L	301	-	3,3,3	0.53	0	2,2,2	0.22	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	L	304	-	-	1/1/1/1	-
4	EDO	H	304	-	-	1/1/1/1	-
4	EDO	H	303	-	-	1/1/1/1	-
4	EDO	L	303	-	-	1/1/1/1	-
6	P33	L	305	-	-	12/19/19/19	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	H	302	-	-	1/1/1/1	-
4	EDO	H	307	-	-	1/1/1/1	-
4	EDO	H	306	-	-	0/1/1/1	-
7	PG4	L	306	-	-	4/10/10/10	-
5	PEG	H	309	-	-	4/4/4/4	-
4	EDO	H	301	-	-	1/1/1/1	-
4	EDO	H	308	-	-	1/1/1/1	-
4	EDO	H	305	-	-	1/1/1/1	-
4	EDO	L	302	-	-	0/1/1/1	-
4	EDO	L	301	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (29) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	L	305	P33	C18-C17-O16-C15
6	L	305	P33	O7-C8-C9-O10
6	L	305	P33	O19-C20-C21-O22
7	L	306	PG4	O4-C7-C8-O5
6	L	305	P33	O13-C14-C15-O16
4	H	304	EDO	O1-C1-C2-O2
4	L	303	EDO	O1-C1-C2-O2
4	H	301	EDO	O1-C1-C2-O2
6	L	305	P33	O10-C11-C12-O13
5	H	309	PEG	C4-C3-O2-C2
5	H	309	PEG	O2-C3-C4-O4
6	L	305	P33	O1-C2-C3-O4
6	L	305	P33	O16-C17-C18-O19
4	H	303	EDO	O1-C1-C2-O2
4	H	302	EDO	O1-C1-C2-O2
4	H	305	EDO	O1-C1-C2-O2
6	L	305	P33	C12-C11-O10-C9
6	L	305	P33	C8-C9-O10-C11
4	L	304	EDO	O1-C1-C2-O2
6	L	305	P33	C2-C3-O4-C5
7	L	306	PG4	O2-C3-C4-O3
7	L	306	PG4	O3-C5-C6-O4
5	H	309	PEG	C1-C2-O2-C3

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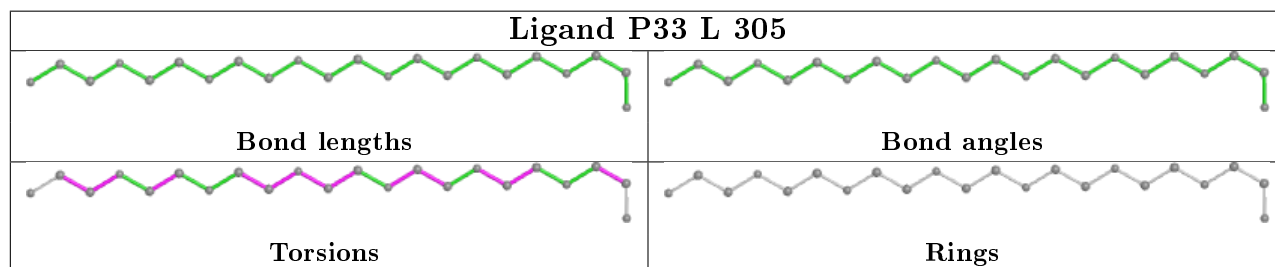
Mol	Chain	Res	Type	Atoms
4	H	307	EDO	O1-C1-C2-O2
6	L	305	P33	C15-C14-O13-C12
5	H	309	PEG	O1-C1-C2-O2
7	L	306	PG4	C4-C3-O2-C2
6	L	305	P33	O4-C5-C6-O7
4	H	308	EDO	O1-C1-C2-O2

There are no ring outliers.

6 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	H	304	EDO	1	0
4	L	303	EDO	1	0
6	L	305	P33	3	0
7	L	306	PG4	1	0
5	H	309	PEG	1	0
4	H	305	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

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	D	230/275 (83%)	0.57	16 (6%) 16 13	38, 63, 82, 94	3 (1%)
2	H	219/224 (97%)	-0.22	0 100 100	19, 31, 53, 74	0
3	L	212/216 (98%)	-0.23	1 (0%) 91 91	17, 30, 47, 62	0
All	All	661/715 (92%)	0.05	17 (2%) 56 52	17, 38, 76, 94	3 (0%)

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	202	ALA	6.6
1	D	220	TYR	4.2
1	D	200	ALA	3.6
1	D	184	TYR	3.2
1	D	124	PRO	2.8
1	D	28	LEU	2.7
3	L	1	SER	2.7
1	D	186	ARG	2.6
1	D	262	LYS	2.4
1	D	29	ASP	2.3
1	D	96	ILE	2.3
1	D	129	SER	2.2
1	D	128	ASP	2.2
1	D	95	THR	2.2
1	D	215	LEU	2.1
1	D	214	ILE	2.1
1	D	197	VAL	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](#)

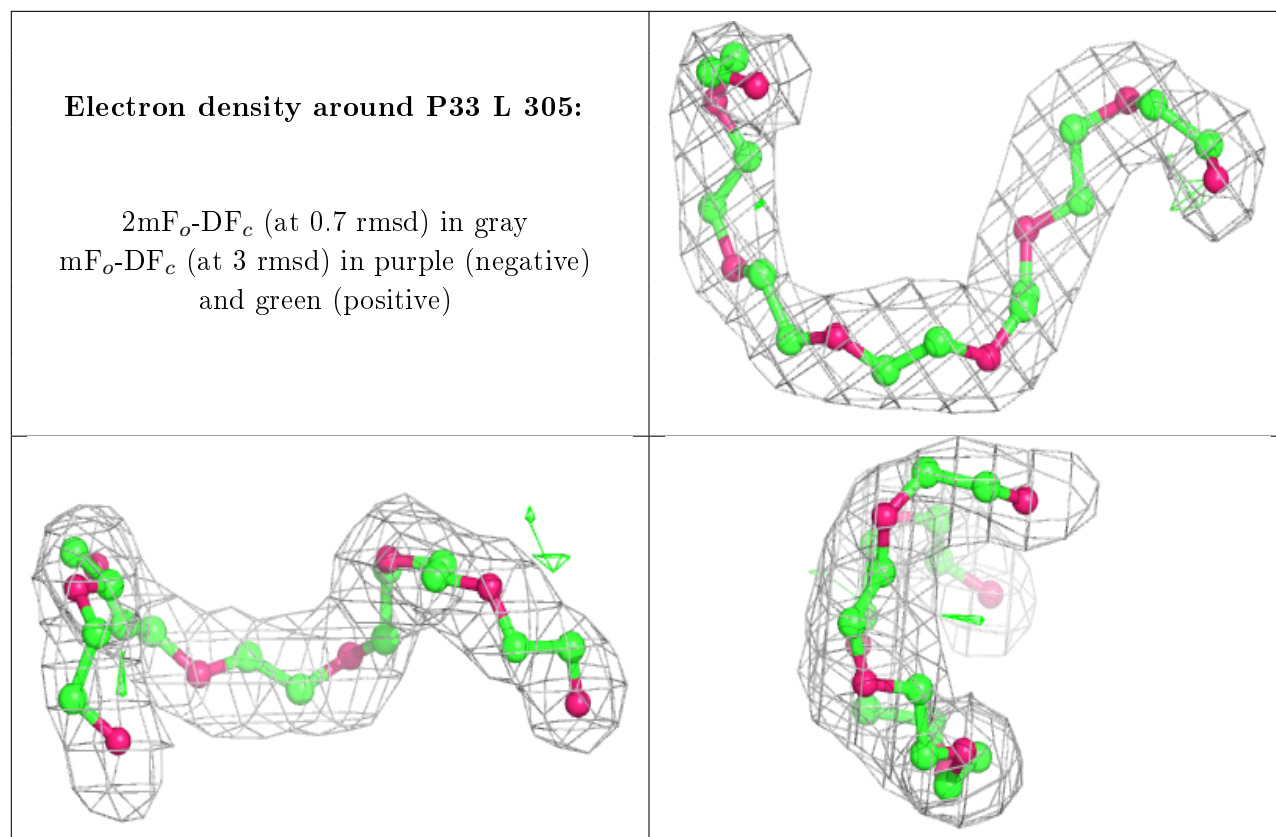
There are no carbohydrates in this entry.

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	H	306	4/4	0.83	0.25	43,50,50,53	0
4	EDO	L	303	4/4	0.85	0.20	43,44,45,46	0
4	EDO	L	301	4/4	0.85	0.23	39,45,49,53	0
5	PEG	H	309	7/7	0.86	0.26	43,48,53,54	0
4	EDO	H	304	4/4	0.87	0.16	42,43,49,53	0
4	EDO	L	302	4/4	0.89	0.16	31,35,42,43	0
7	PG4	L	306	13/13	0.90	0.18	35,41,60,63	0
4	EDO	L	304	4/4	0.92	0.17	26,34,35,40	0
4	EDO	H	301	4/4	0.93	0.19	37,39,40,40	0
4	EDO	H	308	4/4	0.93	0.21	29,31,35,37	0
4	EDO	H	307	4/4	0.93	0.12	37,39,39,52	0
6	P33	L	305	22/22	0.93	0.15	28,34,40,45	0
4	EDO	H	303	4/4	0.94	0.17	37,37,38,39	0
4	EDO	H	302	4/4	0.94	0.17	34,41,44,48	0
4	EDO	H	305	4/4	0.95	0.20	28,31,37,41	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.