



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 10:17 PM UTC

PDB ID : 4LW9 / pdb_00004lw9
Title : Crystal structure of Vibrio cholera major pseudopilin EpsG
Authors : Vago, F.S.; Raghunathan, K.; Jens, J.C.; Wedemeyer, W.J.; Bagdasarian, M.;
Brunzelle, J.S.; Arvidson, D.N.
Deposited on : 2013-07-26
Resolution : 1.90 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:

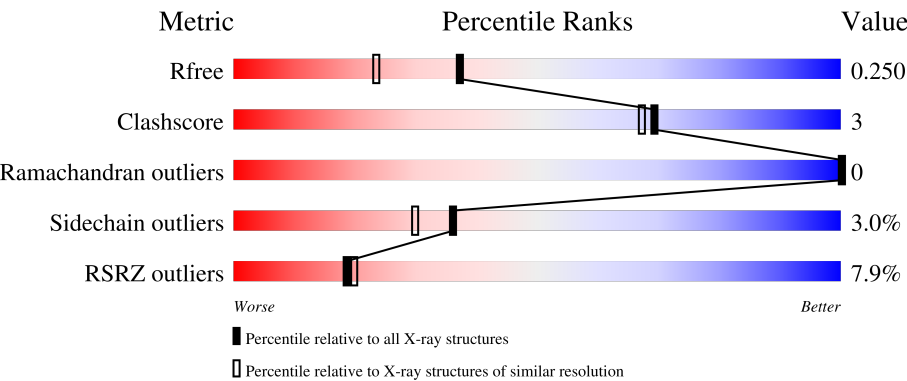
MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry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

1 Overall quality at a glance i

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

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	120	8% 88% 12%
1	B	120	3% 91% 8%
1	C	120	8% 92%
1	D	120	7% 89% 10%
1	E	120	5% 88% 10%

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Mol	Chain	Length	Quality of chain
1	F	120	
1	I	120	
1	J	120	
1	K	120	
1	L	120	
1	Q	120	
1	R	120	

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
5	CL	B	207	-	-	-	X
5	CL	D	207	-	-	X	X

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 11720 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 Type II secretion system protein G.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	119	Total	C	N	O	S	0	0	0
			925	576	160	188	1			
1	B	118	Total	C	N	O	S	0	0	0
			924	575	160	188	1			
1	C	118	Total	C	N	O	S	0	0	0
			908	569	157	181	1			
1	D	119	Total	C	N	O	S	0	0	0
			912	568	156	187	1			
1	E	118	Total	C	N	O	S	0	0	0
			916	572	160	183	1			
1	F	114	Total	C	N	O	S	0	0	0
			868	542	152	173	1			
1	I	117	Total	C	N	O	S	0	0	0
			896	559	153	183	1			
1	J	119	Total	C	N	O	S	0	0	0
			912	568	157	186	1			
1	K	117	Total	C	N	O	S	0	0	0
			887	556	151	179	1			
1	L	118	Total	C	N	O	S	0	0	0
			920	573	160	186	1			
1	Q	119	Total	C	N	O	S	0	0	0
			927	577	160	189	1			
1	R	118	Total	C	N	O	S	0	0	0
			918	572	158	187	1			

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	138	LEU	-	expression tag	UNP P45773
A	139	GLU	-	expression tag	UNP P45773
A	140	HIS	-	expression tag	UNP P45773
A	141	HIS	-	expression tag	UNP P45773
A	142	HIS	-	expression tag	UNP P45773

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Chain	Residue	Modelled	Actual	Comment	Reference
A	143	HIS	-	expression tag	UNP P45773
A	144	HIS	-	expression tag	UNP P45773
A	145	HIS	-	expression tag	UNP P45773
B	138	LEU	-	expression tag	UNP P45773
B	139	GLU	-	expression tag	UNP P45773
B	140	HIS	-	expression tag	UNP P45773
B	141	HIS	-	expression tag	UNP P45773
B	142	HIS	-	expression tag	UNP P45773
B	143	HIS	-	expression tag	UNP P45773
B	144	HIS	-	expression tag	UNP P45773
B	145	HIS	-	expression tag	UNP P45773
C	138	LEU	-	expression tag	UNP P45773
C	139	GLU	-	expression tag	UNP P45773
C	140	HIS	-	expression tag	UNP P45773
C	141	HIS	-	expression tag	UNP P45773
C	142	HIS	-	expression tag	UNP P45773
C	143	HIS	-	expression tag	UNP P45773
C	144	HIS	-	expression tag	UNP P45773
C	145	HIS	-	expression tag	UNP P45773
D	138	LEU	-	expression tag	UNP P45773
D	139	GLU	-	expression tag	UNP P45773
D	140	HIS	-	expression tag	UNP P45773
D	141	HIS	-	expression tag	UNP P45773
D	142	HIS	-	expression tag	UNP P45773
D	143	HIS	-	expression tag	UNP P45773
D	144	HIS	-	expression tag	UNP P45773
D	145	HIS	-	expression tag	UNP P45773
E	138	LEU	-	expression tag	UNP P45773
E	139	GLU	-	expression tag	UNP P45773
E	140	HIS	-	expression tag	UNP P45773
E	141	HIS	-	expression tag	UNP P45773
E	142	HIS	-	expression tag	UNP P45773
E	143	HIS	-	expression tag	UNP P45773
E	144	HIS	-	expression tag	UNP P45773
E	145	HIS	-	expression tag	UNP P45773
F	138	LEU	-	expression tag	UNP P45773
F	139	GLU	-	expression tag	UNP P45773
F	140	HIS	-	expression tag	UNP P45773
F	141	HIS	-	expression tag	UNP P45773
F	142	HIS	-	expression tag	UNP P45773
F	143	HIS	-	expression tag	UNP P45773
F	144	HIS	-	expression tag	UNP P45773

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Chain	Residue	Modelled	Actual	Comment	Reference
F	145	HIS	-	expression tag	UNP P45773
I	138	LEU	-	expression tag	UNP P45773
I	139	GLU	-	expression tag	UNP P45773
I	140	HIS	-	expression tag	UNP P45773
I	141	HIS	-	expression tag	UNP P45773
I	142	HIS	-	expression tag	UNP P45773
I	143	HIS	-	expression tag	UNP P45773
I	144	HIS	-	expression tag	UNP P45773
I	145	HIS	-	expression tag	UNP P45773
J	138	LEU	-	expression tag	UNP P45773
J	139	GLU	-	expression tag	UNP P45773
J	140	HIS	-	expression tag	UNP P45773
J	141	HIS	-	expression tag	UNP P45773
J	142	HIS	-	expression tag	UNP P45773
J	143	HIS	-	expression tag	UNP P45773
J	144	HIS	-	expression tag	UNP P45773
J	145	HIS	-	expression tag	UNP P45773
K	138	LEU	-	expression tag	UNP P45773
K	139	GLU	-	expression tag	UNP P45773
K	140	HIS	-	expression tag	UNP P45773
K	141	HIS	-	expression tag	UNP P45773
K	142	HIS	-	expression tag	UNP P45773
K	143	HIS	-	expression tag	UNP P45773
K	144	HIS	-	expression tag	UNP P45773
K	145	HIS	-	expression tag	UNP P45773
L	138	LEU	-	expression tag	UNP P45773
L	139	GLU	-	expression tag	UNP P45773
L	140	HIS	-	expression tag	UNP P45773
L	141	HIS	-	expression tag	UNP P45773
L	142	HIS	-	expression tag	UNP P45773
L	143	HIS	-	expression tag	UNP P45773
L	144	HIS	-	expression tag	UNP P45773
L	145	HIS	-	expression tag	UNP P45773
Q	138	LEU	-	expression tag	UNP P45773
Q	139	GLU	-	expression tag	UNP P45773
Q	140	HIS	-	expression tag	UNP P45773
Q	141	HIS	-	expression tag	UNP P45773
Q	142	HIS	-	expression tag	UNP P45773
Q	143	HIS	-	expression tag	UNP P45773
Q	144	HIS	-	expression tag	UNP P45773
Q	145	HIS	-	expression tag	UNP P45773
R	138	LEU	-	expression tag	UNP P45773

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Chain	Residue	Modelled	Actual	Comment	Reference
R	139	GLU	-	expression tag	UNP P45773
R	140	HIS	-	expression tag	UNP P45773
R	141	HIS	-	expression tag	UNP P45773
R	142	HIS	-	expression tag	UNP P45773
R	143	HIS	-	expression tag	UNP P45773
R	144	HIS	-	expression tag	UNP P45773
R	145	HIS	-	expression tag	UNP P45773

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	3	Total 3	Zn 3	0	0
2	B	1	Total 1	Zn 1	0	0
2	C	3	Total 3	Zn 3	0	0
2	D	3	Total 3	Zn 3	0	0
2	E	4	Total 4	Zn 4	0	0
2	F	2	Total 2	Zn 2	0	0
2	I	3	Total 3	Zn 3	0	0
2	J	2	Total 2	Zn 2	0	0
2	K	4	Total 4	Zn 4	0	0
2	L	3	Total 3	Zn 3	0	0
2	Q	3	Total 3	Zn 3	0	0
2	R	1	Total 1	Zn 1	0	0

- Molecule 3 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total 2	Na 2	0	0
3	B	3	Total 3	Na 3	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	1	Total 1	Na 1	0	0

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total 1	Ca 1	0	0
4	B	1	Total 1	Ca 1	0	0
4	C	1	Total 1	Ca 1	0	0
4	D	1	Total 1	Ca 1	0	0
4	E	1	Total 1	Ca 1	0	0
4	F	2	Total 2	Ca 2	0	0
4	I	1	Total 1	Ca 1	0	0
4	J	1	Total 1	Ca 1	0	0
4	K	1	Total 1	Ca 1	0	0
4	L	1	Total 1	Ca 1	0	0
4	Q	2	Total 2	Ca 2	0	0
4	R	1	Total 1	Ca 1	0	0

- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total 1	Cl 1	0	0
5	B	1	Total 1	Cl 1	0	0
5	D	1	Total 1	Cl 1	0	0
5	E	2	Total 2	Cl 2	0	0

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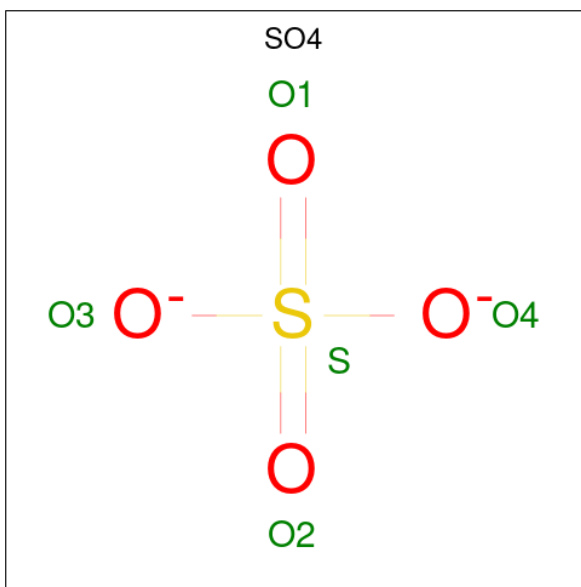
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	K	1	Total	Cl	0	0
			1	1		
5	L	1	Total	Cl	0	0
			1	1		
5	R	2	Total	Cl	0	0
			2	2		

- Molecule 6 is PLATINUM (II) ION (CCD ID: PT) (formula: Pt).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Pt	0	0
			1	1		
6	B	1	Total	Pt	0	0
			1	1		
6	C	1	Total	Pt	0	0
			1	1		
6	D	1	Total	Pt	0	0
			1	1		
6	E	1	Total	Pt	0	0
			1	1		
6	F	1	Total	Pt	0	0
			1	1		
6	I	1	Total	Pt	0	0
			1	1		
6	J	1	Total	Pt	0	0
			1	1		
6	K	1	Total	Pt	0	0
			1	1		
6	L	1	Total	Pt	0	0
			1	1		
6	Q	1	Total	Pt	0	0
			1	1		
6	R	1	Total	Pt	0	0
			1	1		

- Molecule 7 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	O	S	0	0
			5	4	1		
7	B	1	Total	O	S	0	0
			5	4	1		
7	C	1	Total	O	S	0	0
			5	4	1		
7	D	1	Total	O	S	0	0
			5	4	1		
7	D	1	Total	O	S	0	0
			5	4	1		
7	E	1	Total	O	S	0	0
			5	4	1		
7	F	1	Total	O	S	0	0
			5	4	1		
7	I	1	Total	O	S	0	0
			5	4	1		
7	I	1	Total	O	S	0	0
			5	4	1		
7	J	1	Total	O	S	0	0
			5	4	1		
7	K	1	Total	O	S	0	0
			5	4	1		
7	K	1	Total	O	S	0	0
			5	4	1		
7	Q	1	Total	O	S	0	0
			5	4	1		
7	R	1	Total	O	S	0	0
			5	4	1		

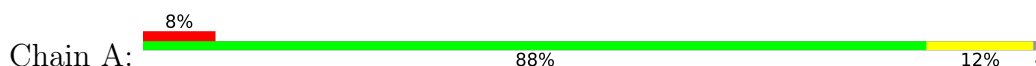
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	56	Total 56	O 56	0	0
8	B	59	Total 59	O 59	0	0
8	C	53	Total 53	O 53	0	0
8	D	72	Total 72	O 72	0	0
8	E	58	Total 58	O 58	0	0
8	F	34	Total 34	O 34	0	0
8	I	67	Total 67	O 67	0	0
8	J	54	Total 54	O 54	0	0
8	K	44	Total 44	O 44	0	0
8	L	60	Total 60	O 60	0	0
8	Q	56	Total 56	O 56	0	0
8	R	51	Total 51	O 51	0	0

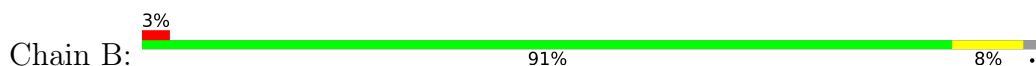
3 Residue-property plots [i](#)

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.

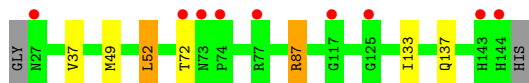
- Molecule 1: Type II secretion system protein G



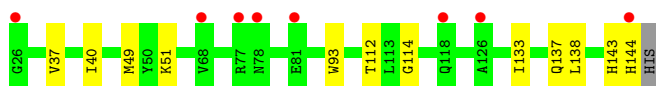
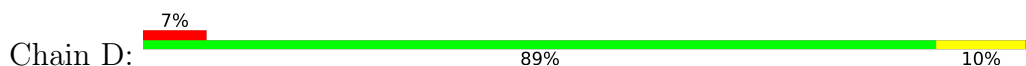
- Molecule 1: Type II secretion system protein G



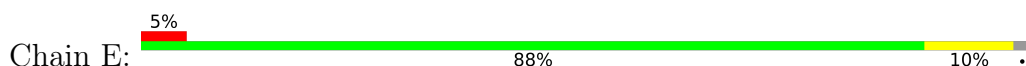
- Molecule 1: Type II secretion system protein G



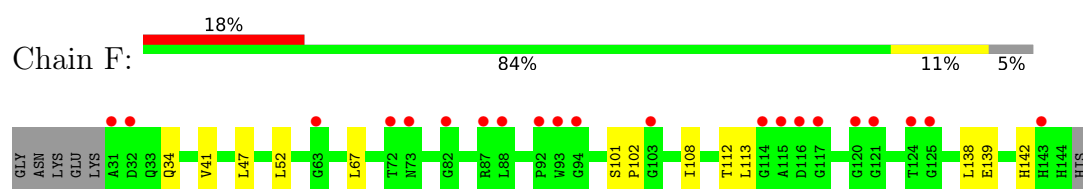
- Molecule 1: Type II secretion system protein G



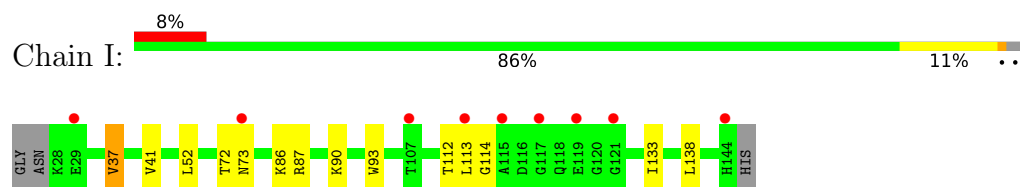
- Molecule 1: Type II secretion system protein G



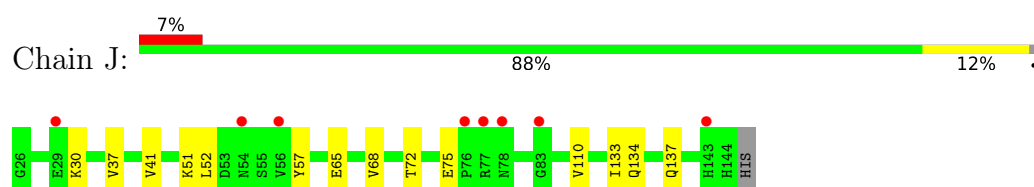
- Molecule 1: Type II secretion system protein G



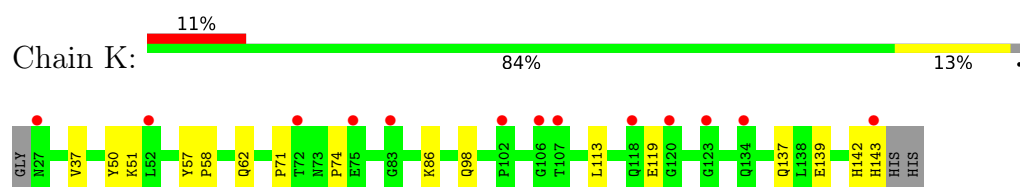
- Molecule 1: Type II secretion system protein G



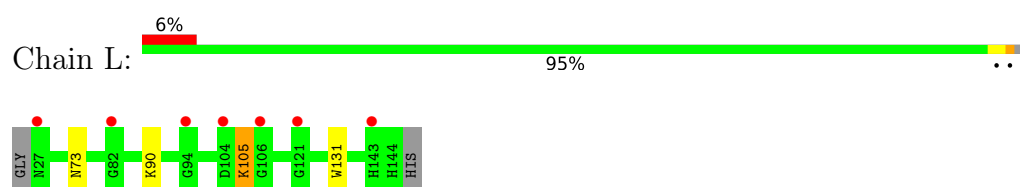
- Molecule 1: Type II secretion system protein G



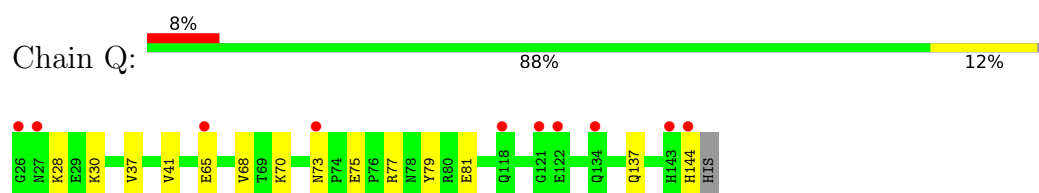
- Molecule 1: Type II secretion system protein G



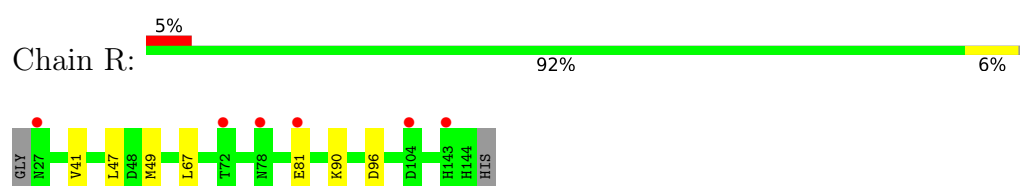
- Molecule 1: Type II secretion system protein G



- Molecule 1: Type II secretion system protein G



- Molecule 1: Type II secretion system protein G



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	88.61Å 70.02Å 131.54Å 90.00° 103.29° 90.00°	Depositor
Resolution (Å)	29.54 – 1.90 29.54 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.8 (29.54-1.90) 99.7 (29.54-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.04 (at 1.91Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.202 , 0.245 0.209 , 0.250	Depositor DCC
R_{free} test set	6178 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	27.7	Xtriage
Anisotropy	0.008	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 46.0	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	0.95	EDS
Total number of atoms	11720	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.48% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PT, ZN, SO4, CL, CA, NA

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	0.74	0/948	0.89	2/1289 (0.2%)
1	B	0.68	0/947	0.80	0/1288
1	C	0.69	0/931	0.86	0/1267
1	D	0.66	0/934	0.86	0/1272
1	E	0.60	0/939	0.80	0/1277
1	F	0.58	0/891	0.77	0/1218
1	I	0.69	0/918	0.87	0/1252
1	J	0.63	0/934	0.83	0/1272
1	K	0.64	0/909	0.86	0/1240
1	L	0.62	0/943	0.88	1/1283 (0.1%)
1	Q	0.67	0/949	0.85	0/1289
1	R	0.73	0/941	0.84	0/1281
All	All	0.66	0/11184	0.84	3/15228 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	44	GLU	OE1-CD-OE2	-5.42	109.90	122.90
1	L	73	ASN	CB-CA-C	-5.15	106.52	111.00
1	A	44	GLU	CG-CD-OE1	5.14	130.22	118.40

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	925	0	854	10	0
1	B	924	0	851	8	0
1	C	908	0	837	7	0
1	D	912	0	831	10	0
1	E	916	0	848	7	0
1	F	868	0	784	7	0
1	I	896	0	813	11	0
1	J	912	0	834	7	0
1	K	887	0	808	11	1
1	L	920	0	847	1	0
1	Q	927	0	860	6	0
1	R	918	0	841	6	0
2	A	3	0	0	0	0
2	B	1	0	0	0	0
2	C	3	0	0	0	0
2	D	3	0	0	0	0
2	E	4	0	0	0	0
2	F	2	0	0	0	0
2	I	3	0	0	0	0
2	J	2	0	0	0	0
2	K	4	0	0	0	0
2	L	3	0	0	0	0
2	Q	3	0	0	0	0
2	R	1	0	0	0	0
3	A	2	0	0	0	0
3	B	3	0	0	0	0
3	D	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	2	0	0	0	0
4	I	1	0	0	0	0
4	J	1	0	0	0	0
4	K	1	0	0	0	0
4	L	1	0	0	0	0
4	Q	2	0	0	0	0
4	R	1	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	1	0	0	2	0
5	E	2	0	0	0	0
5	K	1	0	0	0	0
5	L	1	0	0	0	0
5	R	2	0	0	1	1
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
6	E	1	0	0	0	0
6	F	1	0	0	0	0
6	I	1	0	0	0	0
6	J	1	0	0	0	0
6	K	1	0	0	0	0
6	L	1	0	0	0	0
6	Q	1	0	0	0	0
6	R	1	0	0	0	0
7	A	5	0	0	1	0
7	B	5	0	0	0	0
7	C	5	0	0	0	0
7	D	10	0	0	0	0
7	E	5	0	0	0	0
7	F	5	0	0	0	0
7	I	10	0	0	0	0
7	J	5	0	0	0	0
7	K	10	0	0	0	0
7	Q	5	0	0	0	0
7	R	5	0	0	0	0
8	A	56	0	0	0	0
8	B	59	0	0	1	0
8	C	53	0	0	0	0
8	D	72	0	0	1	0
8	E	58	0	0	0	0
8	F	34	0	0	0	0
8	I	67	0	0	2	0
8	J	54	0	0	0	0
8	K	44	0	0	1	0
8	L	60	0	0	0	0
8	Q	56	0	0	0	0
8	R	51	0	0	0	0
All	All	11720	0	10008	73	1

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 (73) 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:D:143:HIS:HA	1:D:144:HIS:C	2.07	0.79
1:B:37:VAL:HG11	1:B:137:GLN:HG2	1.71	0.72
1:D:49:MET:HE2	5:D:207:CL:CL	2.28	0.71
1:B:49:MET:HE2	5:B:207:CL:CL	2.28	0.70
1:I:37:VAL:HA	1:I:133:ILE:HD11	1.87	0.56
1:K:113:LEU:HD12	1:K:119:GLU:HA	1.88	0.56
1:E:52:LEU:HD21	1:F:138:LEU:HD21	1.87	0.55
1:E:113:LEU:HD13	1:E:118:GLN:HA	1.88	0.55
1:B:134:GLN:HB2	8:B:327:HOH:O	2.06	0.55
1:C:37:VAL:HG11	1:C:137:GLN:HG2	1.88	0.55
1:A:41:VAL:HG11	1:B:41:VAL:CG1	2.38	0.54
1:A:138:LEU:HD21	1:B:52:LEU:HD21	1.92	0.52
1:A:37:VAL:HG11	1:A:137:GLN:HG2	1.92	0.52
1:K:62:GLN:NE2	1:K:74:PRO:O	2.41	0.52
1:I:86:LYS:HG2	8:I:358:HOH:O	2.09	0.52
1:K:37:VAL:HG11	1:K:137:GLN:HG2	1.92	0.52
1:A:41:VAL:CG1	1:B:41:VAL:HG11	2.41	0.51
1:D:143:HIS:CA	1:D:144:HIS:C	2.82	0.50
1:Q:41:VAL:CG1	1:R:41:VAL:HG11	2.42	0.50
1:R:49:MET:HB2	5:R:205:CL:CL	2.49	0.50
1:K:139:GLU:OE2	1:K:142:HIS:CE1	2.64	0.49
1:K:98:GLN:HG3	1:K:113:LEU:CD2	2.43	0.49
1:Q:41:VAL:HG11	1:R:41:VAL:CG1	2.43	0.49
1:I:41:VAL:HG11	1:J:41:VAL:CG1	2.43	0.48
1:D:37:VAL:HG11	1:D:137:GLN:HG2	1.95	0.48
1:E:41:VAL:HG11	1:F:41:VAL:CG1	2.44	0.48
1:I:138:LEU:HD21	1:J:52:LEU:HD21	1.95	0.48
1:I:86:LYS:NZ	8:I:363:HOH:O	2.47	0.47
1:D:37:VAL:HA	1:D:133:ILE:HD11	1.96	0.47
1:R:90:LYS:NZ	1:R:96:ASP:OD1	2.34	0.47
1:D:40:ILE:HD11	1:D:112:THR:HG22	1.96	0.47
1:J:65:GLU:O	1:J:68:VAL:HG22	2.14	0.47
1:E:47:LEU:HD13	1:E:108:ILE:HD12	1.97	0.46
1:I:37:VAL:HB	1:I:133:ILE:HD11	1.97	0.46
1:J:51:LYS:HD2	1:J:57:TYR:CZ	2.50	0.46
1:J:37:VAL:HG11	1:J:137:GLN:HG2	1.98	0.46
1:F:139:GLU:OE1	1:F:142:HIS:CE1	2.69	0.45
1:K:50:TYR:CD2	1:K:58:PRO:HD3	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:139:GLU:OE2	1:E:144:HIS:HE1	1.94	0.45
1:K:51:LYS:HD2	1:K:57:TYR:CE2	2.52	0.44
1:F:101:SER:HA	1:F:102:PRO:C	2.42	0.44
1:Q:70:LYS:HE2	1:Q:79:TYR:HB3	1.98	0.44
1:Q:65:GLU:O	1:Q:68:VAL:HG22	2.18	0.44
1:A:37:VAL:HA	1:A:133:ILE:HD11	2.00	0.44
1:E:41:VAL:CG1	1:F:41:VAL:HG11	2.48	0.43
1:R:47:LEU:HD23	1:R:67:LEU:HD21	2.00	0.43
1:C:49:MET:HE3	1:C:49:MET:HA	2.01	0.43
1:A:41:VAL:HG11	1:B:41:VAL:HG11	2.00	0.43
1:J:41:VAL:HG23	1:J:133:ILE:CD1	2.48	0.43
1:A:93:TRP:CZ3	1:A:114:GLY:HA2	2.54	0.43
1:D:51:LYS:HE3	8:D:367:HOH:O	2.18	0.43
1:C:52:LEU:HD11	1:D:138:LEU:HD21	2.01	0.43
1:D:49:MET:HB2	5:D:207:CL:CL	2.56	0.42
1:F:47:LEU:HD23	1:F:67:LEU:HD21	2.01	0.42
1:K:98:GLN:HG3	1:K:113:LEU:HD21	2.00	0.42
1:I:93:TRP:CZ3	1:I:114:GLY:HA2	2.54	0.42
1:L:105:LYS:HG3	1:L:131:TRP:CD2	2.55	0.41
1:F:47:LEU:HD13	1:F:108:ILE:HD12	2.01	0.41
1:K:51:LYS:HD2	1:K:57:TYR:CD2	2.54	0.41
1:I:52:LEU:HD21	1:J:30:LYS:HE3	2.02	0.41
1:C:87:ARG:HD3	1:I:90:LYS:HD2	2.03	0.41
1:D:93:TRP:CZ3	1:D:114:GLY:HA2	2.56	0.41
1:Q:41:VAL:CG1	1:R:41:VAL:CG1	2.97	0.41
1:C:37:VAL:HA	1:C:133:ILE:HD11	2.02	0.41
1:E:71:PRO:HD2	1:E:76:PRO:HG3	2.03	0.41
1:C:87:ARG:CZ	1:I:90:LYS:HG3	2.51	0.41
1:K:71:PRO:HB3	8:K:341:HOH:O	2.20	0.41
1:A:101:SER:HB2	1:A:108:ILE:HG22	2.02	0.40
1:A:140:HIS:N	7:A:209:SO4:O1	2.45	0.40
1:K:51:LYS:CD	1:K:57:TYR:CE2	3.04	0.40
1:Q:37:VAL:HG11	1:Q:137:GLN:HG2	2.04	0.40
1:A:52:LEU:HD21	1:B:30:LYS:HE3	2.04	0.40
1:C:87:ARG:NE	1:I:90:LYS:HG3	2.37	0.40

All (1) 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)
1:K:143:HIS:NE2	5:R:203:CL:CL[2_757]	2.16	0.04

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	117/120 (98%)	114 (97%)	3 (3%)	0	100	100
1	B	116/120 (97%)	115 (99%)	1 (1%)	0	100	100
1	C	116/120 (97%)	113 (97%)	3 (3%)	0	100	100
1	D	117/120 (98%)	116 (99%)	1 (1%)	0	100	100
1	E	116/120 (97%)	113 (97%)	3 (3%)	0	100	100
1	F	112/120 (93%)	110 (98%)	2 (2%)	0	100	100
1	I	115/120 (96%)	112 (97%)	3 (3%)	0	100	100
1	J	117/120 (98%)	114 (97%)	3 (3%)	0	100	100
1	K	115/120 (96%)	113 (98%)	2 (2%)	0	100	100
1	L	116/120 (97%)	113 (97%)	3 (3%)	0	100	100
1	Q	117/120 (98%)	115 (98%)	2 (2%)	0	100	100
1	R	116/120 (97%)	113 (97%)	3 (3%)	0	100	100
All	All	1390/1440 (96%)	1361 (98%)	29 (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	96/99 (97%)	94 (98%)	2 (2%)	47	44
1	B	96/99 (97%)	94 (98%)	2 (2%)	47	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	92/99 (93%)	89 (97%)	3 (3%)	33	26
1	D	93/99 (94%)	93 (100%)	0	100	100
1	E	94/99 (95%)	92 (98%)	2 (2%)	47	44
1	F	87/99 (88%)	83 (95%)	4 (5%)	24	16
1	I	91/99 (92%)	85 (93%)	6 (7%)	15	8
1	J	93/99 (94%)	89 (96%)	4 (4%)	26	18
1	K	89/99 (90%)	88 (99%)	1 (1%)	65	67
1	L	95/99 (96%)	93 (98%)	2 (2%)	47	44
1	Q	96/99 (97%)	89 (93%)	7 (7%)	13	6
1	R	95/99 (96%)	94 (99%)	1 (1%)	65	67
All	All	1117/1188 (94%)	1083 (97%)	34 (3%)	36	30

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	86	LYS
1	A	118	GLN
1	B	87	ARG
1	B	144	HIS
1	C	52	LEU
1	C	72	THR
1	C	87	ARG
1	E	51	LYS
1	E	86	LYS
1	F	34	GLN
1	F	52	LEU
1	F	112	THR
1	F	113	LEU
1	I	37	VAL
1	I	72	THR
1	I	73	ASN
1	I	87	ARG
1	I	112	THR
1	I	113	LEU
1	J	72	THR
1	J	75	GLU
1	J	110	VAL
1	J	134	GLN

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Mol	Chain	Res	Type
1	K	86	LYS
1	L	90	LYS
1	L	105	LYS
1	Q	28	LYS
1	Q	30	LYS
1	Q	73	ASN
1	Q	75	GLU
1	Q	77	ARG
1	Q	81	GLU
1	Q	144	HIS
1	R	81	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	33	GLN
1	C	144	HIS
1	E	45	ASN
1	I	98	GLN
1	I	134	GLN
1	K	45	ASN
1	K	134	GLN
1	L	34	GLN
1	R	34	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 87 ligands modelled in this entry, 73 are monoatomic - leaving 14 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	$\# Z > 2$
7	SO4	I	207	-	4,4,4	0.24	0	6,6,6	0.15	0
7	SO4	K	209	-	4,4,4	0.24	0	6,6,6	0.27	0
7	SO4	E	209	-	4,4,4	0.28	0	6,6,6	0.24	0
7	SO4	A	209	-	4,4,4	0.18	0	6,6,6	0.37	0
7	SO4	K	208	-	4,4,4	0.24	0	6,6,6	0.07	0
7	SO4	D	208	-	4,4,4	0.25	0	6,6,6	0.13	0
7	SO4	D	209	-	4,4,4	0.24	0	6,6,6	0.32	0
7	SO4	C	206	-	4,4,4	0.31	0	6,6,6	0.24	0
7	SO4	B	208	-	4,4,4	0.24	0	6,6,6	0.22	0
7	SO4	J	205	-	4,4,4	0.34	0	6,6,6	0.24	0
7	SO4	I	206	-	4,4,4	0.25	0	6,6,6	0.47	0
7	SO4	Q	207	-	4,4,4	0.20	0	6,6,6	0.20	0
7	SO4	F	206	-	4,4,4	0.24	0	6,6,6	0.17	0
7	SO4	R	206	-	4,4,4	0.35	0	6,6,6	0.23	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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	209	SO4	1	0

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	119/120 (99%)	0.59	10 (8%) 17 18	16, 28, 48, 54	0
1	B	118/120 (98%)	0.29	4 (3%) 48 51	16, 27, 44, 50	0
1	C	118/120 (98%)	0.64	9 (7%) 20 21	16, 31, 50, 60	0
1	D	119/120 (99%)	0.64	8 (6%) 24 25	17, 31, 48, 53	0
1	E	118/120 (98%)	0.55	6 (5%) 33 36	21, 30, 45, 52	0
1	F	114/120 (95%)	1.19	21 (18%) 3 3	23, 38, 60, 62	0
1	I	117/120 (97%)	0.74	9 (7%) 19 21	17, 32, 53, 57	0
1	J	119/120 (99%)	0.77	8 (6%) 24 25	20, 33, 54, 59	0
1	K	117/120 (97%)	0.91	13 (11%) 10 11	20, 37, 53, 58	0
1	L	118/120 (98%)	0.69	7 (5%) 28 30	19, 35, 48, 54	0
1	Q	119/120 (99%)	0.56	10 (8%) 17 18	15, 29, 46, 56	0
1	R	118/120 (98%)	0.25	6 (5%) 33 36	16, 25, 38, 46	0
All	All	1414/1440 (98%)	0.65	111 (7%) 18 20	15, 31, 51, 62	0

All (111) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	26	GLY	6.9
1	K	72	THR	5.6
1	Q	26	GLY	5.6
1	C	143	HIS	5.0
1	C	72	THR	4.7
1	F	31	ALA	4.7
1	E	27	ASN	4.5
1	D	78	ASN	4.4
1	C	74	PRO	4.2
1	K	143	HIS	4.2
1	L	143	HIS	4.0

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Mol	Chain	Res	Type	RSRZ
1	B	27	ASN	3.9
1	J	143	HIS	3.7
1	E	143	HIS	3.6
1	K	102	PRO	3.6
1	Q	27	ASN	3.4
1	Q	73	ASN	3.4
1	D	144	HIS	3.3
1	F	143	HIS	3.3
1	Q	144	HIS	3.2
1	F	93	TRP	3.2
1	A	26	GLY	3.2
1	B	143	HIS	3.2
1	I	144	HIS	3.2
1	D	77	ARG	3.2
1	L	106	GLY	3.1
1	E	82	GLY	3.1
1	I	115	ALA	3.1
1	F	120	GLY	3.1
1	L	27	ASN	3.1
1	C	73	ASN	3.0
1	Q	143	HIS	3.0
1	R	143	HIS	3.0
1	I	117	GLY	3.0
1	A	118	GLN	3.0
1	C	27	ASN	3.0
1	A	144	HIS	2.9
1	C	125	GLY	2.9
1	F	94	GLY	2.9
1	A	94	GLY	2.9
1	F	117	GLY	2.9
1	K	27	ASN	2.8
1	K	107	THR	2.8
1	R	72	THR	2.8
1	J	77	ARG	2.8
1	Q	65	GLU	2.8
1	R	104	ASP	2.8
1	F	88	LEU	2.8
1	J	76	PRO	2.8
1	F	87	ARG	2.8
1	A	120	GLY	2.8
1	B	144	HIS	2.8
1	F	72	THR	2.8

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Mol	Chain	Res	Type	RSRZ
1	K	134	GLN	2.7
1	C	117	GLY	2.7
1	Q	121	GLY	2.7
1	F	115	ALA	2.7
1	A	125	GLY	2.7
1	A	134	GLN	2.7
1	Q	122	GLU	2.7
1	F	73	ASN	2.6
1	D	118	GLN	2.6
1	J	54	ASN	2.6
1	J	78	ASN	2.6
1	F	116	ASP	2.6
1	L	121	GLY	2.6
1	D	126	ALA	2.6
1	Q	118	GLN	2.6
1	F	125	GLY	2.5
1	I	107	THR	2.5
1	K	123	GLY	2.4
1	Q	134	GLN	2.4
1	I	119	GLU	2.4
1	R	81	GLU	2.4
1	J	56	VAL	2.4
1	J	29	GLU	2.3
1	C	77	ARG	2.3
1	A	27	ASN	2.3
1	K	120	GLY	2.3
1	K	118	GLN	2.3
1	F	124	THR	2.3
1	I	113	LEU	2.3
1	E	31	ALA	2.2
1	F	103	GLY	2.2
1	F	114	GLY	2.2
1	F	63	GLY	2.2
1	A	143	HIS	2.2
1	I	29	GLU	2.2
1	F	82	GLY	2.2
1	L	82	GLY	2.2
1	I	73	ASN	2.2
1	E	104	ASP	2.2
1	C	144	HIS	2.1
1	E	78	ASN	2.1
1	L	104	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	68	VAL	2.1
1	I	121	GLY	2.1
1	D	81	GLU	2.1
1	R	27	ASN	2.1
1	F	121	GLY	2.1
1	K	83	GLY	2.1
1	A	61	ASP	2.1
1	B	123	GLY	2.1
1	J	83	GLY	2.1
1	F	92	PRO	2.1
1	K	52	LEU	2.1
1	F	32	ASP	2.1
1	K	75	GLU	2.0
1	K	106	GLY	2.0
1	L	94	GLY	2.0
1	R	78	ASN	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
7	SO4	J	205	5/5	0.62	0.19	70,71,71,71	0
5	CL	B	207	1/1	0.67	0.61	33,33,33,33	1
7	SO4	D	209	5/5	0.68	0.16	69,70,70,70	0
7	SO4	Q	207	5/5	0.70	0.17	62,63,64,64	0
7	SO4	E	209	5/5	0.71	0.15	62,63,64,64	0
7	SO4	C	206	5/5	0.72	0.17	69,69,70,70	0
7	SO4	D	208	5/5	0.72	0.13	82,82,83,83	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	CL	D	207	1/1	0.72	0.54	34,34,34,34	1
7	SO4	R	206	5/5	0.73	0.16	64,65,65,66	0
7	SO4	F	206	5/5	0.77	0.14	69,69,69,70	0
7	SO4	A	209	5/5	0.78	0.12	54,54,55,56	0
7	SO4	K	209	5/5	0.78	0.17	70,70,71,71	0
7	SO4	I	207	5/5	0.79	0.16	69,69,70,70	0
2	ZN	J	202	1/1	0.81	0.16	64,64,64,64	0
7	SO4	B	208	5/5	0.84	0.13	48,50,51,52	0
3	NA	A	207	1/1	0.85	0.20	38,38,38,38	0
3	NA	A	204	1/1	0.86	0.19	41,41,41,41	0
5	CL	E	207	1/1	0.86	0.53	34,34,34,34	1
2	ZN	E	203	1/1	0.88	0.14	53,53,53,53	0
7	SO4	K	208	5/5	0.88	0.08	79,80,80,80	0
5	CL	L	206	1/1	0.88	0.35	30,30,30,30	1
6	PT	I	205	1/1	0.88	0.17	30,30,30,30	1
6	PT	K	207	1/1	0.88	0.12	45,45,45,45	1
6	PT	J	204	1/1	0.89	0.12	52,52,52,52	1
5	CL	R	205	1/1	0.89	0.43	25,25,25,25	1
6	PT	B	206	1/1	0.89	0.10	37,37,37,37	1
6	PT	C	205	1/1	0.89	0.19	38,38,38,38	1
2	ZN	D	202	1/1	0.89	0.10	49,49,49,49	0
2	ZN	F	201	1/1	0.90	0.09	47,47,47,47	0
5	CL	E	208	1/1	0.91	0.49	30,30,30,30	1
4	CA	F	202	1/1	0.91	0.10	54,54,54,54	0
5	CL	R	203	1/1	0.91	0.10	45,45,45,45	0
6	PT	F	204	1/1	0.91	0.23	46,46,46,46	1
5	CL	A	206	1/1	0.92	0.08	40,40,40,40	0
2	ZN	K	204	1/1	0.92	0.09	68,68,68,68	0
6	PT	L	205	1/1	0.92	0.10	38,38,38,38	1
2	ZN	C	203	1/1	0.92	0.12	51,51,51,51	0
3	NA	D	204	1/1	0.93	0.16	43,43,43,43	0
2	ZN	D	203	1/1	0.93	0.09	62,62,62,62	0
6	PT	D	206	1/1	0.93	0.10	37,37,37,37	1
4	CA	F	203	1/1	0.94	0.06	38,38,38,38	0
6	PT	Q	206	1/1	0.94	0.17	39,39,39,39	1
2	ZN	L	204	1/1	0.94	0.10	61,61,61,61	0
5	CL	K	205	1/1	0.95	0.17	44,44,44,44	0
6	PT	E	206	1/1	0.95	0.21	32,32,32,32	1
4	CA	K	206	1/1	0.95	0.08	44,44,44,44	0
4	CA	B	202	1/1	0.96	0.04	34,34,34,34	0
3	NA	B	204	1/1	0.96	0.08	37,37,37,37	0
7	SO4	I	206	5/5	0.96	0.11	38,38,39,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	CA	I	204	1/1	0.97	0.06	45,45,45,45	0
2	ZN	I	202	1/1	0.97	0.04	32,32,32,32	0
4	CA	L	203	1/1	0.97	0.04	33,33,33,33	0
4	CA	Q	204	1/1	0.97	0.05	33,33,33,33	0
4	CA	Q	205	1/1	0.97	0.05	29,29,29,29	0
6	PT	A	208	1/1	0.97	0.18	27,27,27,27	1
4	CA	A	205	1/1	0.97	0.06	42,42,42,42	0
2	ZN	K	202	1/1	0.97	0.05	31,31,31,31	0
3	NA	B	201	1/1	0.97	0.09	33,33,33,33	0
2	ZN	Q	201	1/1	0.97	0.04	33,33,33,33	0
4	CA	C	204	1/1	0.98	0.05	39,39,39,39	0
4	CA	D	205	1/1	0.98	0.06	40,40,40,40	0
2	ZN	L	201	1/1	0.98	0.05	31,31,31,31	0
2	ZN	L	202	1/1	0.98	0.03	29,29,29,29	0
2	ZN	F	205	1/1	0.98	0.03	30,30,30,30	0
4	CA	J	203	1/1	0.98	0.03	28,28,28,28	0
3	NA	B	205	1/1	0.98	0.12	27,27,27,27	0
2	ZN	A	202	1/1	0.98	0.03	26,26,26,26	0
2	ZN	R	201	1/1	0.98	0.04	28,28,28,28	0
6	PT	R	204	1/1	0.98	0.19	27,27,27,27	1
2	ZN	J	201	1/1	0.98	0.03	27,27,27,27	0
4	CA	R	202	1/1	0.98	0.04	23,23,23,23	0
2	ZN	D	201	1/1	0.99	0.04	27,27,27,27	0
2	ZN	K	201	1/1	0.99	0.04	24,24,24,24	0
2	ZN	E	204	1/1	0.99	0.03	29,29,29,29	0
2	ZN	B	203	1/1	0.99	0.02	29,29,29,29	0
2	ZN	A	201	1/1	0.99	0.03	21,21,21,21	0
2	ZN	I	201	1/1	0.99	0.03	29,29,29,29	0
2	ZN	E	201	1/1	0.99	0.03	29,29,29,29	0
2	ZN	I	203	1/1	0.99	0.03	25,25,25,25	0
2	ZN	Q	203	1/1	0.99	0.03	22,22,22,22	0
2	ZN	E	202	1/1	0.99	0.03	27,27,27,27	0
4	CA	E	205	1/1	0.99	0.02	25,25,25,25	0
2	ZN	K	203	1/1	1.00	0.01	26,26,26,26	0
2	ZN	C	202	1/1	1.00	0.02	23,23,23,23	0
2	ZN	Q	202	1/1	1.00	0.02	21,21,21,21	0
2	ZN	A	203	1/1	1.00	0.01	20,20,20,20	0
2	ZN	C	201	1/1	1.00	0.02	22,22,22,22	0

6.5 Other polymers ⓘ

There are no such residues in this entry.