Full wwPDB X-ray Structure Validation Report (i)

Aug 20, 2023 – 06:12 PM EDT

PDB ID	:	2NR9
Title	:	Crystal structure of GlpG, Rhomboid Peptidase from Haemophilus influenzae
Authors	:	Lemieux, M.J.; Fischer, S.J.; Cherney, M.M.; Bateman, K.S.; James, M.N.G.
Deposited on	:	2006-11-01
Resolution	:	2.20 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 (i) 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 (i)) were used in the production of this report:

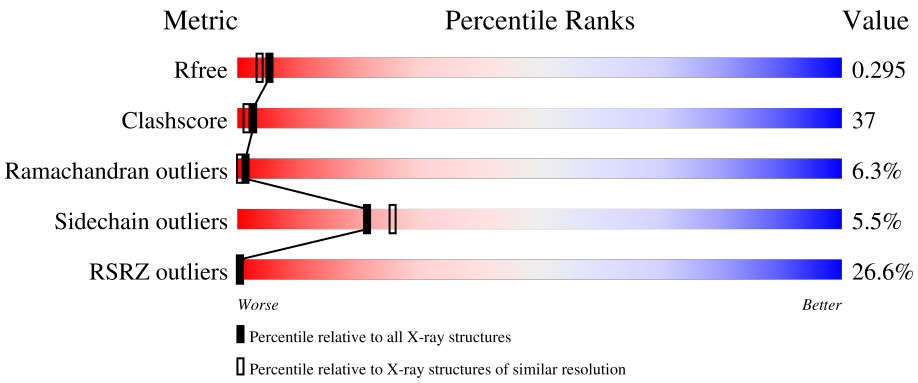
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	196	26% 54% 37% 6% • •

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
2	PA6	A	203	-	-	-	X

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 1754 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.

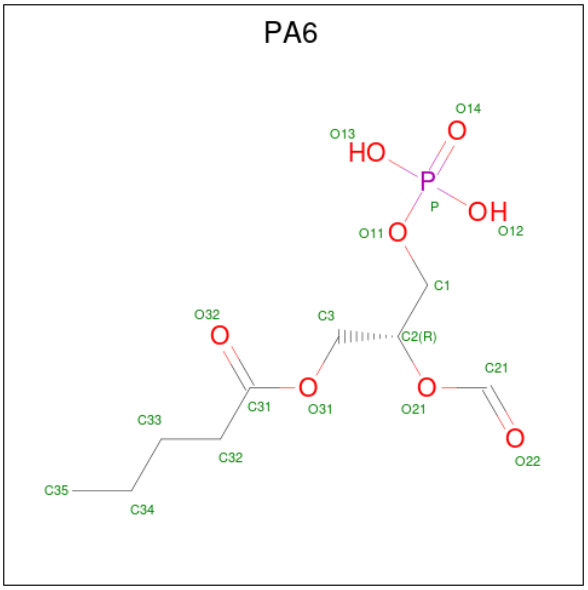
- Molecule 1 is a protein called Protein glpG homolog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	192	1554	1046	240	261	7	0	7	0

There are 6 discrepancies between the modelled and reference sequences:

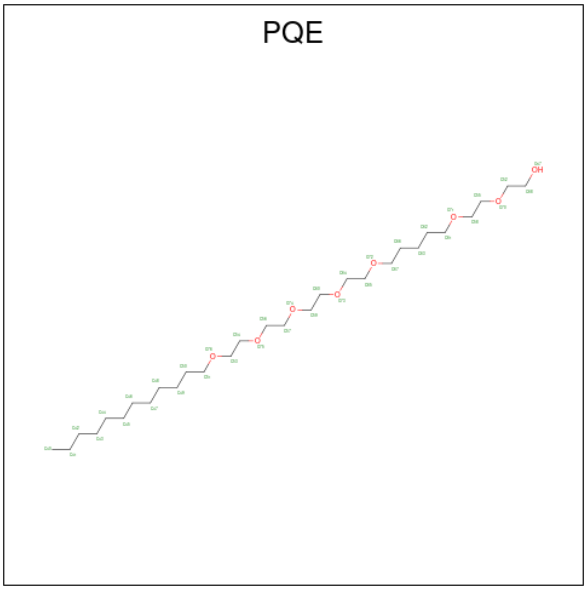
Chain	Residue	Modelled	Actual	Comment	Reference
A	2	GLU	LYS	engineered mutation	UNP P44783
A	24	ILE	LEU	engineered mutation	UNP P44783
A	193	LEU	-	cloning artifact	UNP P44783
A	194	VAL	-	cloning artifact	UNP P44783
A	195	PRO	-	cloning artifact	UNP P44783
A	196	ARG	-	cloning artifact	UNP P44783

- Molecule 2 is (R)-2-(FORMYLOXY)-3-(PHOSPHONOOXY)PROPYL PENTANOATE (three-letter code: PA6) (formula: $C_9H_{17}O_8P$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	P		
2	A	1	18	9	8	1	0	0
			Total	C	O	P		
2	A	1	18	9	8	1	0	0
			Total	C	O	P		
2	A	1	18	9	8	1	0	0

- Molecule 3 is 3,6,12,15,18,21,24-HEPTAOXAHEXATRIACONTAN-1-OL (three-letter code: PQE) (formula: $C_{29}H_{60}O_8$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	37	29	8	0	0
			Total	C	O		
3	A	1	47	36	11	0	1

- Molecule 4 is water.

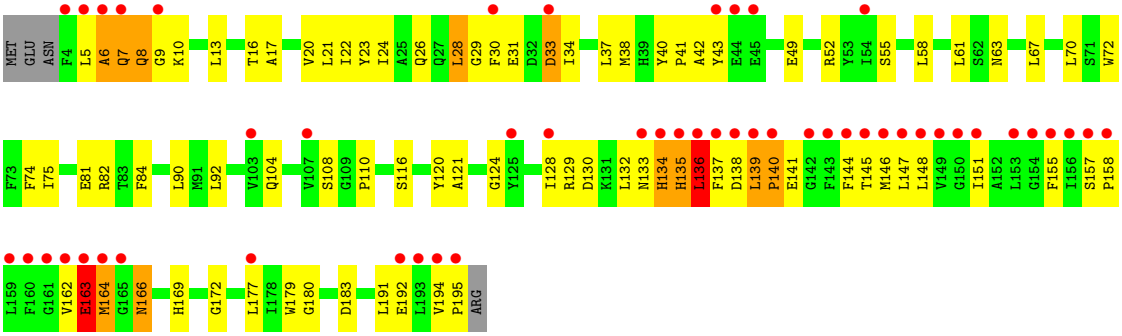
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	62	62	62	0	0

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: Protein glpG homolog

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	121.29Å 35.05Å 52.93Å 90.00° 104.02° 90.00°	Depositor
Resolution (Å)	25.00 – 2.20 24.98 – 2.20	Depositor EDS
% Data completeness (in resolution range)	95.0 (25.00-2.20) 95.0 (24.98-2.20)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.48 (at 2.19Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.233 , 0.295 0.237 , 0.295	Depositor DCC
R_{free} test set	513 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å^2)	43.4	Xtriage
Anisotropy	0.082	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 112.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	1754	wwPDB-VP
Average B, all atoms (Å^2)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.93% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: PA6, PQE

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	0.30	0/1628	0.48	0/2213

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	1554	0	1571	120	0
2	A	54	0	45	4	0
3	A	84	0	94	12	0
4	A	62	0	0	3	0
All	All	1754	0	1710	127	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 37.

All (127) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:128[A]:ILE:HD11	1:A:180:GLY:HA3	1.34	1.07
1:A:155:PHE:HB2	1:A:166:ASN:HB3	1.03	1.03
1:A:37:LEU:HD23	1:A:37:LEU:O	1.57	1.02
1:A:155:PHE:CB	1:A:166:ASN:HB3	1.87	1.02
1:A:61:LEU:HD12	1:A:163:GLU:HB2	1.42	1.01
1:A:155:PHE:HB2	1:A:166:ASN:CB	1.94	0.97
1:A:26:GLN:HB3	1:A:31:GLU:HG2	1.44	0.97
3:A:205[B]:PQE:H662	3:A:205[B]:PQE:H582	1.50	0.90
1:A:128[A]:ILE:HD12	1:A:129:ARG:N	1.87	0.88
1:A:191:LEU:O	1:A:194[A]:VAL:HG22	1.74	0.87
1:A:30:PHE:CE1	1:A:33:ASP:CB	2.60	0.85
1:A:61:LEU:HD12	1:A:163:GLU:CB	2.05	0.85
1:A:166:ASN:HD21	3:A:204:PQE:H482	1.42	0.85
1:A:30:PHE:CE1	1:A:33:ASP:HB3	2.12	0.84
1:A:128[A]:ILE:CD1	1:A:180:GLY:HA3	2.09	0.83
1:A:166:ASN:ND2	3:A:204:PQE:H491	1.95	0.82
1:A:194[B]:VAL:HG13	1:A:195:PRO:HD2	1.58	0.82
1:A:166:ASN:ND2	3:A:204:PQE:H482	2.00	0.77
1:A:194[B]:VAL:CG1	1:A:195:PRO:HD2	2.16	0.74
1:A:146:MET:O	1:A:148:LEU:N	2.20	0.73
1:A:8:GLN:NE2	1:A:8:GLN:H	1.87	0.72
1:A:49:GLU:OE1	1:A:52:ARG:NE	2.20	0.71
1:A:136:LEU:HD13	1:A:137:PHE:CD1	2.26	0.71
1:A:30:PHE:HE1	1:A:33:ASP:HB2	1.56	0.70
1:A:140:PRO:HG2	1:A:145:THR:OG1	1.93	0.69
1:A:146:MET:C	1:A:148:LEU:H	1.96	0.68
1:A:5:LEU:HD23	1:A:7:GLN:H	1.58	0.68
1:A:30:PHE:HE1	1:A:33:ASP:CB	2.04	0.68
1:A:116:SER:CB	1:A:162:VAL:HG11	2.25	0.67
1:A:30:PHE:CE1	1:A:33:ASP:HB2	2.28	0.66
1:A:26:GLN:CB	1:A:31:GLU:HG2	2.24	0.66
1:A:136:LEU:HD13	1:A:137:PHE:CE1	2.31	0.66
1:A:55:SER:HB3	2:A:201:PA6:H331	1.77	0.66
1:A:192:GLU:HB3	4:A:239:HOH:O	1.96	0.66
1:A:128[A]:ILE:HG23	1:A:177:LEU:CD2	2.26	0.65
1:A:37:LEU:HD23	1:A:37:LEU:C	2.18	0.64
1:A:30:PHE:HD1	1:A:33:ASP:H	1.47	0.63
1:A:37:LEU:O	1:A:37:LEU:CD2	2.42	0.62
1:A:166:ASN:HD22	3:A:204:PQE:H491	1.62	0.62
1:A:61:LEU:CD1	1:A:163:GLU:HB2	2.25	0.61
1:A:42:ALA:CB	1:A:110:PRO:HG3	2.31	0.61
1:A:166:ASN:ND2	3:A:204:PQE:C48	2.62	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:129:ARG:NH2	1:A:183:ASP:HB3	2.15	0.61
1:A:166:ASN:ND2	3:A:204:PQE:C49	2.63	0.60
1:A:128[A]:ILE:CG2	1:A:177:LEU:HD22	2.33	0.59
1:A:8:GLN:H	1:A:8:GLN:HE21	1.53	0.57
1:A:37:LEU:C	1:A:37:LEU:CD2	2.73	0.56
1:A:128[A]:ILE:HG23	1:A:177:LEU:HD22	1.86	0.56
1:A:23:TYR:OH	1:A:63:ASN:ND2	2.38	0.56
1:A:61:LEU:HD12	1:A:163:GLU:CG	2.35	0.56
1:A:5:LEU:CD2	1:A:6:ALA:N	2.68	0.55
1:A:5:LEU:C	1:A:7:GLN:H	2.11	0.54
1:A:72:TRP:CH2	1:A:144:PHE:HD2	2.26	0.54
1:A:128[A]:ILE:HD12	1:A:129:ARG:H	1.67	0.54
1:A:157:SER:HB3	4:A:226:HOH:O	2.08	0.54
2:A:203:PA6:O31	2:A:203:PA6:H21	2.09	0.53
1:A:9:GLY:HA3	1:A:81:GLU:OE1	2.09	0.53
1:A:61:LEU:HD12	1:A:163:GLU:HG3	1.90	0.53
1:A:5:LEU:HD23	1:A:7:GLN:N	2.24	0.53
1:A:116:SER:HB3	1:A:162:VAL:HG11	1.90	0.52
1:A:155:PHE:CG	1:A:166:ASN:HB3	2.42	0.52
1:A:162:VAL:HB	1:A:169:HIS:CE1	2.44	0.52
1:A:61:LEU:HB2	1:A:163:GLU:HG3	1.91	0.51
1:A:84:PHE:CE2	1:A:136:LEU:HD22	2.46	0.51
1:A:42:ALA:HB1	1:A:110:PRO:HG3	1.93	0.51
1:A:24:ILE:HG22	1:A:28:LEU:HD11	1.94	0.50
1:A:116:SER:OG	1:A:162:VAL:HG11	2.11	0.50
1:A:138:ASP:O	1:A:139:LEU:HB2	2.12	0.50
1:A:40:TYR:CD2	1:A:41:PRO:HD2	2.47	0.49
1:A:13[A]:LEU:HD23	1:A:74:PHE:HE1	1.77	0.49
1:A:5:LEU:HD11	1:A:10:LYS:HG2	1.94	0.49
1:A:9:GLY:HA3	1:A:81:GLU:CD	2.33	0.49
1:A:130:ASP:O	1:A:134[A]:HIS:HB2	2.13	0.49
2:A:203:PA6:O13	2:A:203:PA6:H341	2.13	0.49
1:A:16:THR:HG23	1:A:70:LEU:HD13	1.94	0.49
1:A:92[A]:LEU:HD23	1:A:179:TRP:CE3	2.47	0.49
1:A:136:LEU:CD1	1:A:137:PHE:CD1	2.96	0.48
1:A:146:MET:C	1:A:148:LEU:N	2.63	0.47
1:A:42:ALA:HB2	1:A:110:PRO:HG3	1.96	0.47
1:A:166:ASN:OD1	1:A:166:ASN:N	2.45	0.47
1:A:26:GLN:HB3	1:A:31:GLU:CG	2.32	0.47
1:A:121:ALA:HA	1:A:172:GLY:O	2.14	0.47
1:A:162:VAL:O	1:A:164:MET:N	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:205[A]:PQE:H661	3:A:205[A]:PQE:H611	1.44	0.47
1:A:130:ASP:O	1:A:134[B]:HIS:HB3	2.15	0.47
1:A:5:LEU:C	1:A:7:GLN:N	2.68	0.46
1:A:84:PHE:CZ	1:A:136:LEU:HD22	2.50	0.46
1:A:29:GLY:O	1:A:30:PHE:HB3	2.16	0.46
1:A:17:ALA:O	1:A:21:LEU:HG	2.16	0.46
1:A:42:ALA:HB2	1:A:110:PRO:CG	2.45	0.46
1:A:8:GLN:NE2	1:A:8:GLN:N	2.62	0.46
1:A:42:ALA:HB2	1:A:110:PRO:CB	2.45	0.46
1:A:135:HIS:C	1:A:137:PHE:H	2.19	0.45
1:A:162:VAL:O	1:A:163:GLU:C	2.54	0.45
1:A:40:TYR:CG	1:A:41:PRO:HD2	2.51	0.44
1:A:120:TYR:OH	1:A:151:ILE:CD1	2.65	0.43
2:A:203:PA6:O31	2:A:203:PA6:C21	2.66	0.43
1:A:128[A]:ILE:CG2	1:A:177:LEU:CD2	2.94	0.43
1:A:34:ILE:O	1:A:38:MET:CG	2.67	0.43
3:A:205[A]:PQE:C55	3:A:205[A]:PQE:H622	2.49	0.42
1:A:5:LEU:HD22	1:A:6:ALA:N	2.34	0.42
1:A:124:GLY:O	1:A:128[A]:ILE:HG13	2.20	0.42
1:A:135:HIS:O	1:A:137:PHE:N	2.53	0.42
1:A:63:ASN:H	3:A:205[A]:PQE:H552	1.84	0.42
1:A:104:GLN:HE21	1:A:108:SER:HB2	1.85	0.42
3:A:204:PQE:H671	3:A:204:PQE:H641	1.58	0.41
1:A:63:ASN:CG	3:A:205[A]:PQE:H551	2.40	0.41
1:A:20:VAL:O	1:A:24:ILE:HG12	2.21	0.41
1:A:82:ARG:NH2	4:A:222:HOH:O	2.52	0.41
1:A:128[A]:ILE:HG23	1:A:177:LEU:HD23	2.01	0.41
1:A:140:PRO:HB2	1:A:141:GLU:H	1.71	0.41
1:A:194[B]:VAL:CG1	1:A:195:PRO:CD	2.95	0.41
1:A:70:LEU:HD23	1:A:70:LEU:HA	1.87	0.40
1:A:5:LEU:O	1:A:7:GLN:N	2.55	0.40
1:A:22:ILE:O	1:A:26:GLN:HG3	2.22	0.40
1:A:135:HIS:C	1:A:137:PHE:N	2.75	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	197/196 (100%)	169 (86%)	15 (8%)	13 (7%)	1 0

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	147	LEU
1	A	163	GLU
1	A	140	PRO
1	A	133	ASN
1	A	134[A]	HIS
1	A	134[B]	HIS
1	A	135	HIS
1	A	136	LEU
1	A	158	PRO
1	A	164	MET
1	A	6	ALA
1	A	7	GLN
1	A	139	LEU

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	170/167 (102%)	161 (95%)	9 (5%)	22 27

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	GLN
1	A	28	LEU
1	A	33	ASP
1	A	43	TYR
1	A	58	LEU
1	A	90	LEU
1	A	136	LEU
1	A	163	GLU
1	A	166	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	GLN
1	A	63	ASN
1	A	69	ASN
1	A	104	GLN
1	A	133	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

6 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	PA6	A	203	-	17,17,17	1.96	3 (17%)	19,21,21	1.44	2 (10%)
2	PA6	A	202	-	17,17,17	1.96	3 (17%)	19,21,21	1.49	2 (10%)
2	PA6	A	201	-	17,17,17	1.97	3 (17%)	19,21,21	1.50	2 (10%)
3	PQE	A	205[A]	-	36,36,36	0.42	0	35,35,35	0.39	0
3	PQE	A	204	-	36,36,36	0.40	0	35,35,35	0.41	0
3	PQE	A	205[B]	-	36,36,36	0.41	0	35,35,35	0.40	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PA6	A	203	-	-	11/18/18/18	-
2	PA6	A	202	-	-	16/18/18/18	-
2	PA6	A	201	-	-	9/18/18/18	-
3	PQE	A	205[A]	-	-	19/34/34/34	-
3	PQE	A	204	-	-	21/34/34/34	-
3	PQE	A	205[B]	-	-	19/34/34/34	-

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	203	PA6	O21-C21	5.80	1.46	1.33
2	A	201	PA6	O21-C21	5.75	1.45	1.33
2	A	202	PA6	O21-C21	5.73	1.45	1.33
2	A	201	PA6	O31-C31	4.42	1.46	1.33
2	A	203	PA6	O31-C31	4.30	1.45	1.33
2	A	202	PA6	O31-C31	4.25	1.45	1.33
2	A	202	PA6	O21-C2	-3.22	1.43	1.46
2	A	201	PA6	O21-C2	-3.03	1.43	1.46
2	A	203	PA6	O21-C2	-2.94	1.43	1.46

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	202	PA6	O21-C21-O22	-4.39	119.98	125.57

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	201	PA6	O21-C21-O22	-4.29	120.11	125.57
2	A	203	PA6	O21-C21-O22	-4.21	120.21	125.57
2	A	201	PA6	O31-C31-C32	2.77	120.59	111.91
2	A	202	PA6	O31-C31-C32	2.67	120.28	111.91
2	A	203	PA6	O31-C31-C32	2.56	119.95	111.91

There are no chirality outliers.

All (95) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	201	PA6	C1-C2-O21-C21
2	A	201	PA6	O22-C21-O21-C2
2	A	202	PA6	C3-C2-O21-C21
2	A	202	PA6	C1-C2-O21-C21
2	A	202	PA6	O22-C21-O21-C2
2	A	202	PA6	C1-O11-P-O13
2	A	202	PA6	C1-O11-P-O12
2	A	203	PA6	C3-C2-O21-C21
2	A	203	PA6	C1-C2-O21-C21
2	A	203	PA6	O22-C21-O21-C2
2	A	203	PA6	C1-O11-P-O13
2	A	203	PA6	C1-O11-P-O12
2	A	201	PA6	O32-C31-O31-C3
2	A	201	PA6	C32-C31-O31-C3
3	A	205[B]	PQE	O70-C52-C68-O47
3	A	205[A]	PQE	C56-C57-O74-C59
3	A	205[B]	PQE	C56-C57-O74-C59
3	A	205[A]	PQE	C62-C61-O71-C58
3	A	204	PQE	O70-C55-C58-O71
3	A	205[A]	PQE	O76-C53-C54-O75
3	A	205[B]	PQE	O76-C53-C54-O75
3	A	204	PQE	C64-C65-O72-C67
3	A	204	PQE	O75-C56-C57-O74
3	A	205[B]	PQE	O70-C55-C58-O71
3	A	205[A]	PQE	O75-C56-C57-O74
3	A	205[B]	PQE	O75-C56-C57-O74
2	A	203	PA6	C31-C32-C33-C34
3	A	205[B]	PQE	O71-C61-C62-C63
3	A	205[A]	PQE	C61-C62-C63-C66
3	A	204	PQE	O74-C59-C60-O73
3	A	205[A]	PQE	O71-C61-C62-C63
3	A	204	PQE	C63-C66-C67-O72

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Mol	Chain	Res	Type	Atoms
3	A	205[A]	PQE	C46-C47-C48-C49
3	A	205[B]	PQE	C46-C47-C48-C49
2	A	202	PA6	C31-C32-C33-C34
3	A	205[A]	PQE	C42-C43-C44-C45
3	A	205[B]	PQE	C42-C43-C44-C45
2	A	201	PA6	C1-C2-C3-O31
3	A	204	PQE	C47-C48-C49-C50
3	A	204	PQE	C45-C46-C47-C48
3	A	204	PQE	C41-C42-C43-C44
3	A	205[A]	PQE	C48-C49-C50-C51
3	A	205[B]	PQE	C48-C49-C50-C51
3	A	204	PQE	C48-C49-C50-C51
2	A	202	PA6	C32-C31-O31-C3
2	A	202	PA6	C32-C33-C34-C35
3	A	205[B]	PQE	C62-C63-C66-C67
2	A	202	PA6	O32-C31-O31-C3
3	A	204	PQE	O70-C52-C68-O47
2	A	202	PA6	C1-C2-C3-O31
3	A	205[A]	PQE	C62-C63-C66-C67
2	A	202	PA6	C1-O11-P-O14
2	A	203	PA6	C1-O11-P-O14
3	A	205[A]	PQE	C65-C64-O73-C60
3	A	205[B]	PQE	C65-C64-O73-C60
3	A	204	PQE	C62-C63-C66-C67
3	A	205[A]	PQE	C41-C42-C43-C44
3	A	205[B]	PQE	C41-C42-C43-C44
3	A	204	PQE	C40-C41-C42-C43
2	A	202	PA6	O11-C1-C2-C3
3	A	205[A]	PQE	O70-C55-C58-O71
2	A	203	PA6	C32-C33-C34-C35
3	A	204	PQE	C49-C50-C51-O76
3	A	205[B]	PQE	C62-C61-O71-C58
2	A	202	PA6	O11-C1-C2-O21
3	A	205[A]	PQE	C40-C41-C42-C43
3	A	205[B]	PQE	C40-C41-C42-C43
2	A	201	PA6	O11-C1-C2-C3
3	A	204	PQE	C53-C54-O75-C56
2	A	201	PA6	O21-C2-C3-O31
2	A	202	PA6	O21-C2-C3-O31
3	A	204	PQE	C62-C61-O71-C58
3	A	205[A]	PQE	C55-C58-O71-C61
2	A	201	PA6	O11-C1-C2-O21

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Mol	Chain	Res	Type	Atoms
3	A	204	PQE	C44-C45-C46-C47
3	A	204	PQE	C66-C67-O72-C65
3	A	205[A]	PQE	C54-C53-O76-C51
3	A	205[B]	PQE	C54-C53-O76-C51
3	A	205[A]	PQE	C59-C60-O73-C64
3	A	205[B]	PQE	C59-C60-O73-C64
3	A	204	PQE	C56-C57-O74-C59
3	A	204	PQE	C55-C58-O71-C61
2	A	201	PA6	C32-C33-C34-C35
2	A	202	PA6	O31-C31-C32-C33
2	A	203	PA6	O11-C1-C2-O21
2	A	203	PA6	O31-C31-C32-C33
3	A	205[A]	PQE	O73-C64-C65-O72
3	A	205[B]	PQE	O73-C64-C65-O72
3	A	204	PQE	O73-C64-C65-O72
3	A	205[B]	PQE	C61-C62-C63-C66
2	A	203	PA6	O32-C31-C32-C33
3	A	204	PQE	O76-C53-C54-O75
2	A	202	PA6	O32-C31-C32-C33
3	A	205[A]	PQE	O74-C59-C60-O73
3	A	205[B]	PQE	O74-C59-C60-O73

There are no ring outliers.

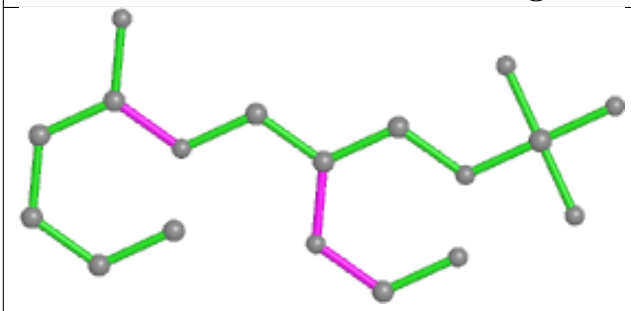
5 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	203	PA6	3	0
2	A	201	PA6	1	0
3	A	205[A]	PQE	4	0
3	A	204	PQE	7	0
3	A	205[B]	PQE	1	0

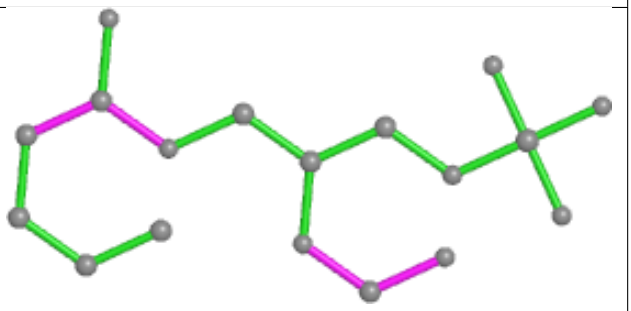
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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.

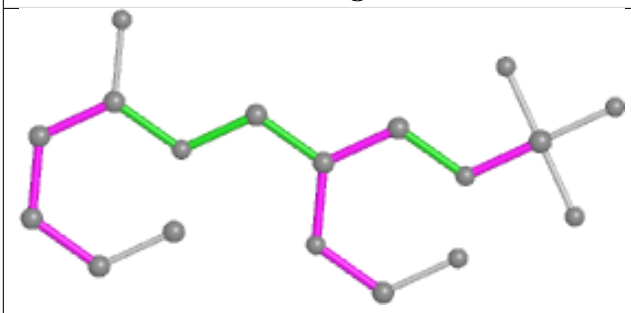
Ligand PA6 A 203



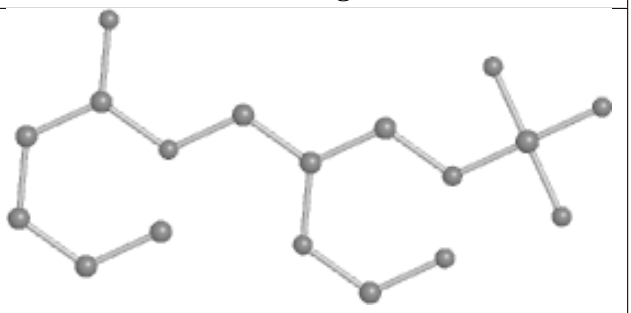
Bond lengths



Bond angles

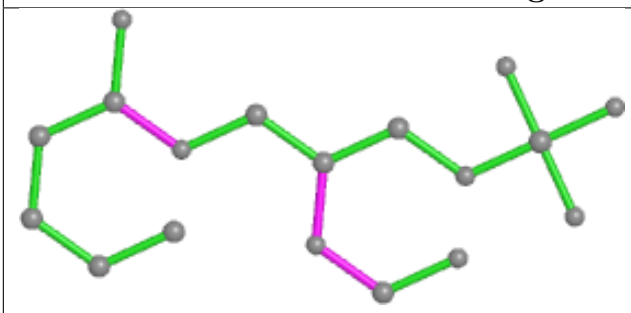


Torsions

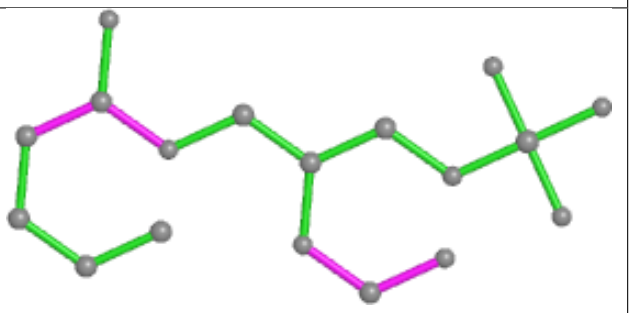


Rings

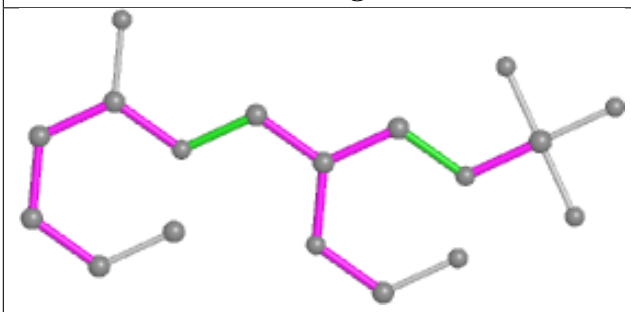
Ligand PA6 A 202



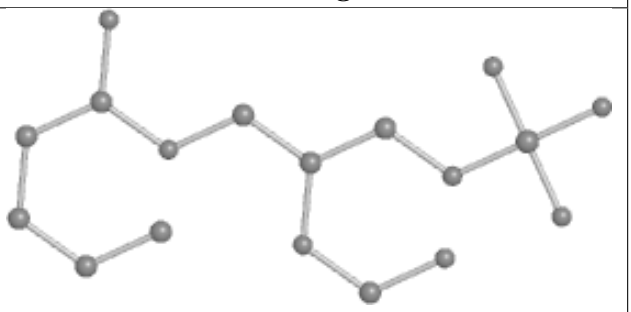
Bond lengths



Bond angles

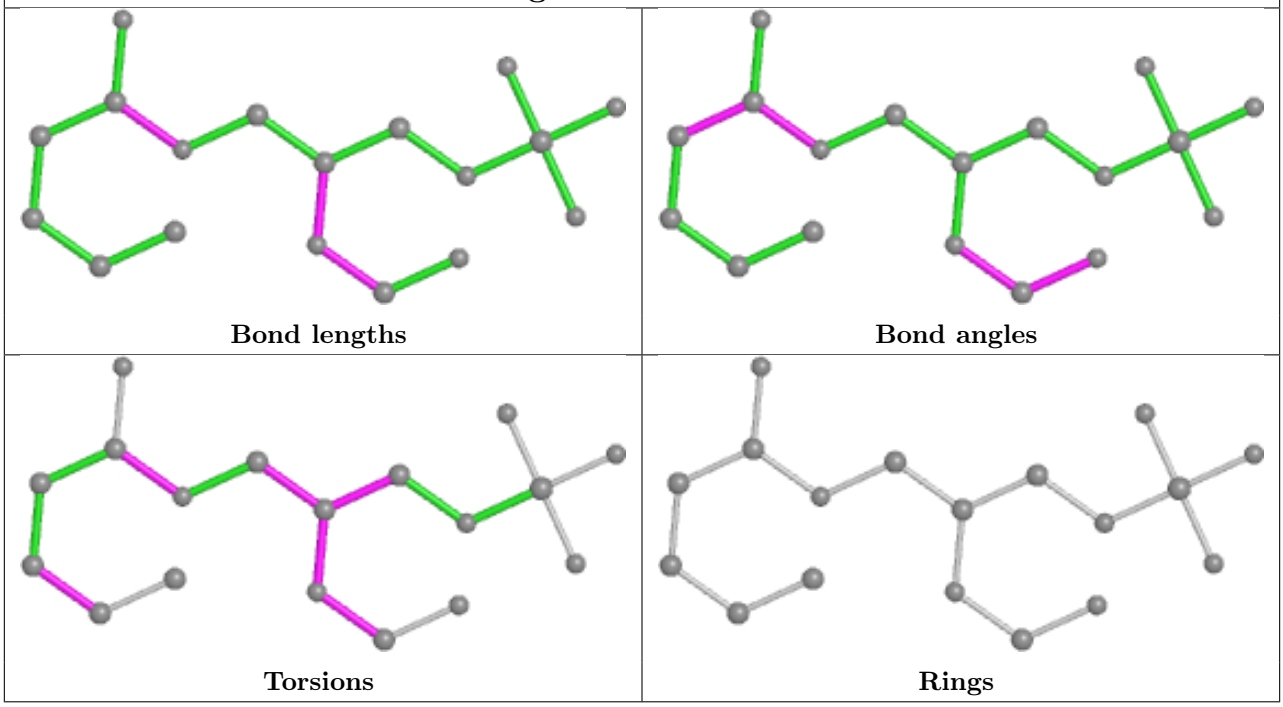


Torsions

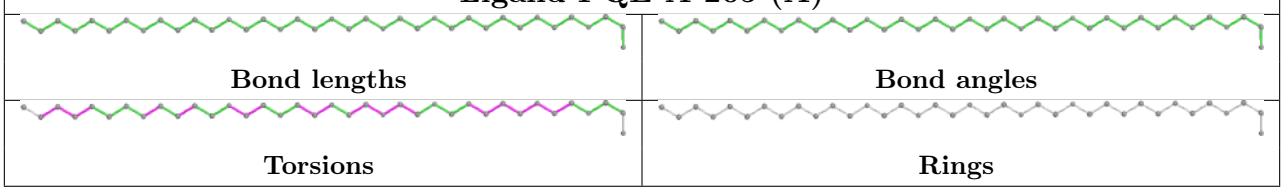


Rings

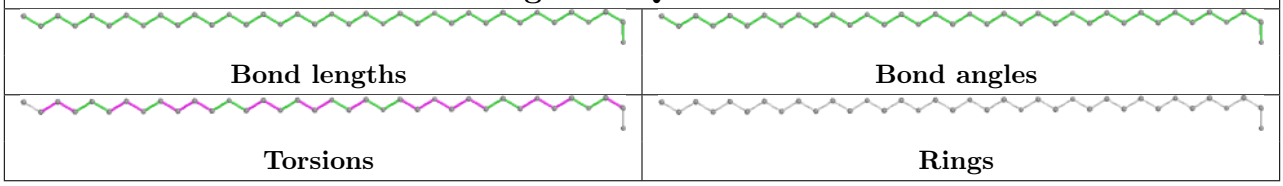
Ligand PA6 A 201



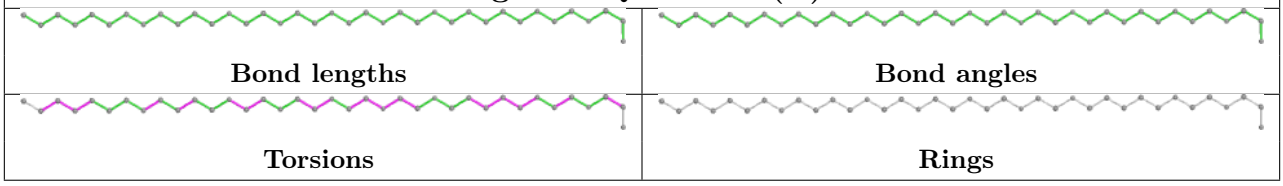
Ligand PQE A 205 (A)



Ligand PQE A 204



Ligand PQE A 205 (B)



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	192/196 (97%)	1.95	51 (26%) 0 0	41, 54, 125, 128	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	164	MET	17.7
1	A	150	GLY	16.6
1	A	139	LEU	15.4
1	A	154	GLY	11.4
1	A	162	VAL	11.0
1	A	140	PRO	10.8
1	A	143	PHE	10.0
1	A	161	GLY	9.4
1	A	160	PHE	9.3
1	A	4	PHE	8.5
1	A	156	ILE	8.1
1	A	155	PHE	7.7
1	A	163	GLU	7.4
1	A	147	LEU	7.3
1	A	145	THR	7.0
1	A	193	LEU	7.0
1	A	157	SER	6.9
1	A	30	PHE	6.6
1	A	194[A]	VAL	6.0
1	A	44	GLU	5.8
1	A	6	ALA	5.8
1	A	158	PRO	5.5
1	A	165	GLY	5.4
1	A	135	HIS	5.1
1	A	146	MET	5.0
1	A	144	PHE	5.0
1	A	159	LEU	4.9

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Mol	Chain	Res	Type	RSRZ
1	A	149	VAL	4.5
1	A	138	ASP	4.5
1	A	33	ASP	4.3
1	A	7	GLN	4.1
1	A	43	TYR	4.1
1	A	142	GLY	4.0
1	A	133	ASN	3.9
1	A	136	LEU	3.6
1	A	137	PHE	3.5
1	A	151	ILE	3.3
1	A	195	PRO	3.3
1	A	192	GLU	3.2
1	A	9	GLY	3.1
1	A	148	LEU	3.0
1	A	134[A]	HIS	2.9
1	A	5	LEU	2.9
1	A	177	LEU	2.8
1	A	125	TYR	2.4
1	A	153	LEU	2.3
1	A	54[A]	ILE	2.3
1	A	45	GLU	2.2
1	A	103	VAL	2.1
1	A	128[A]	ILE	2.1
1	A	107	VAL	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)

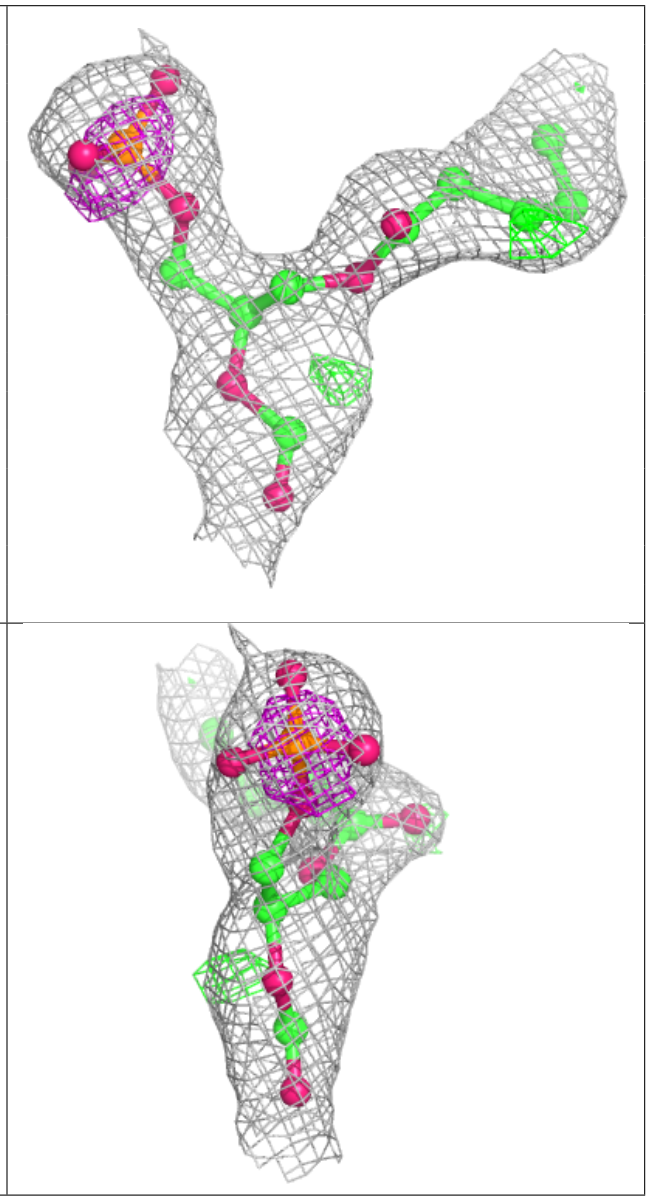
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	PA6	A	202	18/18	0.56	0.31	100,103,105,105	0
3	PQE	A	205[A]	37/37	0.60	0.35	57,72,85,85	10
3	PQE	A	205[B]	37/37	0.60	0.35	61,72,85,85	10
2	PA6	A	203	18/18	0.64	0.56	126,126,127,127	0
3	PQE	A	204	37/37	0.71	0.29	73,77,91,91	0
2	PA6	A	201	18/18	0.79	0.27	94,98,99,99	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.

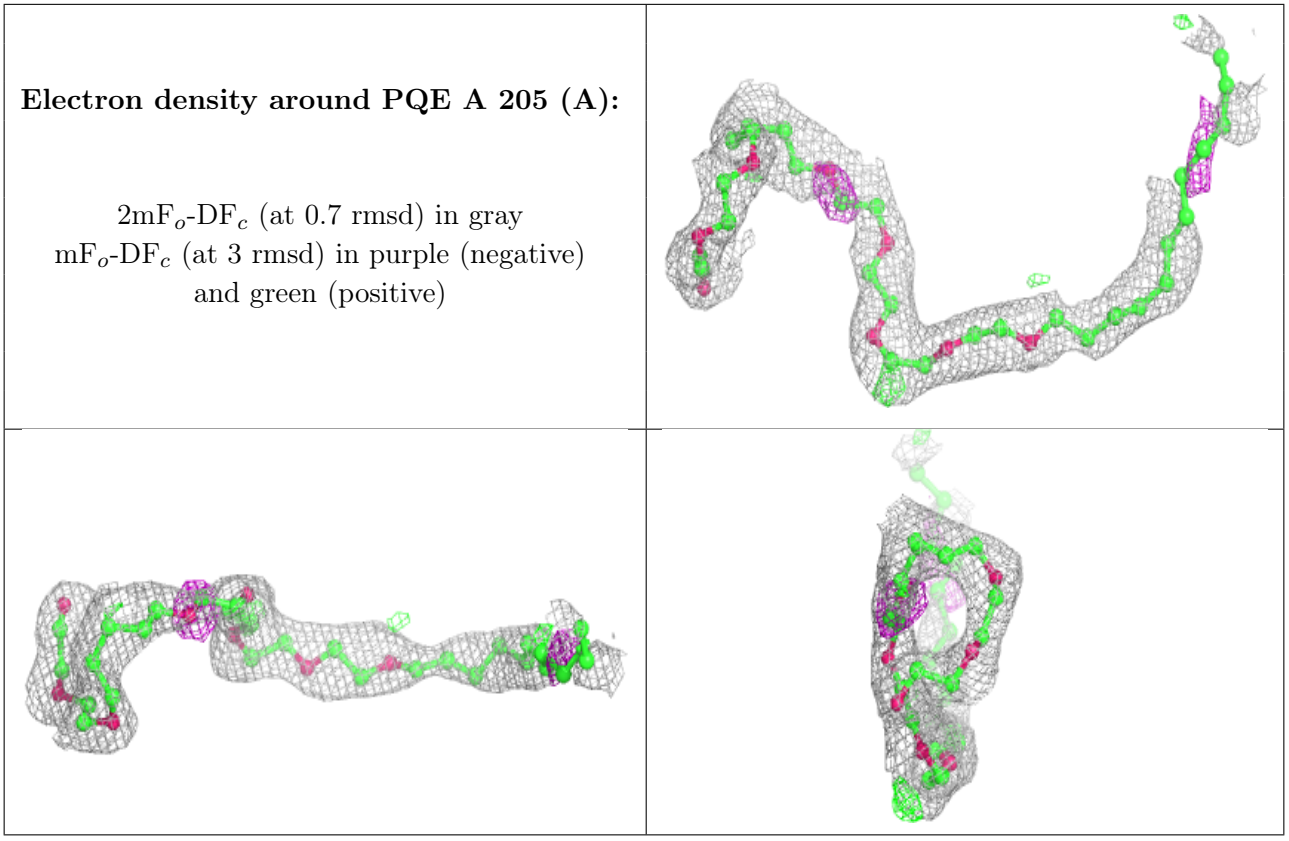
Electron density around PA6 A 202:

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 PQE A 205 (A):

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



Electron density around PQE A 205 (B):

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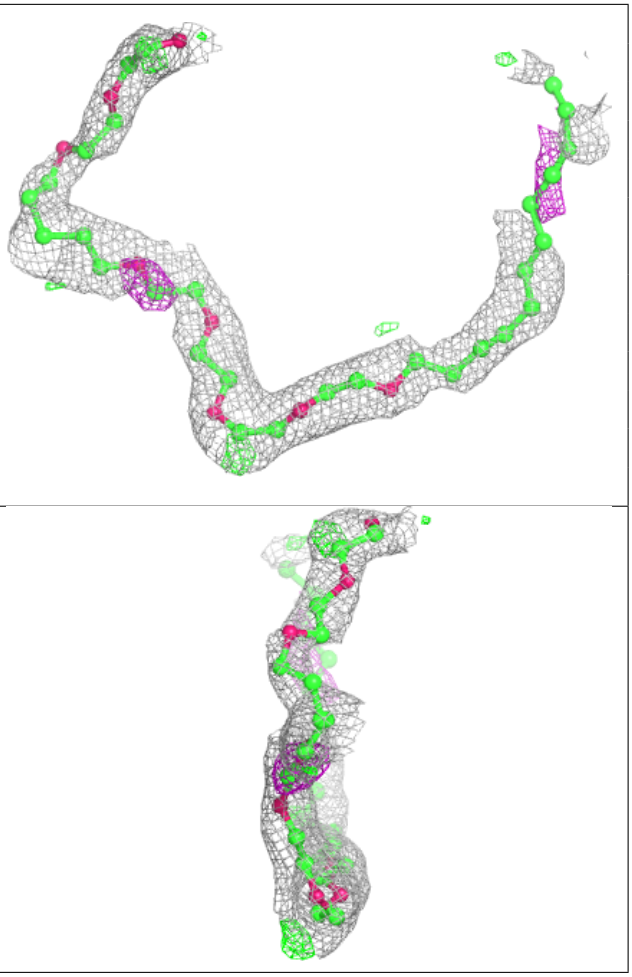
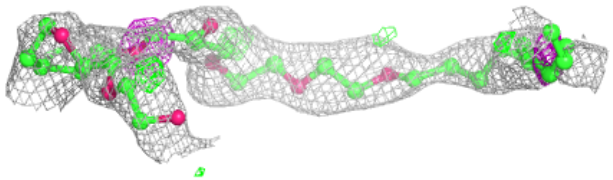
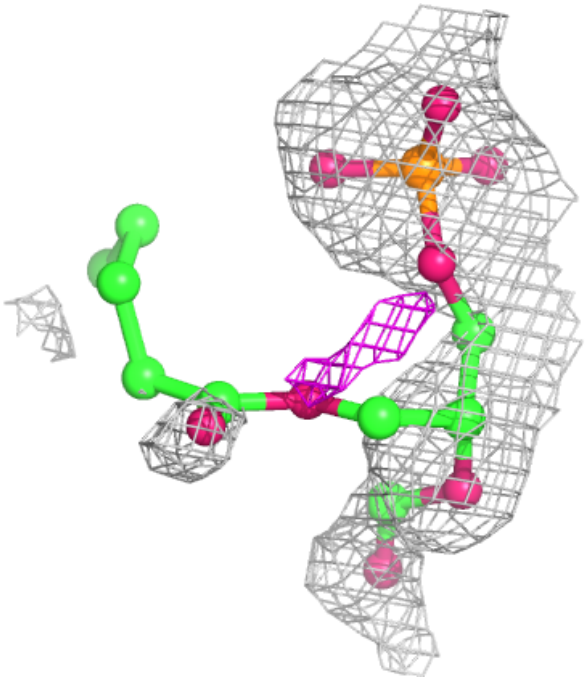
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

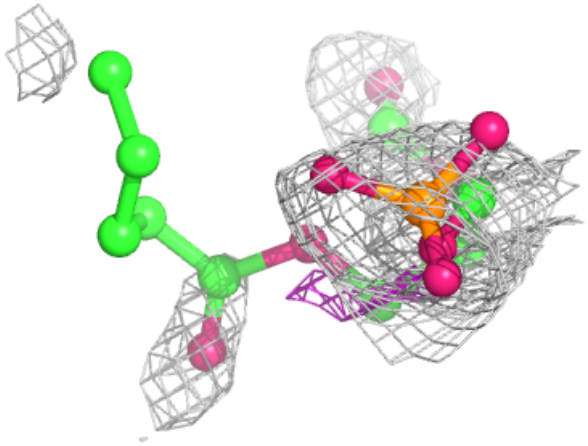


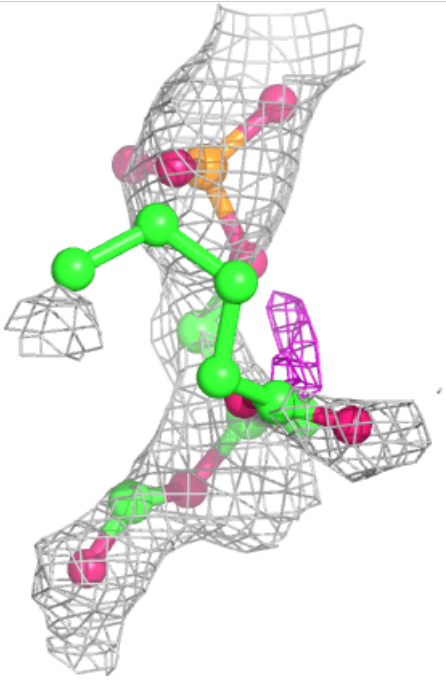


Electron density around PA6 A 203:

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

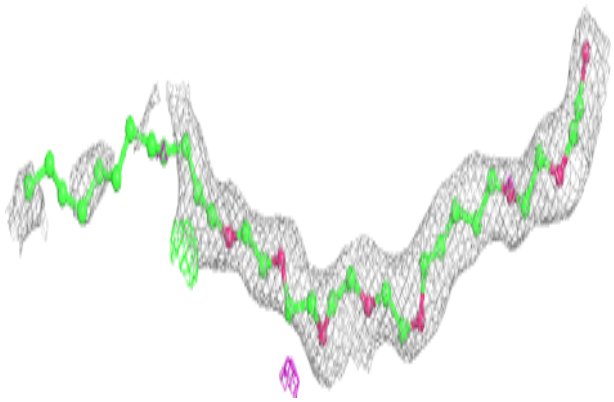


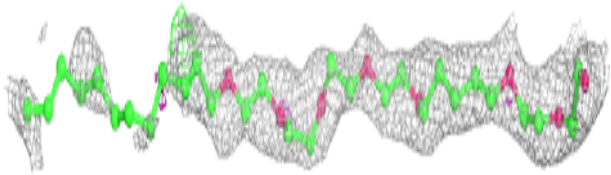


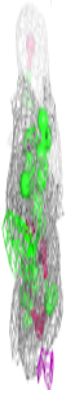


Electron density around PQE A 204:

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

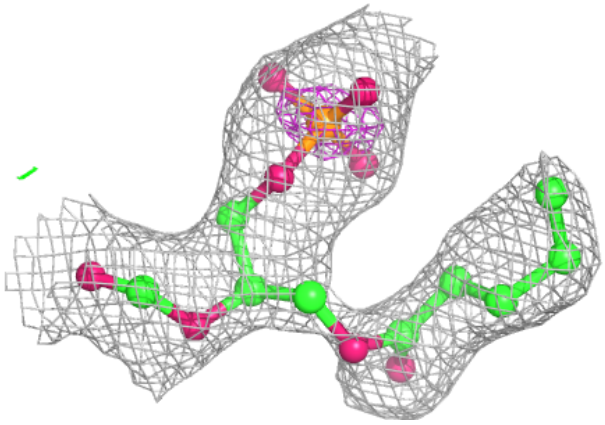


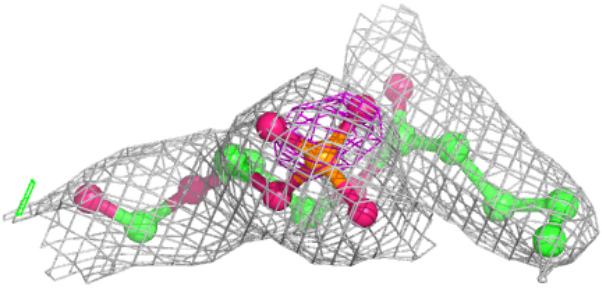


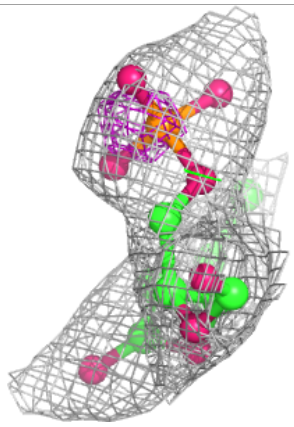


Electron density around PA6 A 201:

$2mF_o$-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.