Full wwPDB X-ray Structure Validation Report (i)

Jan 31, 2016 – 08:22 PM GMT

PDB ID	:	1K24
Title	:	Crystal Structure of the OpcA Outer Membrane Adhesin/Invasin from Neisseria meningitidis
Authors	:	Prince, S.M.; Achtman, M.; Derrick, J.P.
Deposited on	:	2001-09-26
Resolution	:	2.03 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

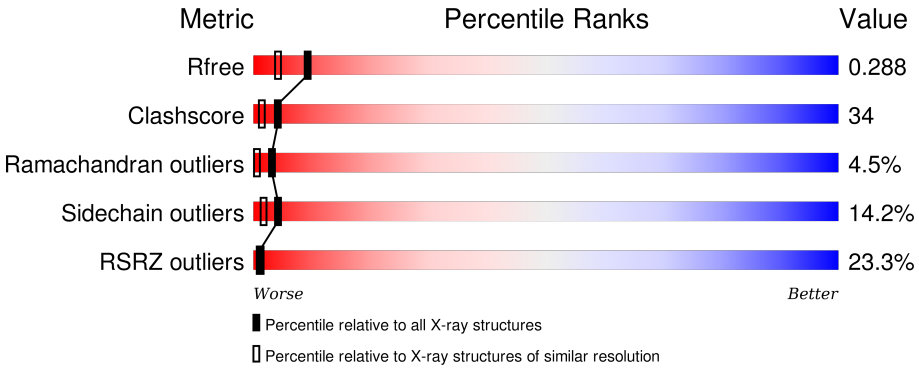
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 2.03 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}	91344	7858 (2.04-2.00)
Clashscore	102246	9060 (2.04-2.00)
Ramachandran outliers	100387	8952 (2.04-2.00)
Sidechain outliers	100360	8951 (2.04-2.00)
RSRZ outliers	91569	7873 (2.04-2.00)

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. 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	253	23% 61% 26% 9%

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
3	1PE	A	302	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2131 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.

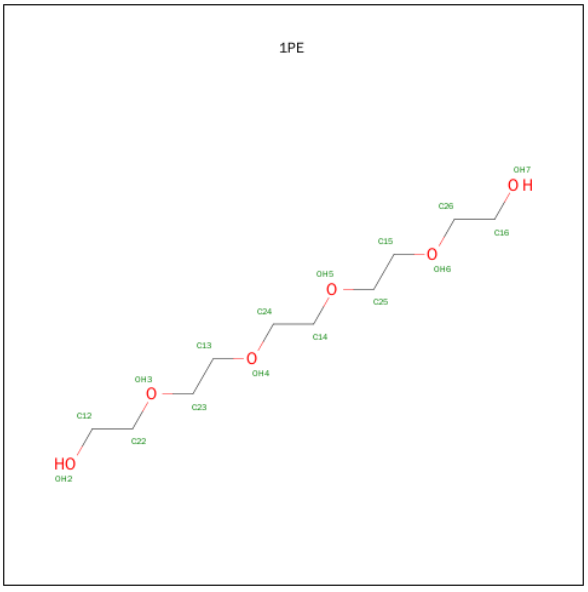
- Molecule 1 is a protein called outer membrane protein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	249	Total	C	N	O	0	0	0
			1952	1232	347	373			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	3	Total	Zn	0	0
			3	3		

- Molecule 3 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: $C_{10}H_{22}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			16	10	6		
3	A	1	Total	C	O	0	0
			16	10	6		

- Molecule 4 is water.

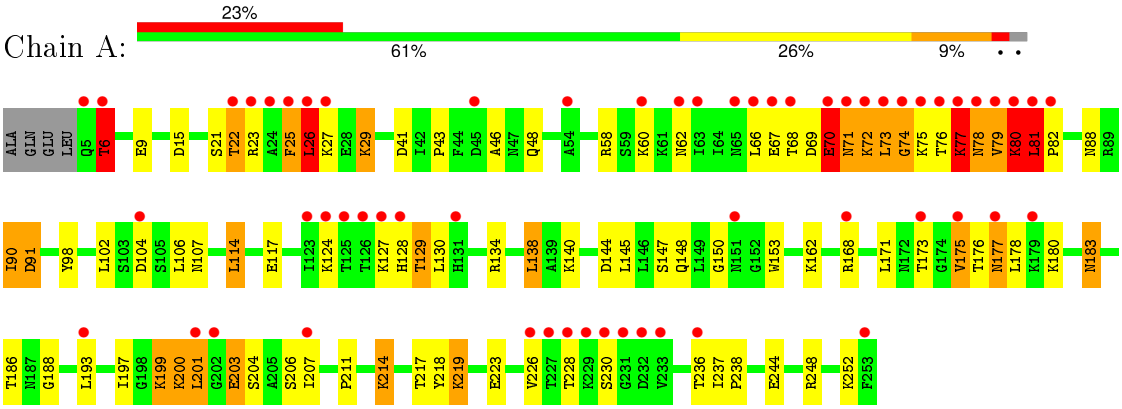
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	144	Total	O	0	0
			144	144		

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 errors 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: outer membrane protein

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	96.86Å 46.35Å 73.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.50 – 2.03 36.40 – 2.03	Depositor EDS
% Data completeness (in resolution range)	98.5 (36.50-2.03) 98.5 (36.40-2.03)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) >$ [1]	2.00 (at 2.03Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.235 , 0.274 0.254 , 0.288	Depositor DCC
R_{free} test set	1093 reflections (5.27%)	DCC
Wilson B-factor (Å^2)	38.2	Xtriage
Anisotropy	0.369	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 71.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Outliers	2 of 21847 reflections (0.009%)	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	2131	wwPDB-VP
Average B, all atoms (Å^2)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.08% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, 1PE

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	0.89	0/1990	0.98	8/2680 (0.3%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	81	LEU	N-CA-C	-10.44	82.81	111.00
1	A	144	ASP	CB-CG-OD2	6.34	124.00	118.30
1	A	104	ASP	CB-CG-OD2	6.23	123.91	118.30
1	A	80	LYS	N-CA-C	-6.04	94.69	111.00
1	A	6	THR	N-CA-C	-5.78	95.40	111.00
1	A	193	LEU	CA-CB-CG	5.61	128.19	115.30
1	A	138	LEU	CA-CB-CG	5.46	127.87	115.30
1	A	91	ASP	CB-CG-OD2	5.26	123.03	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1952	0	1961	134	1
2	A	3	0	0	0	0
3	A	32	0	44	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	144	0	0	9	1
All	All	2131	0	2005	134	2

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 34.

All (134) 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:168:ARG:HD3	1:A:183:ASN:HD21	1.15	1.11
1:A:72:LYS:HE2	1:A:81:LEU:HD11	1.29	1.09
1:A:173:THR:HG22	1:A:178:LEU:HD13	1.08	1.07
1:A:70:GLU:OE2	1:A:228:THR:HG23	1.53	1.07
1:A:69:ASP:C	1:A:71:ASN:H	1.55	1.05
1:A:173:THR:HG22	1:A:178:LEU:CD1	1.91	1.01
1:A:80:LYS:HD2	1:A:82:PRO:HG3	1.45	0.98
1:A:168:ARG:HD3	1:A:183:ASN:ND2	1.79	0.97
1:A:168:ARG:NH2	4:A:545:HOH:O	1.98	0.93
1:A:173:THR:CG2	1:A:178:LEU:HD13	1.98	0.93
1:A:80:LYS:HB3	1:A:81:LEU:HA	1.48	0.92
1:A:72:LYS:HE2	1:A:81:LEU:CD1	1.99	0.92
1:A:186:THR:HG22	1:A:186:THR:O	1.65	0.92
1:A:176:THR:O	1:A:176:THR:HG23	1.67	0.91
1:A:68:THR:HG22	1:A:73:LEU:HB2	1.50	0.90
1:A:80:LYS:HD2	1:A:82:PRO:CG	2.01	0.90
1:A:80:LYS:HD2	1:A:82:PRO:CD	2.02	0.88
1:A:80:LYS:HD2	1:A:82:PRO:HD3	1.54	0.88
1:A:176:THR:O	1:A:178:LEU:HD12	1.75	0.86
1:A:140:LYS:NZ	4:A:493:HOH:O	1.75	0.84
1:A:117:GLU:OE2	1:A:162:LYS:NZ	2.10	0.84
1:A:69:ASP:C	1:A:71:ASN:N	2.32	0.82
1:A:69:ASP:O	1:A:71:ASN:N	2.13	0.81
1:A:128:HIS:CD2	1:A:176:THR:OG1	2.35	0.80
1:A:134:ARG:NH2	1:A:186:THR:HG21	1.98	0.79
1:A:248:ARG:NH2	4:A:494:HOH:O	2.06	0.78
1:A:102:LEU:HB2	1:A:106:LEU:HD12	1.67	0.75
1:A:70:GLU:HA	1:A:176:THR:HG23	1.70	0.74
1:A:70:GLU:OE2	1:A:228:THR:CG2	2.33	0.73
1:A:90:ILE:HD12	1:A:91:ASP:N	2.03	0.73
1:A:78:ASN:O	1:A:79:VAL:HB	1.89	0.73
1:A:26:LEU:H	1:A:26:LEU:HD13	1.54	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:148:GLN:OE1	4:A:492:HOH:O	2.07	0.72
1:A:76:THR:O	1:A:77:LYS:HD2	1.87	0.72
1:A:73:LEU:O	1:A:75:LYS:N	2.23	0.71
1:A:80:LYS:CD	1:A:82:PRO:HG3	2.20	0.71
1:A:70:GLU:HA	1:A:178:LEU:HD11	1.72	0.70
1:A:80:LYS:HB3	1:A:81:LEU:CA	2.21	0.70
1:A:80:LYS:CD	1:A:82:PRO:HD3	2.21	0.70
1:A:173:THR:CG2	1:A:178:LEU:CD1	2.65	0.69
1:A:244:GLU:OE2	4:A:536:HOH:O	2.11	0.69
1:A:176:THR:O	1:A:176:THR:CG2	2.40	0.68
1:A:173:THR:HG23	1:A:176:THR:CG2	2.24	0.67
1:A:214:LYS:HE3	4:A:538:HOH:O	1.93	0.67
1:A:70:GLU:HB3	1:A:178:LEU:HD11	1.75	0.67
1:A:128:HIS:NE2	1:A:176:THR:OG1	2.28	0.67
1:A:197:ILE:HG21	3:A:301:1PE:OH7	1.95	0.67
1:A:134:ARG:HH22	1:A:186:THR:HG21	1.59	0.66
1:A:66:LEU:HD22	1:A:80:LYS:HE2	1.79	0.65
1:A:173:THR:CG2	1:A:176:THR:HG22	2.26	0.65
1:A:199:LYS:O	1:A:201:LEU:HD23	1.97	0.64
1:A:153:TRP:CD2	1:A:199:LYS:HG2	2.31	0.64
1:A:6:THR:HG23	1:A:6:THR:O	1.97	0.64
1:A:25:PHE:O	1:A:27:LYS:N	2.31	0.63
1:A:173:THR:HG23	1:A:176:THR:HG22	1.81	0.62
1:A:58:ARG:HD3	1:A:88:ASN:OD1	2.00	0.62
1:A:106:LEU:C	1:A:106:LEU:HD13	2.20	0.62
1:A:106:LEU:HD11	1:A:145:LEU:HD22	1.83	0.61
1:A:70:GLU:CA	1:A:178:LEU:HD11	2.30	0.61
1:A:70:GLU:HA	1:A:176:THR:CG2	2.29	0.61
1:A:219:LYS:NZ	4:A:445:HOH:O	2.34	0.60
1:A:228:THR:HG22	1:A:230:SER:H	1.66	0.60
1:A:21:SER:OG	1:A:22:THR:N	2.34	0.60
1:A:153:TRP:CE3	3:A:301:1PE:H261	2.36	0.60
1:A:80:LYS:CG	1:A:82:PRO:HD3	2.31	0.60
1:A:69:ASP:C	1:A:70:GLU:HG2	2.21	0.60
1:A:186:THR:HG23	1:A:219:LYS:O	2.01	0.59
1:A:168:ARG:CD	1:A:183:ASN:ND2	2.62	0.59
1:A:71:ASN:ND2	1:A:130:LEU:HD12	2.18	0.59
1:A:186:THR:HG22	1:A:218:TYR:HB3	1.84	0.59
1:A:70:GLU:HB3	1:A:178:LEU:CD1	2.33	0.59
1:A:176:THR:HG23	1:A:178:LEU:CD1	2.33	0.58
1:A:71:ASN:HD22	1:A:130:LEU:HD12	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:129:THR:O	1:A:129:THR:OG1	2.18	0.58
1:A:106:LEU:HD23	1:A:147:SER:HB2	1.85	0.57
1:A:206:SER:HB2	1:A:252:LYS:HB3	1.85	0.56
1:A:173:THR:CG2	1:A:176:THR:CG2	2.83	0.56
1:A:186:THR:CG2	1:A:186:THR:O	2.41	0.56
1:A:70:GLU:CB	1:A:178:LEU:HD11	2.35	0.55
1:A:106:LEU:HD13	1:A:107:ASN:N	2.21	0.55
1:A:58:ARG:CD	1:A:88:ASN:OD1	2.55	0.54
1:A:128:HIS:CE1	1:A:176:THR:HA	2.42	0.54
1:A:197:ILE:HG21	3:A:301:1PE:H262	1.88	0.54
1:A:102:LEU:HD12	1:A:106:LEU:CD1	2.37	0.54
1:A:6:THR:HG21	1:A:46:ALA:CB	2.38	0.54
1:A:186:THR:CG2	1:A:218:TYR:HB3	2.38	0.53
1:A:153:TRP:CZ3	3:A:301:1PE:H261	2.44	0.52
1:A:73:LEU:HD22	1:A:74:GLY:H	1.75	0.51
1:A:168:ARG:NH1	4:A:519:HOH:O	2.42	0.51
1:A:73:LEU:HD13	1:A:74:GLY:N	2.25	0.51
1:A:80:LYS:CE	1:A:82:PRO:HG3	2.40	0.51
1:A:9:GLU:HG3	1:A:41:ASP:HB2	1.92	0.50
1:A:176:THR:O	1:A:178:LEU:CD1	2.53	0.49
1:A:23:ARG:HE	1:A:27:LYS:HD3	1.77	0.49
1:A:102:LEU:HD12	1:A:106:LEU:HD12	1.95	0.48
1:A:124:LYS:HD3	1:A:129:THR:HB	1.94	0.48
1:A:173:THR:C	1:A:175:VAL:N	2.65	0.48
1:A:173:THR:HG22	1:A:176:THR:HG22	1.96	0.47
1:A:66:LEU:HD22	1:A:80:LYS:CE	2.44	0.47
1:A:173:THR:O	1:A:176:THR:HG22	2.14	0.47
1:A:70:GLU:HB3	1:A:178:LEU:CG	2.45	0.47
1:A:70:GLU:O	1:A:71:ASN:HB2	2.15	0.46
1:A:6:THR:HG21	1:A:46:ALA:HB1	1.98	0.46
1:A:203:GLU:O	1:A:204:SER:HB2	2.14	0.46
1:A:80:LYS:HD3	1:A:80:LYS:HA	1.40	0.46
1:A:188:GLY:HA3	1:A:217:THR:O	2.16	0.46
1:A:127:LYS:HB2	1:A:128:HIS:CD2	2.50	0.46
1:A:150:GLY:HA3	3:A:301:1PE:H132	1.98	0.46
1:A:73:LEU:HD13	1:A:74:GLY:H	1.80	0.45
1:A:173:THR:HG23	1:A:176:THR:HG21	1.98	0.45
1:A:72:LYS:HD2	1:A:72:LYS:HA	1.84	0.45
1:A:6:THR:O	1:A:43:PRO:HG2	2.17	0.44
1:A:219:LYS:HE2	1:A:219:LYS:HB2	1.77	0.43
1:A:201:LEU:CD2	1:A:207:ILE:HG22	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:81:LEU:HD22	1:A:81:LEU:N	2.34	0.43
1:A:197:ILE:CG2	3:A:301:1PE:H262	2.49	0.42
1:A:58:ARG:NH1	4:A:489:HOH:O	2.51	0.42
1:A:58:ARG:HG2	1:A:88:ASN:OD1	2.18	0.42
1:A:90:ILE:C	1:A:90:ILE:HD12	2.39	0.42
1:A:102:LEU:HD12	1:A:106:LEU:HD11	2.00	0.42
1:A:26:LEU:HD13	1:A:26:LEU:N	2.23	0.42
1:A:70:GLU:HB3	1:A:178:LEU:HG	2.01	0.42
1:A:68:THR:HA	1:A:73:LEU:HB2	2.02	0.42
1:A:67:GLU:O	1:A:68:THR:HG23	2.20	0.41
1:A:102:LEU:CB	1:A:106:LEU:HD12	2.44	0.41
1:A:29:LYS:HE3	1:A:29:LYS:HB3	1.84	0.41
1:A:200:LYS:HG2	1:A:206:SER:OG	2.20	0.41
1:A:68:THR:HA	1:A:73:LEU:CG	2.50	0.41
1:A:106:LEU:CD1	1:A:106:LEU:C	2.88	0.41
1:A:48:GLN:HG2	1:A:98:TYR:CD2	2.55	0.41
1:A:114:LEU:HA	1:A:114:LEU:HD22	1.85	0.41
1:A:237:ILE:HA	1:A:238:PRO:HD3	1.89	0.41
1:A:68:THR:CG2	1:A:73:LEU:HB2	2.35	0.40
1:A:68:THR:HA	1:A:73:LEU:HG	2.04	0.40

All (2) 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)
4:A:488:HOH:O	4:A:488:HOH:O[2_655]	1.93	0.27
1:A:177:ASN:OD1	1:A:223:GLU:OE2[3_546]	2.18	0.02

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	247/253 (98%)	224 (91%)	12 (5%)	11 (4%)	3 0

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	6	THR
1	A	26	LEU
1	A	71	ASN
1	A	74	GLY
1	A	79	VAL
1	A	177	ASN
1	A	70	GLU
1	A	72	LYS
1	A	77	LYS
1	A	80	LYS
1	A	203	GLU

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	212/215 (99%)	182 (86%)	30 (14%)	4 2

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	THR
1	A	15	ASP
1	A	22	THR
1	A	25	PHE
1	A	26	LEU
1	A	29	LYS
1	A	60	LYS
1	A	62	ASN
1	A	70	GLU
1	A	73	LEU

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Mol	Chain	Res	Type
1	A	77	LYS
1	A	78	ASN
1	A	80	LYS
1	A	81	LEU
1	A	90	ILE
1	A	114	LEU
1	A	129	THR
1	A	138	LEU
1	A	171	LEU
1	A	175	VAL
1	A	180	LYS
1	A	183	ASN
1	A	199	LYS
1	A	200	LYS
1	A	201	LEU
1	A	211	PRO
1	A	214	LYS
1	A	219	LYS
1	A	226	VAL
1	A	236	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	78	ASN
1	A	183	ASN
1	A	184	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 carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 3 are monoatomic - leaving 2 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	$\#\|Z\| > 2$
3	1PE	A	301	-	15,15,15	1.29	2 (13%)	14,14,14	1.74	5 (35%)
3	1PE	A	302	-	15,15,15	1.32	2 (13%)	14,14,14	1.78	6 (42%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	1PE	A	301	-	-	0/13/13/13	0/0/0/0
3	1PE	A	302	-	-	0/13/13/13	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	301	1PE	C25-C15	-3.18	1.32	1.48
3	A	302	1PE	C24-C14	-3.15	1.32	1.48
3	A	302	1PE	C25-C15	-3.13	1.32	1.48
3	A	301	1PE	C24-C14	-3.08	1.33	1.48

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	301	1PE	OH6-C15-C25	2.01	119.31	110.36
3	A	301	1PE	OH5-C14-C24	2.09	119.66	110.36
3	A	301	1PE	OH3-C22-C12	2.10	120.12	110.43
3	A	302	1PE	OH3-C22-C12	2.13	120.24	110.43
3	A	302	1PE	OH5-C25-C15	2.16	119.98	110.36
3	A	302	1PE	OH4-C13-C23	2.17	119.99	110.36
3	A	302	1PE	OH6-C15-C25	2.23	120.27	110.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	301	1PE	OH4-C24-C14	2.23	120.30	110.36
3	A	302	1PE	OH6-C26-C16	2.31	121.08	110.43
3	A	301	1PE	OH4-C13-C23	2.42	121.11	110.36
3	A	302	1PE	OH5-C14-C24	2.45	121.24	110.36

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	301	1PE	6	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

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, 95^{th} 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	249/253 (98%)	1.40	58 (23%) 1 1	29, 49, 187, 278	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	71	ASN	13.2
1	A	75	LYS	11.2
1	A	24	ALA	11.2
1	A	228	THR	10.7
1	A	25	PHE	10.1
1	A	73	LEU	9.7
1	A	79	VAL	8.9
1	A	63	ILE	8.7
1	A	76	THR	8.1
1	A	72	LYS	7.8
1	A	26	LEU	7.4
1	A	74	GLY	7.3
1	A	80	LYS	7.2
1	A	70	GLU	6.7
1	A	62	ASN	6.3
1	A	78	ASN	6.0
1	A	201	LEU	5.7
1	A	229	LYS	4.9
1	A	226	VAL	4.9
1	A	82	PRO	4.9
1	A	179	LYS	4.2
1	A	231	GLY	4.2
1	A	23	ARG	4.2
1	A	123	ILE	4.1
1	A	77	LYS	4.0
1	A	68	THR	4.0
1	A	232	ASP	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	60	LYS	3.7
1	A	202	GLY	3.7
1	A	66	LEU	3.5
1	A	81	LEU	3.4
1	A	5	GLN	3.3
1	A	22	THR	3.3
1	A	126	THR	3.3
1	A	175	VAL	3.2
1	A	6	THR	3.1
1	A	173	THR	3.1
1	A	207	ILE	3.0
1	A	65	ASN	3.0
1	A	67	GLU	3.0
1	A	45	ASP	3.0
1	A	253	PHE	2.6
1	A	227	THR	2.6
1	A	236	THR	2.5
1	A	27	LYS	2.5
1	A	193	LEU	2.4
1	A	177	ASN	2.4
1	A	124	LYS	2.4
1	A	151	ASN	2.4
1	A	230	SER	2.3
1	A	104	ASP	2.2
1	A	131	HIS	2.2
1	A	127	LYS	2.2
1	A	54	ALA	2.1
1	A	168	ARG	2.1
1	A	125	THR	2.1
1	A	128	HIS	2.1
1	A	233	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 carbohydrates in this entry.

6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} 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	LLDF	B-factors(Å^2)	Q<0.9
3	1PE	A	302	16/16	0.87	0.27	3.52	67,71,77,79	0
2	ZN	A	403	1/1	0.92	0.06	-1.69	77,77,77,77	0
3	1PE	A	301	16/16	0.73	0.39	-	80,82,88,89	0
2	ZN	A	401	1/1	0.99	0.07	-	37,37,37,37	0
2	ZN	A	402	1/1	1.00	0.10	-	32,32,32,32	1

6.5 Other polymers

There are no such residues in this entry.