



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 08:17 PM UTC

PDB ID : 6EPG / pdb_00006epg
Title : Structure of the epsilon_1 / zeta_1 antitoxin / toxin system from *Neisseria gonorrhoeae*.
Authors : Rocker, A.; Meinhart, A.
Deposited on : 2017-10-11
Resolution : 2.40 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

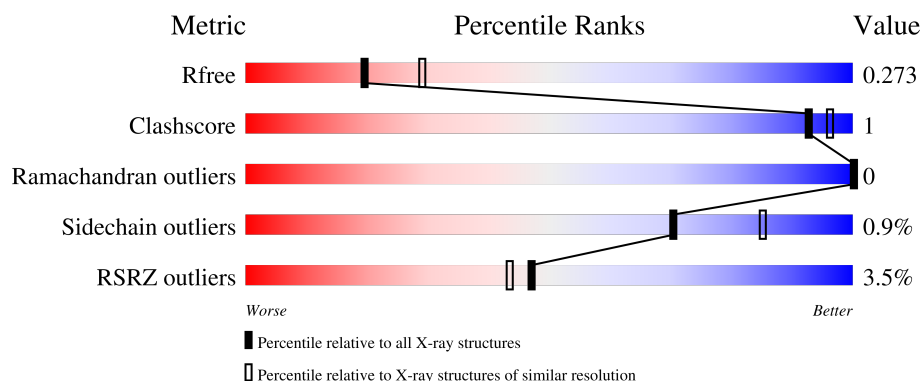
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	61	5% 87% 11%
1	C	61	16% 89% 8%
1	E	61	5% 85% 11%
1	G	61	13% 87% 11%
2	B	401	2% 92% 5%

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Mol	Chain	Length	Quality of chain
2	D	401	3% 93% 5%
2	F	401	2% 95%
2	H	401	2% 95%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14291 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 Epsilon_1 antitoxin.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	54	Total	C	N	O	S	Se	0	0	0
			442	275	83	80	1	3			
1	C	56	Total	C	N	O	S	Se	0	0	0
			458	285	85	84	1	3			
1	E	54	Total	C	N	O	S	Se	0	0	0
			442	275	83	80	1	3			
1	G	54	Total	C	N	O	S	Se	0	0	0
			442	275	83	80	1	3			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	initiating methionine	UNP D5K9E3
C	1	MSE	-	initiating methionine	UNP D5K9E3
E	1	MSE	-	initiating methionine	UNP D5K9E3
G	1	MSE	-	initiating methionine	UNP D5K9E3

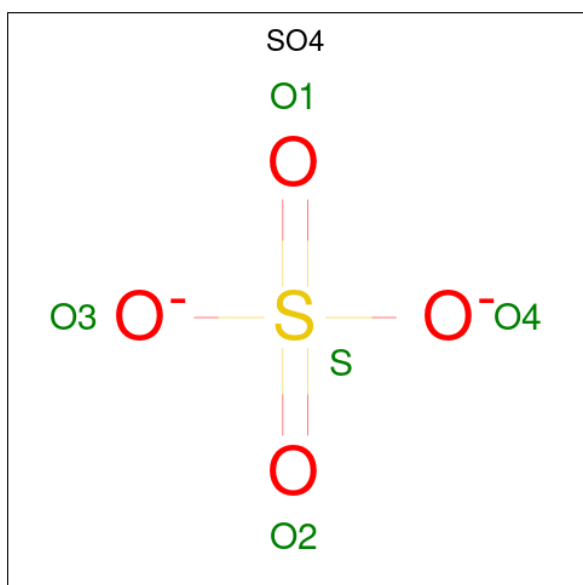
- Molecule 2 is a protein called Zeta_1 toxin.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	390	Total	C	N	O	S	Se	0	0	0
			3045	1896	531	607	3	8			
2	D	394	Total	C	N	O	S	Se	0	0	0
			3075	1914	538	612	3	8			
2	F	395	Total	C	N	O	S	Se	0	0	0
			3083	1919	539	613	3	9			
2	H	395	Total	C	N	O	S	Se	0	0	0
			3084	1921	539	612	3	9			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	MSE	-	initiating methionine	UNP D5K9G7
B	115	ALA	LYS	engineered mutation	UNP D5K9G7
D	1	MSE	-	initiating methionine	UNP D5K9G7
D	115	ALA	LYS	engineered mutation	UNP D5K9G7
F	1	MSE	-	initiating methionine	UNP D5K9G7
F	115	ALA	LYS	engineered mutation	UNP D5K9G7
H	1	MSE	-	initiating methionine	UNP D5K9G7
H	115	ALA	LYS	engineered mutation	UNP D5K9G7

- 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	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	O	0	0
			1	1		
4	B	21	Total	O	0	0
			21	21		
4	C	1	Total	O	0	0
			1	1		
4	D	23	Total	O	0	0
			23	23		
4	F	38	Total	O	0	0
			38	38		

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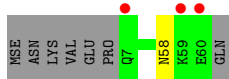
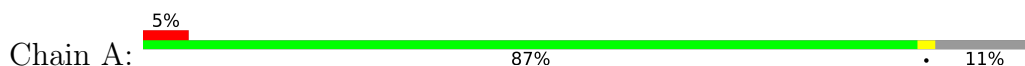
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	H	26	Total	O	0	0
			26	26		

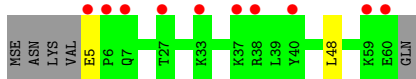
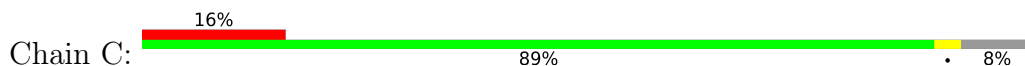
3 Residue-property plots [i](#)

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.

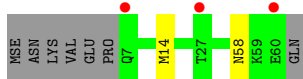
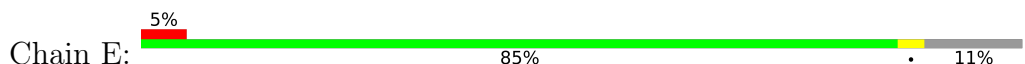
- Molecule 1: Epsilon_1 antitoxin



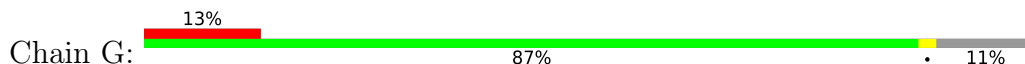
- Molecule 1: Epsilon_1 antitoxin



- Molecule 1: Epsilon_1 antitoxin



- Molecule 1: Epsilon_1 antitoxin

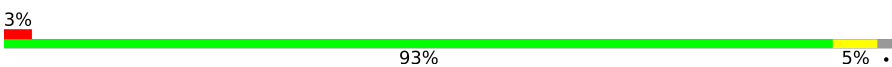


- Molecule 2: Zeta_1 toxin



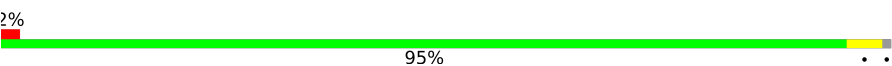
SER
ARG

- Molecule 2: Zeta_1 toxin

Chain D:  3% 93% 5%

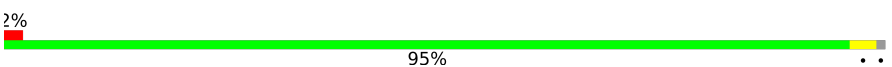


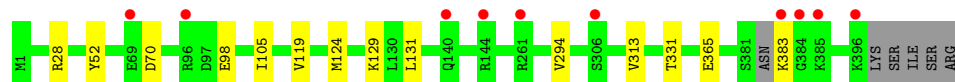
- Molecule 2: Zeta_1 toxin

Chain F:  2% 95% 3%



- Molecule 2: Zeta_1 toxin

Chain H:  2% 95% 3%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	79.76Å 149.58Å 125.09Å 90.00° 94.82° 90.00°	Depositor
Resolution (Å)	48.91 – 2.40 48.91 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.7 (48.91-2.40) 99.7 (48.91-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.38 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.226 , 0.270 0.233 , 0.273	Depositor DCC
R_{free} test set	5687 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	45.3	Xtriage
Anisotropy	0.362	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 23.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	14291	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 40.95 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.5363e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

5.1 Standard geometry

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

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	0.68	0/444	0.92	0/586
1	C	0.73	0/461	1.01	2/610 (0.3%)
1	E	0.72	0/444	0.91	0/586
1	G	0.74	0/444	0.91	0/586
2	B	0.75	0/3074	0.89	0/4117
2	D	0.74	0/3105	0.88	3/4158 (0.1%)
2	F	0.75	0/3113	0.86	0/4168
2	H	0.73	0/3113	0.86	0/4165
All	All	0.74	0/14198	0.88	5/18976 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	382	ASN	N-CA-C	-9.00	95.45	109.76
1	C	5	GLU	CA-C-N	6.85	128.40	119.84
1	C	5	GLU	C-N-CA	6.85	128.40	119.84
2	D	383	LYS	N-CA-C	6.27	119.45	110.24
2	D	381	SER	N-CA-C	5.57	117.48	108.34

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	442	0	457	1	0
1	C	458	0	470	0	0
1	E	442	0	457	2	0
1	G	442	0	457	1	0
2	B	3045	0	3036	14	0
2	D	3075	0	3072	11	0
2	F	3083	0	3084	9	0
2	H	3084	0	3090	7	0
3	B	30	0	0	0	0
3	D	25	0	0	0	0
3	F	30	0	0	0	0
3	H	25	0	0	0	0
4	A	1	0	0	0	0
4	B	21	0	0	0	0
4	C	1	0	0	0	0
4	D	23	0	0	0	0
4	F	38	0	0	0	0
4	H	26	0	0	0	0
All	All	14291	0	14123	41	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 1.

All (41) 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)
2:B:294:VAL:HG13	2:B:316:MSE:HE1	1.69	0.74
1:A:58:ASN:O	2:B:28:ARG:NH2	2.21	0.74
2:D:285:GLN:HG2	2:D:298:THR:HG22	1.80	0.63
2:B:271:MSE:HE2	2:B:276:VAL:HG23	1.80	0.63
2:F:363:ASN:HD22	2:F:384:GLY:HA2	1.62	0.63
2:F:93:VAL:HG11	2:F:130:LEU:HD13	1.82	0.62
2:F:119:VAL:HG13	2:F:131:LEU:HD21	1.82	0.60
2:D:100:GLN:HE21	2:D:126:ASP:HB3	1.69	0.58
2:H:331:THR:OG1	2:H:383:LYS:HE3	2.03	0.58
2:H:119:VAL:HG13	2:H:131:LEU:HD21	1.87	0.57
2:B:93:VAL:HG11	2:B:130:LEU:HD13	1.86	0.56
2:D:271:MSE:HE2	2:D:276:VAL:HG23	1.89	0.54
2:H:119:VAL:HG13	2:H:131:LEU:CD2	2.39	0.53
2:B:313:VAL:HB	2:B:316:MSE:HE2	1.91	0.53
2:F:52:TYR:CE1	2:F:119:VAL:HG11	2.44	0.52
2:D:289:THR:HG22	2:D:294:VAL:HG12	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:105:ILE:HB	2:H:131:LEU:HD12	1.93	0.51
2:B:52:TYR:CE1	2:B:119:VAL:HG11	2.46	0.50
2:B:285:GLN:HG2	2:B:298:THR:HG22	1.94	0.49
2:B:289:THR:HG22	2:B:294:VAL:HG12	1.96	0.48
2:D:163:MSE:HE2	2:D:167:ARG:NH1	2.29	0.47
2:D:271:MSE:HE3	2:D:272:ASP:N	2.32	0.45
2:F:169:SER:HA	2:F:188:MSE:HE1	1.98	0.45
1:E:58:ASN:O	2:F:28:ARG:NH2	2.44	0.45
2:B:271:MSE:HE3	2:B:272:ASP:N	2.32	0.44
2:B:294:VAL:CG1	2:B:316:MSE:HE1	2.44	0.44
2:D:271:MSE:HE2	2:D:276:VAL:CG2	2.49	0.43
2:H:52:TYR:CE1	2:H:119:VAL:HG11	2.53	0.43
2:H:98:GLU:OE1	2:H:129:LYS:NZ	2.51	0.43
2:D:383:LYS:HD3	2:D:383:LYS:HA	1.66	0.43
2:B:219:ARG:NH2	2:B:222:GLU:OE1	2.51	0.43
2:B:271:MSE:HE2	2:B:276:VAL:CG2	2.49	0.43
1:E:14:MSE:HE1	2:F:105:ILE:HD13	2.00	0.43
1:G:58:ASN:O	2:H:28:ARG:NH2	2.47	0.43
2:F:119:VAL:HG13	2:F:131:LEU:CD2	2.48	0.42
2:B:233:MSE:HE3	2:B:234:LEU:HG	2.01	0.42
2:D:52:TYR:CE1	2:D:119:VAL:HG11	2.54	0.42
2:D:51:ARG:NH2	2:D:98:GLU:OE2	2.35	0.42
2:B:285:GLN:CG	2:B:298:THR:HG22	2.51	0.41
2:D:331:THR:OG1	2:D:383:LYS:HE2	2.20	0.41
2:F:110:ILE:HD12	2:F:192:GLN:HB2	2.02	0.41

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	52/61 (85%)	51 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	54/61 (88%)	51 (94%)	3 (6%)	0	100	100
1	E	52/61 (85%)	52 (100%)	0	0	100	100
1	G	52/61 (85%)	51 (98%)	1 (2%)	0	100	100
2	B	386/401 (96%)	381 (99%)	5 (1%)	0	100	100
2	D	392/401 (98%)	387 (99%)	5 (1%)	0	100	100
2	F	393/401 (98%)	386 (98%)	7 (2%)	0	100	100
2	H	391/401 (98%)	383 (98%)	8 (2%)	0	100	100
All	All	1772/1848 (96%)	1742 (98%)	30 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	46/49 (94%)	46 (100%)	0	100	100
1	C	48/49 (98%)	47 (98%)	1 (2%)	47	69
1	E	46/49 (94%)	46 (100%)	0	100	100
1	G	46/49 (94%)	46 (100%)	0	100	100
2	B	332/333 (100%)	329 (99%)	3 (1%)	70	85
2	D	335/333 (101%)	333 (99%)	2 (1%)	78	89
2	F	336/333 (101%)	333 (99%)	3 (1%)	70	85
2	H	336/333 (101%)	331 (98%)	5 (2%)	57	77
All	All	1525/1528 (100%)	1511 (99%)	14 (1%)	70	85

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	124	MSE
2	B	131	LEU

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Mol	Chain	Res	Type
2	B	164	ARG
1	C	48	LEU
2	D	70	ASP
2	D	203	ARG
2	F	141	SER
2	F	294	VAL
2	F	381	SER
2	H	70	ASP
2	H	124	MSE
2	H	294	VAL
2	H	313	VAL
2	H	365	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	325	GLN
2	B	376	ASN
1	C	10	ASN
2	D	100	GLN
2	D	376	ASN
2	F	140	GLN
2	F	241	GLN
2	F	363	ASN
2	F	376	ASN
1	G	22	ASN
1	G	58	ASN
2	H	121	ASN
2	H	241	GLN
2	H	333	GLN
2	H	376	ASN

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

22 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	$\# Z > 2$
3	SO4	D	502	-	4,4,4	0.49	0	6,6,6	0.27	0
3	SO4	F	505	-	4,4,4	0.48	0	6,6,6	0.16	0
3	SO4	F	501	-	4,4,4	0.30	0	6,6,6	0.45	0
3	SO4	H	504	-	4,4,4	0.51	0	6,6,6	0.19	0
3	SO4	B	505	-	4,4,4	0.47	0	6,6,6	0.24	0
3	SO4	F	503	-	4,4,4	0.61	0	6,6,6	0.20	0
3	SO4	B	501	-	4,4,4	0.45	0	6,6,6	0.75	0
3	SO4	D	504	-	4,4,4	0.53	0	6,6,6	0.19	0
3	SO4	B	504	-	4,4,4	0.51	0	6,6,6	0.18	0
3	SO4	B	503	-	4,4,4	0.36	0	6,6,6	0.30	0
3	SO4	H	503	-	4,4,4	0.48	0	6,6,6	0.53	0
3	SO4	H	505	-	4,4,4	0.44	0	6,6,6	0.48	0
3	SO4	D	505	-	4,4,4	0.44	0	6,6,6	0.35	0
3	SO4	B	506	-	4,4,4	0.48	0	6,6,6	0.43	0
3	SO4	F	504	-	4,4,4	0.41	0	6,6,6	0.25	0
3	SO4	H	501	-	4,4,4	0.44	0	6,6,6	0.41	0
3	SO4	H	502	-	4,4,4	0.52	0	6,6,6	0.30	0
3	SO4	D	501	-	4,4,4	0.33	0	6,6,6	0.72	0
3	SO4	D	503	-	4,4,4	0.40	0	6,6,6	0.28	0
3	SO4	F	502	-	4,4,4	0.43	0	6,6,6	0.26	0
3	SO4	F	506	-	4,4,4	0.54	0	6,6,6	0.47	0
3	SO4	B	502	-	4,4,4	0.50	0	6,6,6	0.20	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

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	51/61 (83%)	0.85	3 (5%) 28 24	40, 62, 90, 110	0
1	C	53/61 (86%)	0.95	10 (18%) 3 2	41, 64, 101, 110	0
1	E	51/61 (83%)	0.53	3 (5%) 28 24	35, 55, 78, 92	0
1	G	51/61 (83%)	1.06	8 (15%) 5 4	35, 63, 96, 105	0
2	B	382/401 (95%)	0.31	7 (1%) 67 63	32, 48, 71, 87	0
2	D	386/401 (96%)	0.31	11 (2%) 55 51	31, 47, 71, 101	0
2	F	386/401 (96%)	0.19	9 (2%) 61 57	28, 44, 69, 117	0
2	H	386/401 (96%)	0.25	10 (2%) 57 53	29, 45, 69, 101	0
All	All	1746/1848 (94%)	0.33	61 (3%) 47 43	28, 47, 77, 117	0

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	385	LYS	5.2
2	H	383	LYS	4.8
2	D	384	GLY	4.6
2	H	396	LYS	4.6
2	D	383	LYS	4.3
2	F	384	GLY	4.0
2	D	382	ASN	4.0
1	A	7	GLN	3.8
2	F	385	LYS	3.7
2	H	384	GLY	3.7
2	D	385	LYS	3.7
1	G	60	GLU	3.5
1	A	60	GLU	3.4
1	G	7	GLN	3.3
2	F	382	ASN	3.2
2	B	2	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
1	G	40	TYR	3.1
1	G	38	ARG	3.1
1	C	60	GLU	3.0
2	F	383	LYS	3.0
2	B	381	SER	2.9
1	C	6	PRO	2.9
2	F	2	VAL	2.9
2	D	164	ARG	2.8
1	C	5	GLU	2.7
2	F	96	ARG	2.6
1	G	30	ALA	2.6
2	F	235	SER	2.6
2	H	96	ARG	2.6
2	D	317	LYS	2.6
1	G	20	GLU	2.5
2	H	261	ARG	2.5
2	B	395	ALA	2.4
2	B	164	ARG	2.4
2	D	2	VAL	2.4
2	F	120	LYS	2.4
1	C	33	LYS	2.3
1	G	59	LYS	2.3
1	C	38	ARG	2.3
2	F	352	LYS	2.3
1	E	60	GLU	2.3
2	B	100	GLN	2.2
1	E	27	THR	2.2
1	G	8	GLU	2.2
2	B	96	ARG	2.2
2	D	380	GLY	2.2
2	H	144	ARG	2.2
2	D	232	LYS	2.2
2	B	331	THR	2.1
1	C	40	TYR	2.1
2	D	96	ARG	2.1
2	H	306	SER	2.1
2	H	140	GLN	2.1
1	C	27	THR	2.1
1	C	37	LYS	2.1
1	C	59	LYS	2.1
1	C	7	GLN	2.0
1	E	7	GLN	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	59	LYS	2.0
2	H	69	GLU	2.0
2	D	381	SER	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	SO4	H	503	5/5	0.81	0.14	66,71,82,84	0
3	SO4	H	504	5/5	0.82	0.14	84,87,88,95	0
3	SO4	B	505	5/5	0.83	0.13	87,87,92,94	0
3	SO4	D	504	5/5	0.84	0.12	78,84,86,87	0
3	SO4	F	504	5/5	0.88	0.12	67,75,76,79	0
3	SO4	D	503	5/5	0.90	0.12	66,72,80,85	0
3	SO4	B	503	5/5	0.91	0.11	61,64,70,71	0
3	SO4	B	504	5/5	0.92	0.15	72,75,76,78	0
3	SO4	B	502	5/5	0.93	0.08	68,71,72,77	0
3	SO4	H	502	5/5	0.93	0.10	58,59,64,65	0
3	SO4	B	506	5/5	0.93	0.11	53,53,56,58	0
3	SO4	F	503	5/5	0.93	0.14	65,66,69,70	0
3	SO4	F	506	5/5	0.94	0.14	51,52,58,60	0
3	SO4	D	502	5/5	0.94	0.11	69,69,71,72	0
3	SO4	F	502	5/5	0.94	0.08	62,65,69,72	0
3	SO4	F	505	5/5	0.94	0.13	62,68,72,75	0
3	SO4	D	505	5/5	0.95	0.12	50,54,56,60	0
3	SO4	H	505	5/5	0.95	0.10	55,55,57,58	0
3	SO4	F	501	5/5	0.97	0.11	41,43,44,46	0
3	SO4	B	501	5/5	0.97	0.07	40,40,40,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	SO4	D	501	5/5	0.98	0.07	42,42,46,48	0
3	SO4	H	501	5/5	0.98	0.07	43,44,46,47	0

6.5 Other polymers [i](#)

There are no such residues in this entry.