



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 15, 2026 – 10:04 AM UTC

PDB ID : 1K24 / pdb_00001k24
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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

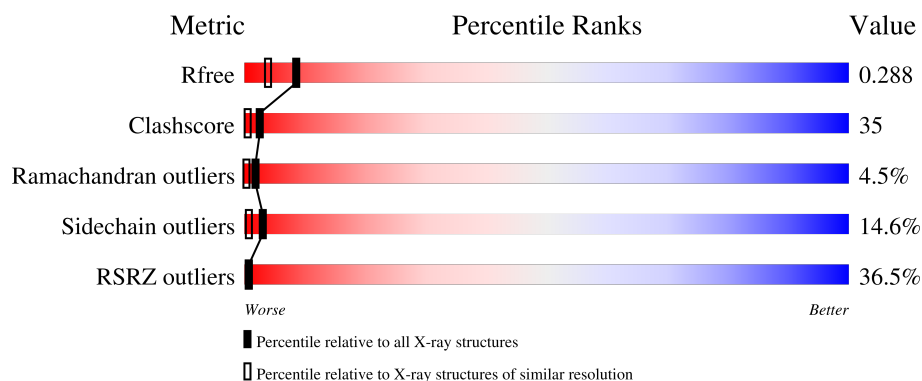
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.03 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}	180053	13299 (2.04-2.00)
Clashscore	190562	1022 (2.02-2.02)
Ramachandran outliers	187476	1014 (2.02-2.02)
Sidechain outliers	187428	1014 (2.02-2.02)
RSRZ outliers	180081	13314 (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 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	253	

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 [i](#)

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.

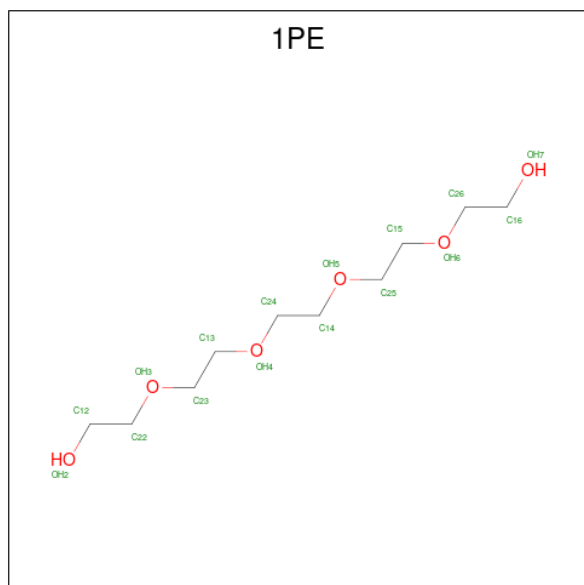
- Molecule 1 is a protein called outer membrane protein.

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 (CCD ID: ZN) (formula: Zn).

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

- Molecule 3 is PENTAETHYLENE GLYCOL (CCD ID: 1PE) (formula: C₁₀H₂₂O₆).



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		

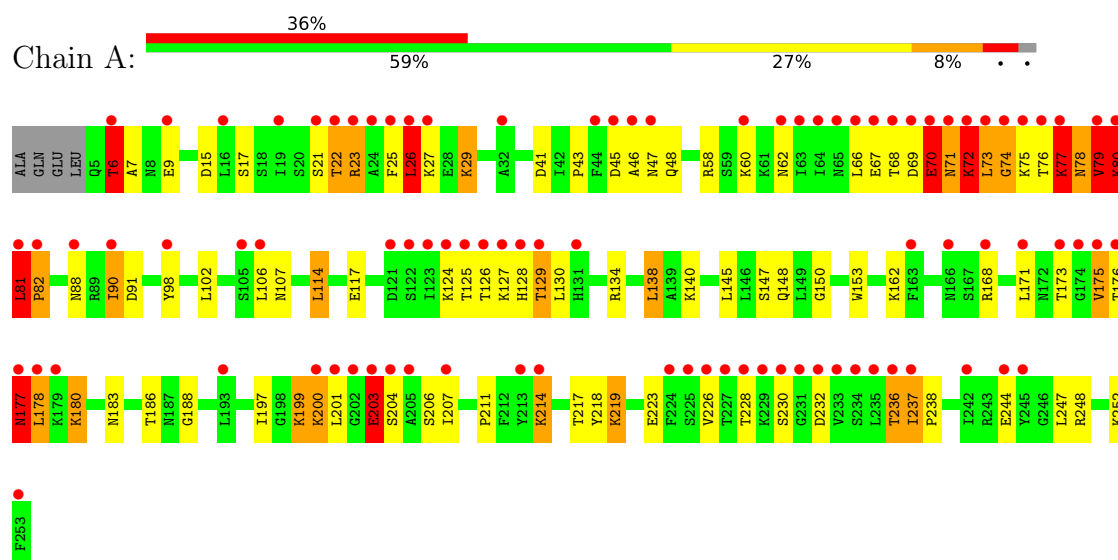
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	144	Total 144	O 144	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: outer membrane protein



4 Data and refinement statistics

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 36.50 – 2.03	Depositor EDS
% Data completeness (in resolution range)	98.5 (36.50-2.03) 98.4 (36.50-2.03)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ 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 (5.00%)	wwPDB-VP
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 , 58.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	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.*

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: 1PE, ZN

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	1.09	0/1990	1.20	18/2680 (0.7%)

There are no bond length outliers.

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	178	LEU	N-CA-C	-11.16	99.21	113.72
1	A	81	LEU	N-CA-C	-10.07	82.81	111.00
1	A	7	ALA	N-CA-C	9.30	123.10	110.55
1	A	232	ASP	N-CA-C	-8.78	97.53	110.52
1	A	80	LYS	N-CA-C	-7.56	94.69	110.80
1	A	6	THR	N-CA-C	-7.23	95.40	110.80
1	A	82	PRO	N-CA-C	6.88	122.47	111.26
1	A	203	GLU	N-CA-C	5.96	123.49	110.80
1	A	236	THR	CA-C-N	-5.83	118.39	122.59
1	A	236	THR	C-N-CA	-5.83	118.39	122.59
1	A	138	LEU	N-CA-C	5.63	117.73	109.24
1	A	17	SER	N-CA-C	5.60	117.69	109.24
1	A	45	ASP	N-CA-C	-5.59	105.23	113.61
1	A	80	LYS	CA-C-N	5.40	131.41	121.70
1	A	80	LYS	C-N-CA	5.40	131.41	121.70
1	A	47	ASN	N-CA-C	-5.22	99.69	110.80
1	A	79	VAL	N-CA-C	5.16	120.07	109.34
1	A	72	LYS	N-CA-C	-5.02	100.11	110.80

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	138	1
2	A	3	0	0	0	0
3	A	32	0	44	6	0
4	A	144	0	0	8	1
All	All	2131	0	2005	138	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 35.

All (138) 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:140:LYS:NZ	4:A:493:HOH:O	1.75	1.17
1:A:168:ARG:HD3	1:A:183:ASN:HD21	1.15	1.11
1:A:69:ASP:C	1:A:71:ASN:H	1.55	1.10
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: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:O	1:A:186:THR:HG22	1.65	0.92
1:A:176:THR:HG23	1:A:176:THR:O	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:69:ASP:C	1:A:71:ASN:N	2.32	0.86
1:A:176:THR:O	1:A:178:LEU:HD12	1.75	0.86
1:A:117:GLU:OE2	1:A:162:LYS:NZ	2.10	0.84
1:A:69:ASP:O	1:A:71:ASN:N	2.13	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:26:LEU:HD13	1:A:26:LEU:H	1.54	0.73
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:78:ASN:O	1:A:79:VAL:HB	1.89	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:106:LEU:C	1:A:106:LEU:HD13	2.20	0.67
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:6:THR:O	1:A:6:THR:HG23	1.97	0.64
1:A:153:TRP:CD2	1:A:199:LYS:HG2	2.31	0.64
1:A:69:ASP:C	1:A:70:GLU:HG2	2.21	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: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:21:SER:OG	1:A:22:THR:N	2.34	0.60
1:A:228:THR:HG22	1:A:230:SER:H	1.66	0.60
1:A:153:TRP:CE3	3:A:301:1PE:H261	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:80:LYS:CG	1:A:82:PRO:HD3	2.31	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
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:O	1:A:186:THR:CG2	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:173:THR:C	1:A:175:VAL:N	2.65	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:23:ARG:HE	1:A:27:LYS:HD3	1.77	0.49
1:A:176:THR:O	1:A:178:LEU:CD1	2.53	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: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:90:ILE:HD12	1:A:90:ILE:C	2.39	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:106:LEU:C	1:A:106:LEU:CD1	2.88	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:125:THR:O	1:A:126:THR:C	2.61	0.44
1:A:6:THR:O	1:A:43:PRO:HG2	2.17	0.44
1:A:219:LYS:HB2	1:A:219:LYS:HE2	1.77	0.43
1:A:201:LEU:CD2	1:A:207:ILE:HG22	2.48	0.43
1:A:81:LEU:N	1:A:81:LEU:HD22	2.34	0.43
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:197:ILE:CG2	3:A:301:1PE:H262	2.49	0.42
1:A:173:THR:C	1:A:175:VAL:H	2.27	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:68:THR:HA	1:A:73:LEU:HB2	2.02	0.42
1:A:70:GLU:HB3	1:A:178:LEU:HG	2.01	0.42
1:A:67:GLU:O	1:A:68:THR:HG23	2.20	0.41
1:A:29:LYS:HB3	1:A:29:LYS:HE3	1.84	0.41
1:A:102:LEU:CB	1:A:106:LEU:HD12	2.44	0.41
1:A:200:LYS:HG2	1:A:206:SER:OG	2.20	0.41
1:A:48:GLN:HG2	1:A:98:TYR:CD2	2.55	0.41
1:A:68:THR:HA	1:A:73:LEU:CG	2.50	0.41
1:A:114:LEU:HD22	1:A:114:LEU:HA	1.85	0.41
1:A:237:ILE:HA	1:A:238:PRO:HD3	1.89	0.41
1:A:178:LEU:C	1:A:180:LYS:H	2.28	0.40
1:A:68:THR:HA	1:A:73:LEU:HG	2.04	0.40
1:A:68:THR:CG2	1:A:73:LEU:HB2	2.35	0.40
1:A:69:ASP:C	1:A:70:GLU:CG	2.92	0.40
1:A:73:LEU:C	1:A:75:LYS:H	2.28	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%)	2 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%)	181 (85%)	31 (15%)	3 1

All (31) 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	23	ARG
1	A	26	LEU
1	A	29	LYS
1	A	60	LYS
1	A	62	ASN
1	A	70	GLU
1	A	73	LEU
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	177	ASN
1	A	180	LYS
1	A	199	LYS
1	A	200	LYS
1	A	211	PRO
1	A	214	LYS
1	A	219	LYS
1	A	226	VAL
1	A	236	THR
1	A	237	ILE
1	A	247	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	71	ASN
1	A	78	ASN
1	A	183	ASN
1	A	184	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	302	-	15,15,15	1.35	2 (13%)	14,14,14	1.78	6 (42%)
3	1PE	A	301	-	15,15,15	1.32	2 (13%)	14,14,14	1.74	5 (35%)

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	302	-	-	9/13/13/13	-
3	1PE	A	301	-	-	8/13/13/13	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	301	1PE	C25-C15	-3.29	1.32	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	302	1PE	C24-C14	-3.26	1.32	1.49
3	A	302	1PE	C25-C15	-3.24	1.32	1.49
3	A	301	1PE	C24-C14	-3.19	1.33	1.49

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	302	1PE	OH6-C26-C16	2.49	121.08	110.11
3	A	302	1PE	OH5-C14-C24	2.39	121.24	110.35
3	A	301	1PE	OH4-C13-C23	2.36	121.11	110.35
3	A	302	1PE	OH3-C22-C12	2.30	120.24	110.11
3	A	301	1PE	OH3-C22-C12	2.27	120.12	110.11
3	A	301	1PE	OH4-C24-C14	2.18	120.30	110.35
3	A	302	1PE	OH6-C15-C25	2.18	120.27	110.35
3	A	301	1PE	OH6-C26-C16	2.13	119.52	110.11
3	A	302	1PE	OH4-C13-C23	2.12	119.99	110.35
3	A	302	1PE	OH5-C25-C15	2.11	119.98	110.35
3	A	301	1PE	OH5-C14-C24	2.04	119.66	110.35

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	302	1PE	C16-C26-OH6-C15
3	A	301	1PE	OH4-C13-C23-OH3
3	A	302	1PE	OH6-C15-C25-OH5
3	A	302	1PE	OH2-C12-C22-OH3
3	A	301	1PE	C24-C14-OH5-C25
3	A	302	1PE	C13-C23-OH3-C22
3	A	301	1PE	C12-C22-OH3-C23
3	A	302	1PE	C14-C24-OH4-C13
3	A	302	1PE	C25-C15-OH6-C26
3	A	301	1PE	C14-C24-OH4-C13
3	A	302	1PE	C23-C13-OH4-C24
3	A	301	1PE	OH2-C12-C22-OH3
3	A	301	1PE	C13-C23-OH3-C22
3	A	302	1PE	C24-C14-OH5-C25
3	A	301	1PE	OH7-C16-C26-OH6
3	A	302	1PE	OH5-C14-C24-OH4
3	A	301	1PE	OH6-C15-C25-OH5

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, 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	249/253 (98%)	1.67	91 (36%) ⓘ ⓘ	29, 49, 186, 278	0

All (91) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	228	THR	6.8
1	A	66	LEU	6.4
1	A	71	ASN	6.3
1	A	68	THR	5.9
1	A	79	VAL	5.7
1	A	226	VAL	5.5
1	A	233	VAL	5.2
1	A	72	LYS	5.1
1	A	47	ASN	5.1
1	A	64	ILE	5.0
1	A	81	LEU	5.0
1	A	73	LEU	5.0
1	A	225	SER	4.8
1	A	69	ASP	4.7
1	A	65	ASN	4.7
1	A	175	VAL	4.6
1	A	70	GLU	4.6
1	A	179	LYS	4.6
1	A	253	PHE	4.5
1	A	126	THR	4.3
1	A	229	LYS	4.2
1	A	24	ALA	4.2
1	A	127	LYS	4.2
1	A	177	ASN	4.2
1	A	76	THR	4.1
1	A	234	SER	4.0
1	A	173	THR	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	25	PHE	3.8
1	A	201	LEU	3.7
1	A	82	PRO	3.7
1	A	63	ILE	3.6
1	A	232	ASP	3.6
1	A	123	ILE	3.6
1	A	67	GLU	3.6
1	A	178	LEU	3.5
1	A	205	ALA	3.5
1	A	45	ASP	3.4
1	A	131	HIS	3.4
1	A	74	GLY	3.4
1	A	62	ASN	3.3
1	A	46	ALA	3.2
1	A	245	TYR	3.2
1	A	231	GLY	3.2
1	A	193	LEU	3.2
1	A	23	ARG	3.2
1	A	227	THR	3.1
1	A	236	THR	3.1
1	A	204	SER	3.1
1	A	6	THR	3.0
1	A	168	ARG	3.0
1	A	237	ILE	3.0
1	A	80	LYS	3.0
1	A	77	LYS	2.9
1	A	98	TYR	2.7
1	A	44	PHE	2.7
1	A	19	ILE	2.7
1	A	235	LEU	2.6
1	A	21	SER	2.6
1	A	121	ASP	2.6
1	A	75	LYS	2.5
1	A	106	LEU	2.5
1	A	129	THR	2.5
1	A	122	SER	2.5
1	A	128	HIS	2.5
1	A	88	ASN	2.5
1	A	203	GLU	2.5
1	A	207	ILE	2.5
1	A	163	PHE	2.4
1	A	26	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	176	THR	2.4
1	A	230	SER	2.4
1	A	32	ALA	2.3
1	A	22	THR	2.3
1	A	124	LYS	2.3
1	A	213	TYR	2.3
1	A	9	GLU	2.2
1	A	200	LYS	2.2
1	A	166	ASN	2.2
1	A	244	GLU	2.2
1	A	105	SER	2.2
1	A	174	GLY	2.2
1	A	214	LYS	2.2
1	A	224	PHE	2.1
1	A	202	GLY	2.1
1	A	60	LYS	2.1
1	A	16	LEU	2.1
1	A	171	LEU	2.1
1	A	90	ILE	2.1
1	A	242	ILE	2.1
1	A	125	THR	2.0
1	A	27	LYS	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 oligosaccharides 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
3	1PE	A	301	16/16	0.73	0.20	80,82,88,89	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	1PE	A	302	16/16	0.85	0.15	67,71,77,79	0
2	ZN	A	403	1/1	0.89	0.10	77,77,77,77	0
2	ZN	A	401	1/1	0.99	0.04	37,37,37,37	0
2	ZN	A	402	1/1	1.00	0.03	32,32,32,32	1

6.5 Other polymers [i](#)

There are no such residues in this entry.