



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:55 PM UTC

PDB ID : 5WTL / pdb_00005wtl
Title : Crystal structure of the periplasmic portion of outer membrane protein A (OmpA) from *Capnocytophaga gingivalis*
Authors : Dai, S.; Tan, K.; Ye, S.; Zhang, R.
Deposited on : 2016-12-13
Resolution : 2.30 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

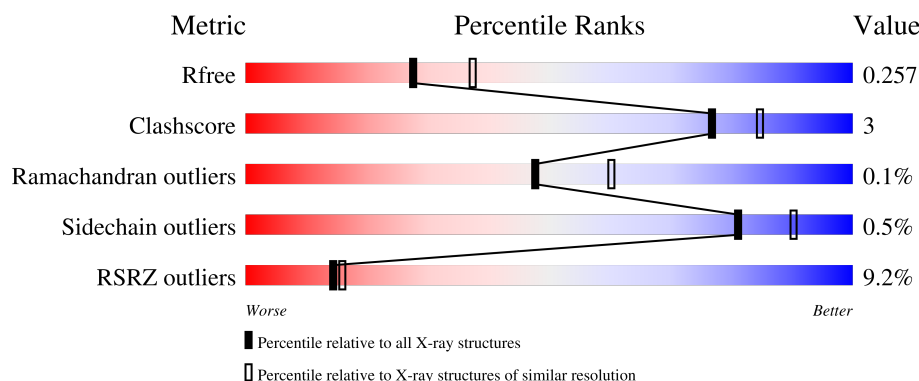
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	261	
1	B	261	
1	C	261	
1	D	261	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8183 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 OmpA family protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	258	Total	C	N	O	S	0	0	0
			1936	1185	335	405	11			
1	B	258	Total	C	N	O	S	0	0	0
			1936	1185	335	405	11			
1	C	260	Total	C	N	O	S	0	0	0
			1951	1194	338	408	11			
1	D	247	Total	C	N	O	S	0	0	0
			1852	1136	321	384	11			

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	11	Total	Ca	0	0
			11	11		
2	B	10	Total	Ca	0	0
			10	10		
2	C	11	Total	Ca	0	0
			11	11		
2	D	9	Total	Ca	0	0
			9	9		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	C	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

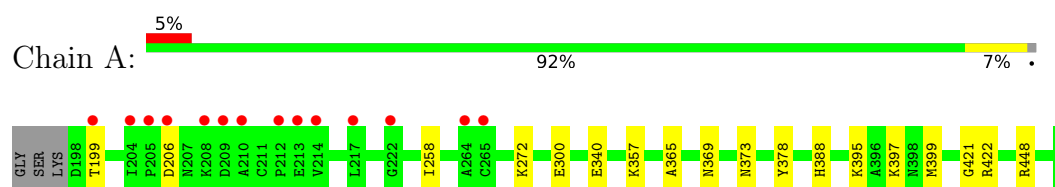
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	129	Total 129	O 129	0	0
5	B	108	Total 108	O 108	0	0
5	C	114	Total 114	O 114	0	0
5	D	94	Total 94	O 94	0	0

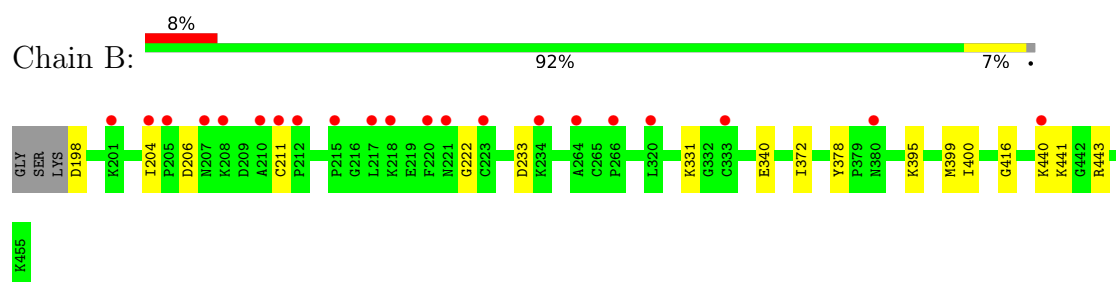
3 Residue-property plots [i](#)

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.

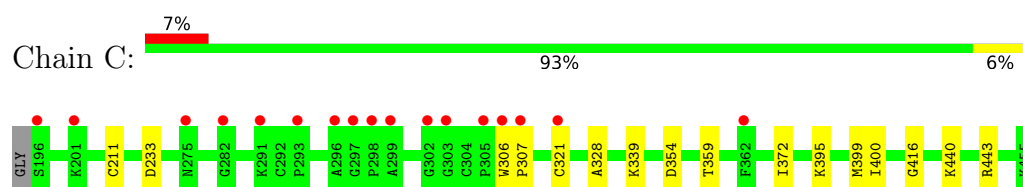
- Molecule 1: OmpA family protein



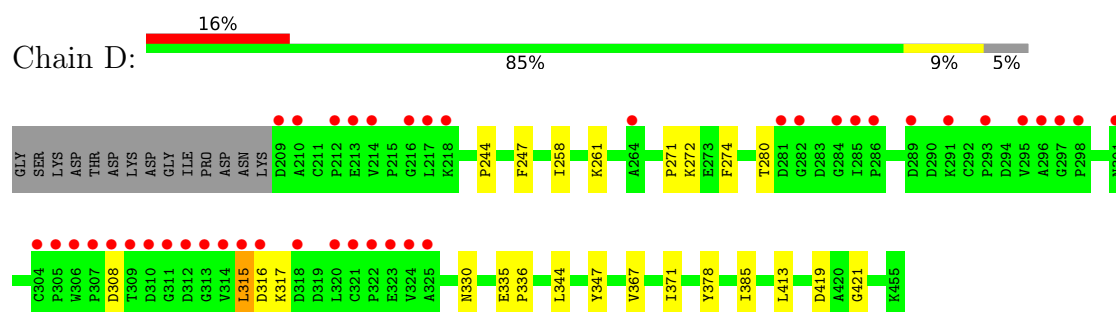
- Molecule 1: OmpA family protein



- Molecule 1: OmpA family protein



- Molecule 1: OmpA family protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	73.20Å 87.34Å 185.46Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.51 – 2.30 42.51 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.6 (42.51-2.30) 98.6 (42.51-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.86 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.203 , 0.255 0.205 , 0.257	Depositor DCC
R_{free} test set	2701 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	35.6	Xtriage
Anisotropy	0.668	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 47.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8183	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.79% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, MES, CA

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.32	0/1972	0.82	0/2666
1	B	0.32	0/1972	0.81	0/2666
1	C	0.32	0/1987	0.81	4/2685 (0.1%)
1	D	0.31	0/1887	0.80	0/2551
All	All	0.32	0/7818	0.81	4/10568 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	321	CYS	CA-C-N	5.25	125.06	119.28
1	C	321	CYS	C-N-CA	5.25	125.06	119.28
1	C	211	CYS	CA-C-N	5.13	124.80	119.56
1	C	211	CYS	C-N-CA	5.13	124.80	119.56

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	1936	0	1850	11	0
1	B	1936	0	1850	10	0
1	C	1951	0	1868	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	1852	0	1774	12	0
2	A	11	0	0	0	0
2	B	10	0	0	0	0
2	C	11	0	0	0	0
2	D	9	0	0	0	0
3	B	5	0	0	0	0
3	C	5	0	0	0	0
4	C	12	0	13	4	0
5	A	129	0	0	3	0
5	B	108	0	0	2	0
5	C	114	0	0	3	0
5	D	94	0	0	1	0
All	All	8183	0	7355	43	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 3.

All (43) 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:B:440:LYS:HD2	1:B:443:ARG:HH21	1.59	0.67
1:A:421:GLY:HA3	1:B:400:ILE:HG23	1.79	0.63
1:A:365:ALA:O	1:A:369:ASN:ND2	2.32	0.62
1:C:372:ILE:HD13	1:C:416:GLY:HA3	1.84	0.59
1:B:198:ASP:N	1:B:206:ASP:OD2	2.37	0.58
1:D:419:ASP:OD1	5:D:601:HOH:O	2.17	0.58
1:B:331:LYS:NZ	5:B:1107:HOH:O	2.36	0.57
1:C:400:ILE:HG23	1:D:421:GLY:HA3	1.87	0.56
1:D:344:LEU:HD11	1:D:371:ILE:HG23	1.88	0.56
1:A:357:LYS:NZ	5:A:1107:HOH:O	2.40	0.54
1:C:440:LYS:H	4:C:1011:MES:H62	1.71	0.54
1:C:440:LYS:HB2	4:C:1011:MES:H21	1.91	0.52
1:D:258:ILE:HD11	1:D:272:LYS:HG2	1.91	0.52
1:D:315:LEU:HD13	1:D:317:LYS:HG3	1.91	0.52
1:B:372:ILE:HD13	1:B:416:GLY:HA3	1.92	0.51
1:C:354:ASP:OD2	1:C:359:THR:OG1	2.29	0.50
1:A:340:GLU:OE1	1:A:378:TYR:OH	2.29	0.50
1:C:443:ARG:HH22	4:C:1011:MES:H82	1.77	0.50
1:A:373:ASN:O	5:A:1101:HOH:O	2.19	0.49
1:A:258:ILE:HD11	1:A:272:LYS:HG2	1.94	0.49
1:D:385:ILE:HD11	1:D:413:LEU:HD12	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:330:ASN:ND2	1:D:335:GLU:HG3	2.31	0.46
1:C:395:LYS:O	1:C:399:MET:HG2	2.16	0.46
1:C:443:ARG:HH12	4:C:1011:MES:HN4	1.64	0.45
1:C:328:ALA:N	5:C:1115:HOH:O	2.50	0.45
1:B:340:GLU:OE1	1:B:378:TYR:OH	2.31	0.44
1:B:395:LYS:O	1:B:399:MET:HG2	2.18	0.44
1:D:244:PRO:HG2	1:D:247:PHE:HD2	1.83	0.43
1:A:422:ARG:NH1	5:A:1106:HOH:O	2.36	0.43
1:D:347:TYR:HB3	1:D:367:VAL:HG13	2.01	0.43
1:D:308:ASP:HA	1:D:316:ASP:OD1	2.18	0.43
1:A:395:LYS:O	1:A:399:MET:HG2	2.19	0.43
1:D:271:PRO:HG2	1:D:274:PHE:HD1	1.83	0.43
1:D:336:PRO:HG3	1:D:378:TYR:CD2	2.54	0.43
1:C:306:TRP:HA	1:C:307:PRO:HD3	1.82	0.43
1:A:388:HIS:HB2	1:A:448:ARG:HG2	2.01	0.42
1:B:233:ASP:OD1	5:B:1101:HOH:O	2.22	0.42
1:A:300:GLU:H	1:A:300:GLU:CD	2.27	0.42
1:C:339:LYS:NZ	5:C:1117:HOH:O	2.51	0.41
1:C:233:ASP:OD1	5:C:1101:HOH:O	2.22	0.41
1:B:441:LYS:HA	1:B:441:LYS:HD2	1.80	0.41
1:B:204:ILE:HD13	1:B:222:GLY:HA2	2.02	0.41
1:A:199:THR:N	1:A:206:ASP:OD1	2.45	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	256/261 (98%)	252 (98%)	4 (2%)	0	100	100
1	B	256/261 (98%)	249 (97%)	7 (3%)	0	100	100
1	C	258/261 (99%)	255 (99%)	3 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	245/261 (94%)	237 (97%)	7 (3%)	1 (0%)	30	38
All	All	1015/1044 (97%)	993 (98%)	21 (2%)	1 (0%)	48	60

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	280	THR

5.3.2 Protein sidechains ⓘ

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	213/215 (99%)	212 (100%)	1 (0%)	81	90
1	B	213/215 (99%)	212 (100%)	1 (0%)	81	90
1	C	215/215 (100%)	215 (100%)	0	100	100
1	D	203/215 (94%)	201 (99%)	2 (1%)	68	82
All	All	844/860 (98%)	840 (100%)	4 (0%)	81	90

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	397	LYS
1	B	211	CYS
1	D	261	LYS
1	D	315	LEU

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

Mol	Chain	Res	Type
1	C	221	ASN
1	C	380	ASN
1	C	439	ASN
1	D	301	ASN

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Mol	Chain	Res	Type
1	D	343	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 44 ligands modelled in this entry, 41 are monoatomic - leaving 3 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	SO4	B	1011	-	4,4,4	0.24	0	6,6,6	0.10	0
4	MES	C	1011	-	12,12,12	2.32	1 (8%)	15,16,16	1.06	0
3	SO4	C	1012	-	4,4,4	0.24	0	6,6,6	0.09	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	MES	C	1011	-	-	0/6/14/14	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	1011	MES	C8-S	-7.79	1.66	1.77

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	1011	MES	4	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	258/261 (98%)	0.31	14 (5%) 31 33	27, 50, 98, 141	0
1	B	258/261 (98%)	0.44	21 (8%) 18 19	25, 50, 113, 151	0
1	C	260/261 (99%)	0.49	17 (6%) 25 27	22, 52, 101, 130	0
1	D	247/261 (94%)	0.74	42 (17%) 4 5	26, 53, 116, 148	0
All	All	1023/1044 (97%)	0.49	94 (9%) 14 16	22, 51, 108, 151	0

All (94) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	311	GLY	6.3
1	D	297	GLY	6.0
1	D	285	ILE	4.9
1	C	296	ALA	4.7
1	D	315	LEU	4.3
1	D	217	LEU	4.2
1	D	306	TRP	4.0
1	D	321	CYS	4.0
1	A	204	ILE	4.0
1	C	306	TRP	3.8
1	D	293	PRO	3.8
1	C	305	PRO	3.8
1	C	297	GLY	3.7
1	D	210	ALA	3.7
1	A	205	PRO	3.7
1	B	210	ALA	3.5
1	D	325	ALA	3.5
1	B	220	PHE	3.5
1	D	305	PRO	3.5
1	B	205	PRO	3.4
1	D	212	PRO	3.4

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Mol	Chain	Res	Type	RSRZ
1	D	313	GLY	3.3
1	A	208	LYS	3.3
1	A	206	ASP	3.2
1	C	362	PHE	3.2
1	D	304	CYS	3.2
1	B	264	ALA	3.1
1	C	303	GLY	3.1
1	D	323	GLU	3.1
1	D	209	ASP	3.1
1	A	222	GLY	3.1
1	B	211	CYS	3.1
1	C	291	LYS	3.1
1	C	299	ALA	3.0
1	C	298	PRO	3.0
1	B	208	LYS	3.0
1	D	298	PRO	3.0
1	A	214	VAL	2.9
1	D	318	ASP	2.9
1	C	307	PRO	2.9
1	B	207	ASN	2.9
1	D	295	VAL	2.9
1	B	320	LEU	2.8
1	C	302	GLY	2.8
1	A	217	LEU	2.8
1	C	196	SER	2.8
1	D	296	ALA	2.8
1	C	293	PRO	2.7
1	A	210	ALA	2.7
1	B	380	ASN	2.7
1	A	209	ASP	2.7
1	D	213	GLU	2.7
1	A	212	PRO	2.7
1	B	221	ASN	2.6
1	B	218	LYS	2.6
1	C	275	ASN	2.6
1	A	265	CYS	2.5
1	A	213	GLU	2.5
1	D	301	ASN	2.5
1	D	312	ASP	2.5
1	A	199	THR	2.5
1	D	308	ASP	2.5
1	B	201	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	D	216	GLY	2.5
1	B	217	LEU	2.4
1	D	309	THR	2.4
1	D	218	LYS	2.4
1	D	286	PRO	2.4
1	D	322	PRO	2.4
1	C	282	GLY	2.3
1	D	314	VAL	2.3
1	D	324	VAL	2.3
1	D	320	LEU	2.3
1	B	234	LYS	2.3
1	D	291	LYS	2.3
1	D	307	PRO	2.3
1	B	440	LYS	2.2
1	D	281	ASP	2.2
1	D	310	ASP	2.2
1	D	316	ASP	2.2
1	C	201	LYS	2.2
1	D	264	ALA	2.2
1	D	214	VAL	2.1
1	D	282	GLY	2.1
1	D	284	GLY	2.1
1	B	215	PRO	2.1
1	B	333	CYS	2.0
1	D	289	ASP	2.0
1	A	264	ALA	2.0
1	B	223	CYS	2.0
1	C	321	CYS	2.0
1	B	204	ILE	2.0
1	B	212	PRO	2.0
1	B	266	PRO	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

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	MES	C	1011	12/12	0.59	0.31	110,115,124,125	12
3	SO4	C	1012	5/5	0.87	0.15	61,61,61,62	5
3	SO4	B	1011	5/5	0.89	0.12	65,65,65,66	5
2	CA	B	1002	1/1	0.93	0.08	92,92,92,92	0
2	CA	C	1008	1/1	0.94	0.08	90,90,90,90	0
2	CA	D	506	1/1	0.95	0.07	82,82,82,82	0
2	CA	A	1002	1/1	0.95	0.10	84,84,84,84	0
2	CA	D	508	1/1	0.96	0.06	67,67,67,67	0
2	CA	A	1001	1/1	0.96	0.11	87,87,87,87	0
2	CA	C	1007	1/1	0.97	0.06	77,77,77,77	0
2	CA	D	501	1/1	0.97	0.07	82,82,82,82	0
2	CA	D	509	1/1	0.97	0.06	62,62,62,62	0
2	CA	D	507	1/1	0.98	0.06	97,97,97,97	0
2	CA	C	1006	1/1	0.98	0.04	51,51,51,51	0
2	CA	B	1001	1/1	0.98	0.07	91,91,91,91	0
2	CA	A	1004	1/1	0.98	0.03	33,33,33,33	0
2	CA	B	1009	1/1	0.98	0.05	37,37,37,37	0
2	CA	C	1004	1/1	0.98	0.09	37,37,37,37	0
2	CA	B	1010	1/1	0.99	0.04	41,41,41,41	0
2	CA	C	1001	1/1	0.99	0.07	46,46,46,46	0
2	CA	C	1002	1/1	0.99	0.04	41,41,41,41	0
2	CA	A	1009	1/1	0.99	0.02	46,46,46,46	0
2	CA	C	1005	1/1	0.99	0.05	44,44,44,44	0
2	CA	A	1010	1/1	0.99	0.03	49,49,49,49	0
2	CA	A	1011	1/1	0.99	0.02	32,32,32,32	0
2	CA	A	1003	1/1	0.99	0.03	41,41,41,41	0
2	CA	C	1009	1/1	0.99	0.03	57,57,57,57	0
2	CA	C	1010	1/1	0.99	0.08	46,46,46,46	0
2	CA	A	1005	1/1	0.99	0.04	28,28,28,28	0
2	CA	D	502	1/1	0.99	0.02	36,36,36,36	0
2	CA	D	503	1/1	0.99	0.03	32,32,32,32	0
2	CA	D	504	1/1	0.99	0.05	43,43,43,43	0
2	CA	D	505	1/1	0.99	0.07	47,47,47,47	0
2	CA	B	1003	1/1	0.99	0.04	48,48,48,48	0
2	CA	B	1004	1/1	0.99	0.04	36,36,36,36	0
2	CA	B	1005	1/1	0.99	0.04	35,35,35,35	0
2	CA	B	1006	1/1	0.99	0.06	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	CA	B	1007	1/1	0.99	0.04	36,36,36,36	0
2	CA	B	1008	1/1	0.99	0.08	36,36,36,36	0
2	CA	A	1007	1/1	0.99	0.06	45,45,45,45	0
2	CA	A	1006	1/1	1.00	0.09	32,32,32,32	0
2	CA	C	1003	1/1	1.00	0.04	37,37,37,37	0
2	CA	A	1008	1/1	1.00	0.04	42,42,42,42	0
2	CA	C	1013	1/1	1.00	0.02	35,35,35,35	0

6.5 Other polymers [i](#)

There are no such residues in this entry.