



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:10 PM UTC

PDB ID : 5LTV / pdb_00005ltv
Title : LIGAND BINDING DOMAIN OF PSEUDOMONAS AERUGINOSA PAO1
AMINO ACID CHEMORECEPTOR PCTC IN COMPLEX WITH GABA
Authors : Gavira, J.A.; Rico-Jimenez, M.; Conejero-Muriel, M.; Krell, T.
Deposited on : 2016-09-07
Resolution : 2.31 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

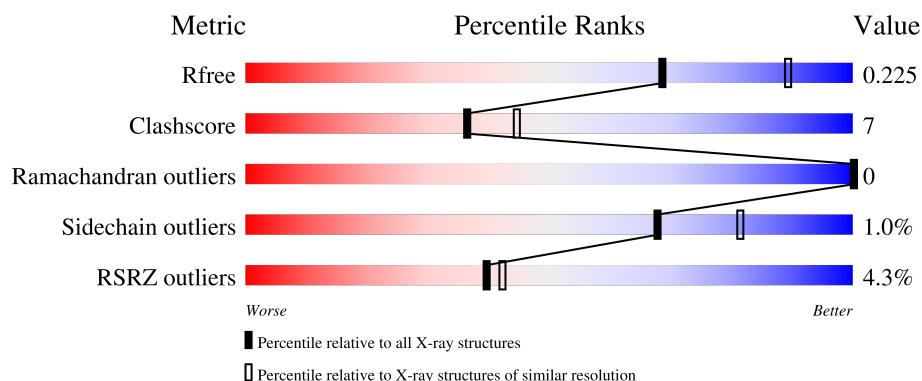
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.31 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	7754 (2.34-2.30)
Clashscore	190562	8383 (2.34-2.30)
Ramachandran outliers	187476	8303 (2.34-2.30)
Sidechain outliers	187428	8303 (2.34-2.30)
RSRZ outliers	180081	7760 (2.34-2.30)

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	273	3% 66% 12% • 21%
1	B	273	2% 68% 8% 23%
1	C	273	2% 72% 10% 18%
1	D	273	• 73% 10% 17%
1	E	273	3% 68% 13% • 18%

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Mol	Chain	Length	Quality of chain
1	F	273	4% 67% 13% 20%
1	G	273	8% 60% 12% 27%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 12780 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 Chemotactic transducer PctC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	215	Total	C	N	O	S	0	7	0
			1697	1085	282	325	5			
1	B	209	Total	C	N	O	S	0	4	0
			1623	1040	272	306	5			
1	C	223	Total	C	N	O	S	0	6	0
			1750	1119	294	332	5			
1	D	226	Total	C	N	O	S	0	9	0
			1791	1139	301	345	6			
1	E	224	Total	C	N	O	S	0	3	0
			1728	1104	287	332	5			
1	F	219	Total	C	N	O	S	0	6	0
			1735	1109	292	329	5			
1	G	200	Total	C	N	O	S	0	7	0
			1589	1020	271	293	5			

There are 154 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	9	MET	-	initiating methionine	UNP A0A080VJ62
A	10	GLY	-	expression tag	UNP A0A080VJ62
A	11	SER	-	expression tag	UNP A0A080VJ62
A	12	SER	-	expression tag	UNP A0A080VJ62
A	13	HIS	-	expression tag	UNP A0A080VJ62
A	14	HIS	-	expression tag	UNP A0A080VJ62
A	15	HIS	-	expression tag	UNP A0A080VJ62
A	16	HIS	-	expression tag	UNP A0A080VJ62
A	17	HIS	-	expression tag	UNP A0A080VJ62
A	18	HIS	-	expression tag	UNP A0A080VJ62
A	19	SER	-	expression tag	UNP A0A080VJ62
A	20	SER	-	expression tag	UNP A0A080VJ62
A	21	GLY	-	expression tag	UNP A0A080VJ62
A	22	LEU	-	expression tag	UNP A0A080VJ62
A	23	VAL	-	expression tag	UNP A0A080VJ62

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Chain	Residue	Modelled	Actual	Comment	Reference
A	24	PRO	-	expression tag	UNP A0A080VJ62
A	25	ARG	-	expression tag	UNP A0A080VJ62
A	26	GLY	-	expression tag	UNP A0A080VJ62
A	27	SER	-	expression tag	UNP A0A080VJ62
A	28	HIS	-	expression tag	UNP A0A080VJ62
A	29	MET	-	expression tag	UNP A0A080VJ62
A	242	SER	ARG	conflict	UNP A0A080VJ62
B	9	MET	-	initiating methionine	UNP A0A080VJ62
B	10	GLY	-	expression tag	UNP A0A080VJ62
B	11	SER	-	expression tag	UNP A0A080VJ62
B	12	SER	-	expression tag	UNP A0A080VJ62
B	13	HIS	-	expression tag	UNP A0A080VJ62
B	14	HIS	-	expression tag	UNP A0A080VJ62
B	15	HIS	-	expression tag	UNP A0A080VJ62
B	16	HIS	-	expression tag	UNP A0A080VJ62
B	17	HIS	-	expression tag	UNP A0A080VJ62
B	18	HIS	-	expression tag	UNP A0A080VJ62
B	19	SER	-	expression tag	UNP A0A080VJ62
B	20	SER	-	expression tag	UNP A0A080VJ62
B	21	GLY	-	expression tag	UNP A0A080VJ62
B	22	LEU	-	expression tag	UNP A0A080VJ62
B	23	VAL	-	expression tag	UNP A0A080VJ62
B	24	PRO	-	expression tag	UNP A0A080VJ62
B	25	ARG	-	expression tag	UNP A0A080VJ62
B	26	GLY	-	expression tag	UNP A0A080VJ62
B	27	SER	-	expression tag	UNP A0A080VJ62
B	28	HIS	-	expression tag	UNP A0A080VJ62
B	29	MET	-	expression tag	UNP A0A080VJ62
B	242	SER	ARG	conflict	UNP A0A080VJ62
C	9	MET	-	initiating methionine	UNP A0A080VJ62
C	10	GLY	-	expression tag	UNP A0A080VJ62
C	11	SER	-	expression tag	UNP A0A080VJ62
C	12	SER	-	expression tag	UNP A0A080VJ62
C	13	HIS	-	expression tag	UNP A0A080VJ62
C	14	HIS	-	expression tag	UNP A0A080VJ62
C	15	HIS	-	expression tag	UNP A0A080VJ62
C	16	HIS	-	expression tag	UNP A0A080VJ62
C	17	HIS	-	expression tag	UNP A0A080VJ62
C	18	HIS	-	expression tag	UNP A0A080VJ62
C	19	SER	-	expression tag	UNP A0A080VJ62
C	20	SER	-	expression tag	UNP A0A080VJ62
C	21	GLY	-	expression tag	UNP A0A080VJ62

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Chain	Residue	Modelled	Actual	Comment	Reference
C	22	LEU	-	expression tag	UNP A0A080VJ62
C	23	VAL	-	expression tag	UNP A0A080VJ62
C	24	PRO	-	expression tag	UNP A0A080VJ62
C	25	ARG	-	expression tag	UNP A0A080VJ62
C	26	GLY	-	expression tag	UNP A0A080VJ62
C	27	SER	-	expression tag	UNP A0A080VJ62
C	28	HIS	-	expression tag	UNP A0A080VJ62
C	29	MET	-	expression tag	UNP A0A080VJ62
C	242	SER	ARG	conflict	UNP A0A080VJ62
D	9	MET	-	initiating methionine	UNP A0A080VJ62
D	10	GLY	-	expression tag	UNP A0A080VJ62
D	11	SER	-	expression tag	UNP A0A080VJ62
D	12	SER	-	expression tag	UNP A0A080VJ62
D	13	HIS	-	expression tag	UNP A0A080VJ62
D	14	HIS	-	expression tag	UNP A0A080VJ62
D	15	HIS	-	expression tag	UNP A0A080VJ62
D	16	HIS	-	expression tag	UNP A0A080VJ62
D	17	HIS	-	expression tag	UNP A0A080VJ62
D	18	HIS	-	expression tag	UNP A0A080VJ62
D	19	SER	-	expression tag	UNP A0A080VJ62
D	20	SER	-	expression tag	UNP A0A080VJ62
D	21	GLY	-	expression tag	UNP A0A080VJ62
D	22	LEU	-	expression tag	UNP A0A080VJ62
D	23	VAL	-	expression tag	UNP A0A080VJ62
D	24	PRO	-	expression tag	UNP A0A080VJ62
D	25	ARG	-	expression tag	UNP A0A080VJ62
D	26	GLY	-	expression tag	UNP A0A080VJ62
D	27	SER	-	expression tag	UNP A0A080VJ62
D	28	HIS	-	expression tag	UNP A0A080VJ62
D	29	MET	-	expression tag	UNP A0A080VJ62
D	242	SER	ARG	conflict	UNP A0A080VJ62
E	9	MET	-	initiating methionine	UNP A0A080VJ62
E	10	GLY	-	expression tag	UNP A0A080VJ62
E	11	SER	-	expression tag	UNP A0A080VJ62
E	12	SER	-	expression tag	UNP A0A080VJ62
E	13	HIS	-	expression tag	UNP A0A080VJ62
E	14	HIS	-	expression tag	UNP A0A080VJ62
E	15	HIS	-	expression tag	UNP A0A080VJ62
E	16	HIS	-	expression tag	UNP A0A080VJ62
E	17	HIS	-	expression tag	UNP A0A080VJ62
E	18	HIS	-	expression tag	UNP A0A080VJ62
E	19	SER	-	expression tag	UNP A0A080VJ62

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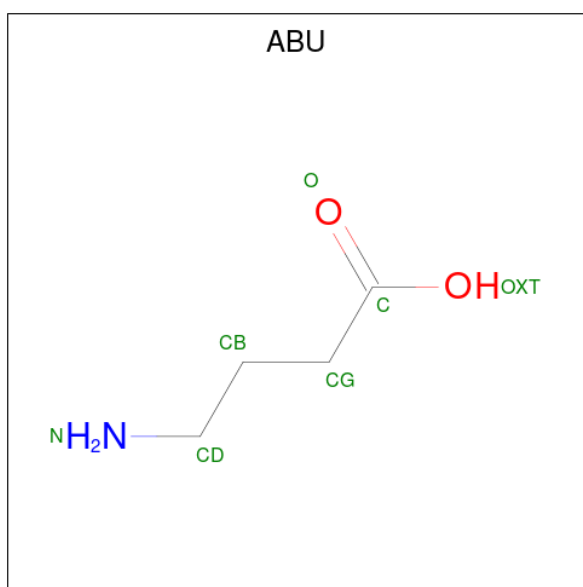
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E	20	SER	-	expression tag	UNP A0A080VJ62
E	21	GLY	-	expression tag	UNP A0A080VJ62
E	22	LEU	-	expression tag	UNP A0A080VJ62
E	23	VAL	-	expression tag	UNP A0A080VJ62
E	24	PRO	-	expression tag	UNP A0A080VJ62
E	25	ARG	-	expression tag	UNP A0A080VJ62
E	26	GLY	-	expression tag	UNP A0A080VJ62
E	27	SER	-	expression tag	UNP A0A080VJ62
E	28	HIS	-	expression tag	UNP A0A080VJ62
E	29	MET	-	expression tag	UNP A0A080VJ62
E	242	SER	ARG	conflict	UNP A0A080VJ62
F	9	MET	-	initiating methionine	UNP A0A080VJ62
F	10	GLY	-	expression tag	UNP A0A080VJ62
F	11	SER	-	expression tag	UNP A0A080VJ62
F	12	SER	-	expression tag	UNP A0A080VJ62
F	13	HIS	-	expression tag	UNP A0A080VJ62
F	14	HIS	-	expression tag	UNP A0A080VJ62
F	15	HIS	-	expression tag	UNP A0A080VJ62
F	16	HIS	-	expression tag	UNP A0A080VJ62
F	17	HIS	-	expression tag	UNP A0A080VJ62
F	18	HIS	-	expression tag	UNP A0A080VJ62
F	19	SER	-	expression tag	UNP A0A080VJ62
F	20	SER	-	expression tag	UNP A0A080VJ62
F	21	GLY	-	expression tag	UNP A0A080VJ62
F	22	LEU	-	expression tag	UNP A0A080VJ62
F	23	VAL	-	expression tag	UNP A0A080VJ62
F	24	PRO	-	expression tag	UNP A0A080VJ62
F	25	ARG	-	expression tag	UNP A0A080VJ62
F	26	GLY	-	expression tag	UNP A0A080VJ62
F	27	SER	-	expression tag	UNP A0A080VJ62
F	28	HIS	-	expression tag	UNP A0A080VJ62
F	29	MET	-	expression tag	UNP A0A080VJ62
F	242	SER	ARG	conflict	UNP A0A080VJ62
G	9	MET	-	initiating methionine	UNP A0A080VJ62
G	10	GLY	-	expression tag	UNP A0A080VJ62
G	11	SER	-	expression tag	UNP A0A080VJ62
G	12	SER	-	expression tag	UNP A0A080VJ62
G	13	HIS	-	expression tag	UNP A0A080VJ62
G	14	HIS	-	expression tag	UNP A0A080VJ62
G	15	HIS	-	expression tag	UNP A0A080VJ62
G	16	HIS	-	expression tag	UNP A0A080VJ62
G	17	HIS	-	expression tag	UNP A0A080VJ62

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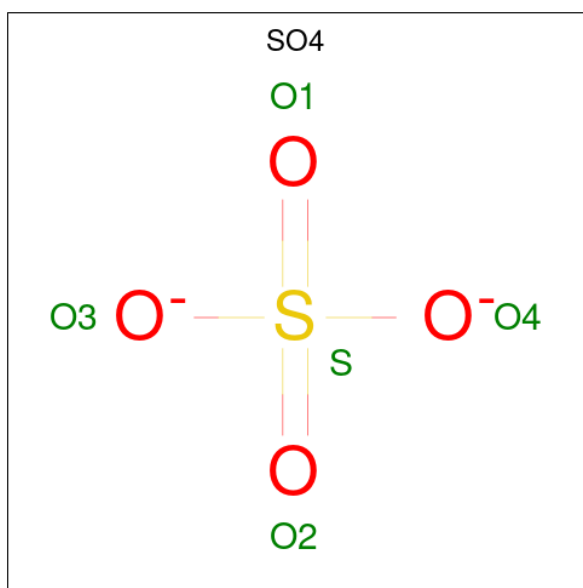
Chain	Residue	Modelled	Actual	Comment	Reference
G	18	HIS	-	expression tag	UNP A0A080VJ62
G	19	SER	-	expression tag	UNP A0A080VJ62
G	20	SER	-	expression tag	UNP A0A080VJ62
G	21	GLY	-	expression tag	UNP A0A080VJ62
G	22	LEU	-	expression tag	UNP A0A080VJ62
G	23	VAL	-	expression tag	UNP A0A080VJ62
G	24	PRO	-	expression tag	UNP A0A080VJ62
G	25	ARG	-	expression tag	UNP A0A080VJ62
G	26	GLY	-	expression tag	UNP A0A080VJ62
G	27	SER	-	expression tag	UNP A0A080VJ62
G	28	HIS	-	expression tag	UNP A0A080VJ62
G	29	MET	-	expression tag	UNP A0A080VJ62
G	242	SER	ARG	conflict	UNP A0A080VJ62

- Molecule 2 is GAMMA-AMINO-BUTANOIC ACID (CCD ID: ABU) (formula: $C_4H_9NO_2$).



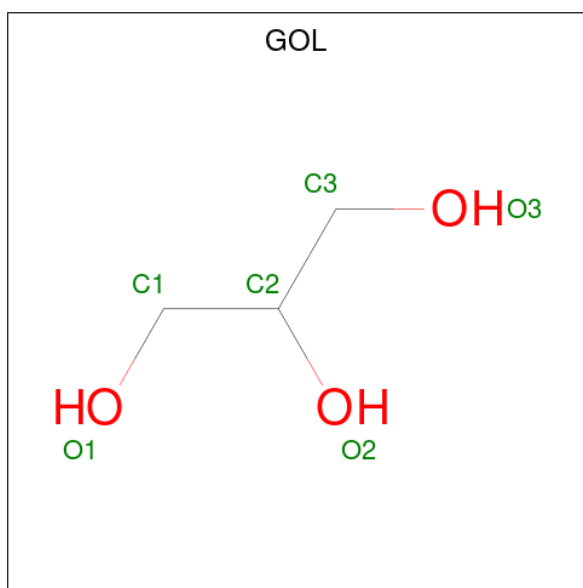
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			7	4	1	2		
2	B	1	Total	C	N	O	0	0
			7	4	1	2		
2	B	1	Total	C	N	O	0	1
			14	8	2	4		
2	D	1	Total	C	N	O	0	1
			14	8	2	4		
2	E	1	Total	C	N	O	0	1
			14	8	2	4		

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



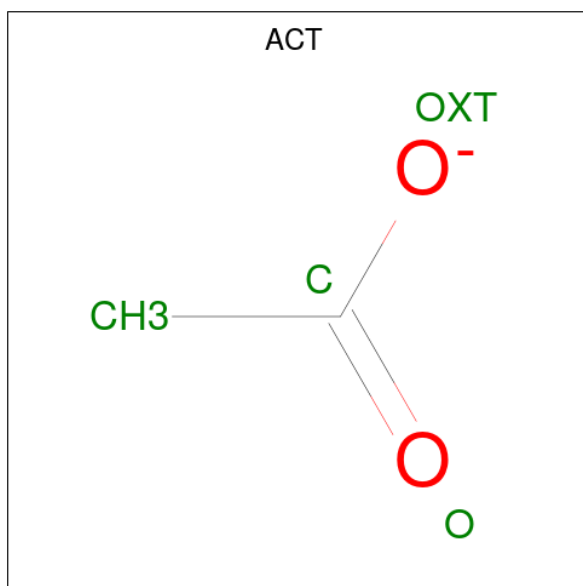
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	F	1	Total	C	O	0	0
			6	3	3		
4	G	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	C	1	Total C O 4 2 2	0	0
5	E	1	Total C O 4 2 2	0	0
5	F	1	Total C O 4 2 2	0	0

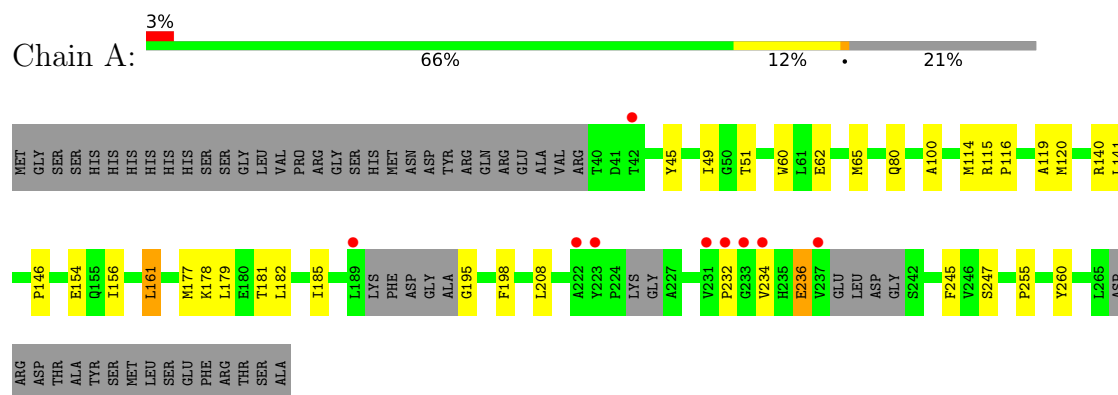
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	100	Total O 100 100	0	0
6	B	105	Total O 105 105	0	0
6	C	86	Total O 86 86	0	0
6	D	120	Total O 120 120	0	0
6	E	108	Total O 108 108	0	0
6	F	91	Total O 91 91	0	0
6	G	94	Total O 94 94	0	0

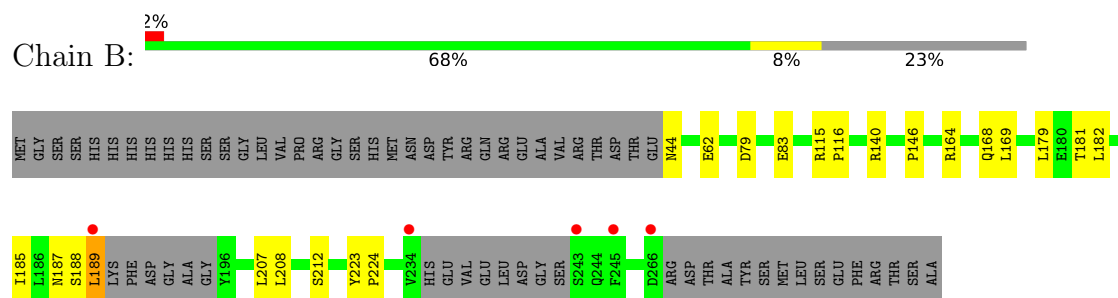
3 Residue-property plots [i](#)

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.

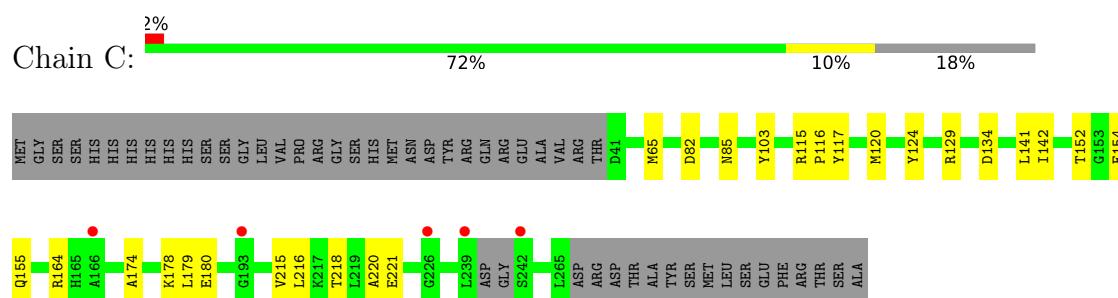
• Molecule 1: Chemotactic transducer PctC



• Molecule 1: Chemotactic transducer PctC

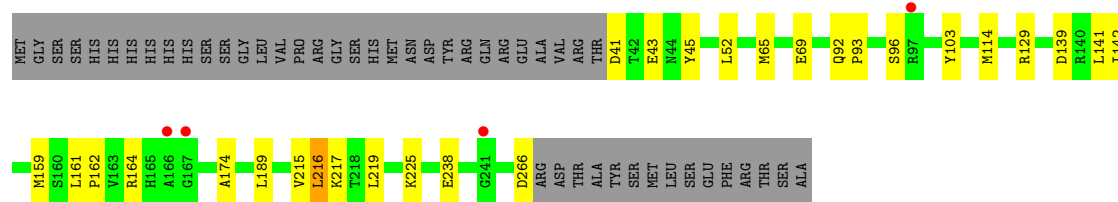


• Molecule 1: Chemotactic transducer PctC

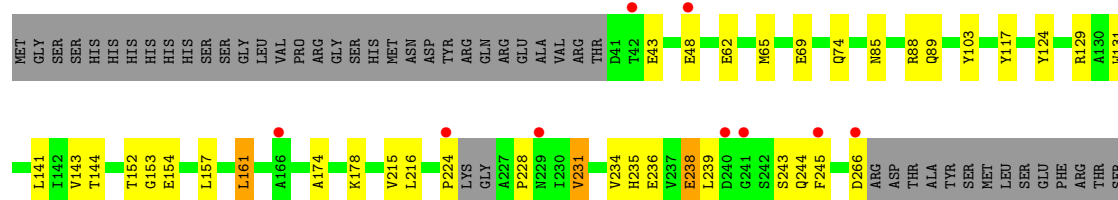


• Molecule 1: Chemotactic transducer PctC

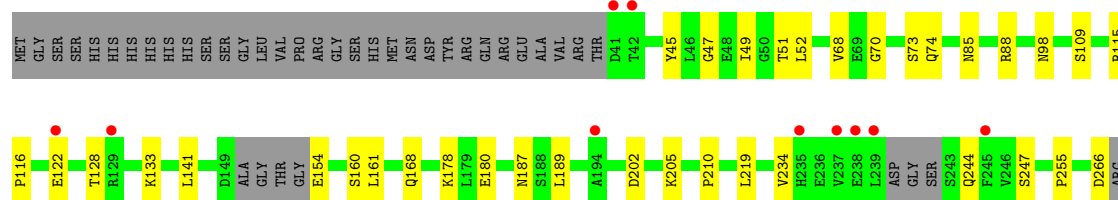




• Molecule 1: Chemotactic transducer PctC



• Molecule 1: Chemotactic transducer PctC



• Molecule 1: Chemotactic transducer PctC



4 Data and refinement statistics

Property	Value	Source
Space group	P 64	Depositor
Cell constants a, b, c, α , β , γ	209.76 Å 209.76 Å 68.89 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.63 – 2.31 48.63 – 2.31	Depositor EDS
% Data completeness (in resolution range)	99.8 (48.63-2.31) 99.8 (48.63-2.31)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.82 (at 2.32 Å)	Xtriage
Refinement program	PHENIX 1.10_2155	Depositor
R, R_{free}	0.177 , 0.226 0.178 , 0.225	Depositor DCC
R_{free} test set	3821 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	37.2	Xtriage
Anisotropy	0.002	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 52.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.027 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	12780	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.95% 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: GOL, ACT, ABU, 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	0.56	1/1731 (0.1%)	0.64	0/2354
1	B	0.52	0/1657	0.74	1/2256 (0.0%)
1	C	0.48	0/1787	0.61	0/2430
1	D	0.53	0/1829	0.62	0/2488
1	E	0.56	0/1765	0.74	6/2404 (0.2%)
1	F	0.56	0/1772	0.63	0/2410
1	G	0.55	0/1622	0.68	0/2204
All	All	0.54	1/12163 (0.0%)	0.67	7/16546 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	G	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	80	GLN	C-N	-5.04	1.22	1.33

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	189	LEU	CB-CG-CD2	-14.85	66.15	110.70
1	E	48	GLU	CB-CG-CD	-9.96	95.67	112.60
1	E	48	GLU	OE1-CD-OE2	-7.71	104.39	122.90
1	E	48	GLU	CG-CD-OE2	6.09	132.41	118.40
1	E	238	GLU	CB-CG-CD	6.03	122.84	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	231	VAL	CG1-CB-CG2	-5.22	99.31	110.80
1	E	238	GLU	CA-CB-CG	-5.07	103.96	114.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	G	178	LYS	Peptide

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	1697	0	1681	21	0
1	B	1623	0	1618	18	0
1	C	1750	0	1739	31	0
1	D	1791	0	1765	21	0
1	E	1728	0	1706	31	0
1	F	1735	0	1712	29	0
1	G	1589	0	1594	31	0
2	A	7	0	0	0	0
2	B	21	0	0	3	0
2	D	14	0	0	0	0
2	E	14	0	0	2	0
3	A	15	0	0	0	0
3	B	10	0	0	0	0
3	C	10	0	0	2	0
3	D	5	0	0	0	0
3	E	10	0	0	0	0
3	F	5	0	0	0	0
3	G	10	0	0	1	0
4	A	6	0	8	0	0
4	F	6	0	8	2	0
4	G	6	0	8	0	0
5	B	12	0	9	0	0
5	C	4	0	3	0	0
5	E	4	0	3	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	F	4	0	3	0	0
6	A	100	0	0	6	2
6	B	105	0	0	5	1
6	C	86	0	0	5	0
6	D	120	0	0	5	1
6	E	108	0	0	6	0
6	F	91	0	0	8	0
6	G	94	0	0	4	0
All	All	12780	0	11857	173	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 7.

All (173) 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:62:GLU:OE2	6:B:401:HOH:O	1.89	0.88
1:E:131:TRP:HE1	1:F:168:GLN:HE22	1.19	0.88
1:G:147:PHE:O	1:G:156:ILE:N	2.07	0.87
1:E:144:THR:OG1	6:E:401:HOH:O	1.92	0.86
1:B:83:GLU:OE1	6:B:402:HOH:O	1.94	0.86
1:D:129[B]:ARG:NH2	6:D:402:HOH:O	2.09	0.85
1:F:202:ASP:OD1	6:F:401:HOH:O	1.96	0.84
1:E:117:TYR:OH	6:E:402:HOH:O	1.97	0.82
1:E:224:PRO:O	6:E:403:HOH:O	1.99	0.81
1:A:140:ARG:NH1	6:A:404:HOH:O	2.13	0.80
1:G:179:LEU:H	1:G:179:LEU:CD1	1.94	0.79
3:C:302:SO4:O3	6:C:401:HOH:O	2.00	0.77
1:A:260:TYR:OH	6:A:401:HOH:O	1.97	0.76
1:D:52:LEU:HD11	1:F:189:LEU:HD21	1.67	0.74
1:C:178[A]:LYS:HE3	1:C:180:GLU:HB2	1.70	0.73
1:E:89:GLN:NE2	6:E:405:HOH:O	2.19	0.73
1:F:45:TYR:O	1:F:49:ILE:HD12	1.87	0.73
1:D:43:GLU:OE1	6:D:401:HOH:O	2.06	0.73
1:G:167:GLY:O	6:G:401:HOH:O	2.07	0.72
1:A:51:THR:OG1	6:A:402:HOH:O	2.06	0.71
1:A:232:PRO:O	6:A:403:HOH:O	2.08	0.71
1:G:179:LEU:H	1:G:179:LEU:HD12	1.53	0.71
1:D:41:ASP:N	1:D:43:GLU:OE1	2.24	0.71
1:F:255:PRO:O	6:F:403:HOH:O	2.08	0.70
1:C:82:ASP:OD1	1:C:85:ASN:N	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:225:LYS:HD3	6:D:501:HOH:O	1.90	0.69
1:E:43:GLU:HG2	1:E:234:VAL:HB	1.73	0.69
1:C:154:GLU:HB3	1:C:178[A]:LYS:HD3	1.73	0.69
1:D:65:MET:HE3	1:D:141:LEU:HD22	1.74	0.68
1:B:44:ASN:N	6:B:406:HOH:O	2.26	0.68
1:G:156:ILE:HA	1:G:178:LYS:HG3	1.76	0.67
3:G:301:SO4:O2	6:G:402:HOH:O	2.10	0.67
1:A:195:GLY:N	6:A:408:HOH:O	2.27	0.67
1:D:215:VAL:HG12	1:D:216:LEU:HD22	1.76	0.67
1:G:178:LYS:HD3	1:G:179:LEU:HD12	1.76	0.66
1:E:85:ASN:OD1	1:E:88:ARG:NH1	2.28	0.66
1:B:79:ASP:O	6:B:403:HOH:O	2.14	0.65
1:E:124:TYR:OH	1:F:168:GLN:NE2	2.29	0.64
1:G:178:LYS:HD3	1:G:179:LEU:CD1	2.28	0.64
1:E:62:GLU:HA	1:E:65:MET:HE2	1.80	0.63
1:B:169:LEU:O	1:C:129[A]:ARG:NH1	2.30	0.63
1:B:140:ARG:NE	6:B:404:HOH:O	2.18	0.63
1:G:181:THR:O	1:G:185:ILE:HD12	1.99	0.63
1:F:244:GLN:NE2	1:F:266:ASP:OD1	2.32	0.63
1:F:154:GLU:N	6:F:410:HOH:O	2.31	0.62
1:G:62:GLU:HA	1:G:65:MET:HE3	1.82	0.62
1:F:128:THR:HA	1:F:133:LYS:HE3	1.81	0.62
1:E:43:GLU:CG	1:E:234:VAL:HB	2.30	0.61
1:C:117:TYR:O	6:C:402:HOH:O	2.16	0.61
1:G:195:GLY:HA2	1:G:264:VAL:O	2.01	0.61
1:B:164[B]:ARG:HH12	2:B:304[B]:ABU:CB	2.13	0.60
1:B:168:GLN:CB	1:C:120:MET:HE1	2.31	0.60
1:A:156:ILE:HG22	1:A:178[A]:LYS:HD3	1.83	0.59
1:F:73:SER:OG	6:F:404:HOH:O	2.16	0.59
1:A:114:MET:HE1	1:A:120:MET:HE3	1.84	0.59
1:D:41:ASP:N	6:D:401:HOH:O	2.36	0.59
1:C:155[B]:GLN:NE2	6:C:405:HOH:O	2.36	0.58
1:D:164[A]:ARG:NH2	1:G:213:GLY:O	2.38	0.57
1:C:218:THR:HG22	1:C:221:GLU:CD	2.29	0.57
1:A:234:VAL:HG22	1:A:247:SER:HB2	1.87	0.56
1:A:236[B]:GLU:HG3	1:A:245:PHE:CE1	2.40	0.56
1:B:168:GLN:HB2	1:C:120:MET:HE1	1.87	0.56
1:A:255:PRO:O	6:A:405:HOH:O	2.17	0.56
1:G:179:LEU:CD1	1:G:179:LEU:N	2.66	0.56
1:D:161:LEU:HD12	1:D:162:PRO:HD2	1.89	0.55
1:D:139:ASP:OD2	6:D:403:HOH:O	2.18	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:119:ALA:O	1:A:120:MET:HE2	2.07	0.55
1:C:218:THR:HG23	1:C:220:ALA:N	2.22	0.54
1:C:103:TYR:CE2	1:C:174:ALA:HB3	2.43	0.53
1:E:65:MET:O	1:E:69:GLU:HG3	2.09	0.53
1:A:62:GLU:HA	1:A:65:MET:HE2	1.91	0.53
1:D:238[B]:GLU:H	1:D:238[B]:GLU:CD	2.16	0.53
1:G:91:GLU:HG3	1:G:115:ARG:HG3	1.92	0.52
1:C:215:VAL:HG12	1:C:216:LEU:HG	1.91	0.52
1:E:103:TYR:CE2	1:E:174:ALA:HB3	2.44	0.52
1:G:61:LEU:O	1:G:65:MET:HG3	2.10	0.52
1:E:178:LYS:NZ	6:E:410:HOH:O	2.42	0.52
1:A:60:TRP:CZ3	1:A:182:LEU:HD21	2.44	0.52
1:B:168:GLN:OE1	2:B:304[B]:ABU:N	2.43	0.51
1:C:154:GLU:HB3	1:C:178[A]:LYS:CD	2.39	0.51
1:B:181:THR:O	1:B:185:ILE:HG12	2.10	0.51
1:C:65:MET:HE3	1:C:141:LEU:HD22	1.92	0.51
1:E:129:ARG:HH11	2:E:301[B]:ABU:N	2.08	0.51
1:E:143:VAL:HG13	1:E:157:LEU:HD13	1.93	0.51
1:C:134:ASP:HB2	1:C:142:ILE:HD13	1.93	0.51
1:F:205:LYS:HE3	6:F:477:HOH:O	2.10	0.51
1:C:154:GLU:HB3	1:C:178[A]:LYS:CE	2.41	0.50
1:E:238:GLU:HG3	1:E:243:SER:HA	1.93	0.50
1:C:178[A]:LYS:HD2	1:C:179:LEU:N	2.27	0.50
1:C:155[A]:GLN:H	1:C:178[A]:LYS:NZ	2.10	0.50
1:E:141:LEU:HA	1:E:161:LEU:HB3	1.94	0.50
1:E:215:VAL:HG12	1:E:216:LEU:HG	1.94	0.50
1:F:68:VAL:HG12	1:F:161:LEU:HD22	1.94	0.50
1:F:47:GLY:O	1:F:51:THR:HG23	2.12	0.49
1:G:246:VAL:HA	1:G:264:VAL:HG22	1.94	0.49
1:B:115:ARG:HA	1:B:116:PRO:C	2.37	0.49
1:E:62:GLU:HG2	1:E:65:MET:HE2	1.93	0.49
1:A:45:TYR:O	1:A:49:ILE:HG13	2.13	0.49
1:C:218:THR:HG23	1:C:220:ALA:H	1.78	0.48
1:A:100:ALA:HB1	1:A:178[A]:LYS:HE2	1.95	0.48
1:E:244:GLN:NE2	1:E:266:ASP:OD2	2.42	0.48
1:B:188:SER:O	1:B:189:LEU:HD12	2.13	0.48
1:G:207:LEU:O	1:G:208:LEU:HD23	2.14	0.48
1:G:247:SER:HB3	1:G:263:LEU:HB2	1.96	0.48
1:C:152:THR:OG1	1:C:154:GLU:HG3	2.13	0.48
1:C:154:GLU:HB3	1:C:178[A]:LYS:HE2	1.96	0.47
1:E:74:GLN:NE2	6:E:413:HOH:O	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:234:VAL:C	1:E:235:HIS:HD1	2.22	0.47
1:F:178:LYS:HB2	4:F:303:GOL:H12	1.96	0.47
1:F:234:VAL:HG22	1:F:247:SER:HB2	1.96	0.47
2:E:301[B]:ABU:N	1:F:168:GLN:NE2	2.63	0.47
1:E:236:GLU:HG3	1:E:245:PHE:CE1	2.50	0.46
1:C:155[A]:GLN:H	1:C:178[A]:LYS:HZ3	1.63	0.46
1:B:182:LEU:HB3	1:B:208:LEU:HD21	1.98	0.46
1:A:141:LEU:HA	1:A:161:LEU:HB3	1.97	0.46
1:A:154:GLU:OE1	1:A:178[A]:LYS:NZ	2.43	0.46
1:F:187:ASN:HD22	1:F:210:PRO:HB3	1.80	0.46
1:G:179:LEU:HD23	1:G:208:LEU:HD22	1.97	0.46
1:G:209:HIS:ND1	1:G:211:ASP:HB2	2.29	0.46
1:B:223:TYR:HA	1:B:224:PRO:HD2	1.73	0.45
1:E:152:THR:OG1	1:E:154:GLU:HG2	2.17	0.45
1:E:228:PRO:HD3	1:E:239:LEU:HD11	1.98	0.45
1:F:88[A]:ARG:NE	6:F:420:HOH:O	2.48	0.45
1:G:103:TYR:CE2	1:G:174:ALA:HB3	2.52	0.45
1:C:178[A]:LYS:HE3	1:C:180:GLU:CB	2.43	0.45
1:B:146:PRO:HB3	1:B:179:LEU:HD11	1.98	0.45
1:G:156:ILE:N	1:G:178:LYS:HE3	2.32	0.45
1:E:231:VAL:CG2	1:E:235:HIS:CD2	3.00	0.45
1:F:109:SER:N	6:F:405:HOH:O	2.17	0.45
1:D:45:TYR:CE1	1:F:45:TYR:HE1	2.34	0.45
1:B:187:ASN:C	1:B:189:LEU:N	2.75	0.44
1:G:168:GLN:HA	6:G:407:HOH:O	2.16	0.44
1:E:234:VAL:C	1:E:235:HIS:ND1	2.76	0.44
1:C:129[A]:ARG:NH2	6:C:413:HOH:O	2.51	0.44
1:F:98:ASN:C	4:F:303:GOL:H32	2.43	0.43
1:F:141:LEU:HA	1:F:160:SER:O	2.18	0.43
1:G:148:VAL:HG12	6:G:417:HOH:O	2.18	0.43
1:A:115:ARG:HA	1:A:116:PRO:C	2.43	0.43
1:G:156:ILE:HA	1:G:178:LYS:CG	2.46	0.43
1:F:70:GLY:O	1:F:74:GLN:HG3	2.18	0.43
1:G:45:TYR:CD1	1:G:46:LEU:HD22	2.53	0.43
1:D:103:TYR:CE2	1:D:174:ALA:HB3	2.54	0.43
1:C:164[A]:ARG:NH2	6:C:412:HOH:O	2.51	0.43
1:E:231:VAL:HG23	1:E:235:HIS:CD2	2.54	0.43
1:C:155[A]:GLN:OE1	1:C:215:VAL:HG11	2.19	0.42
1:F:219:LEU:HD23	1:F:219:LEU:HA	1.91	0.42
1:D:189:LEU:HD21	1:F:52:LEU:HD22	2.01	0.42
1:A:198:PHE:HB2	1:A:208:LEU:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:115:ARG:HA	1:C:116:PRO:C	2.43	0.42
1:D:142:ILE:O	1:D:159:MET:HA	2.20	0.42
1:E:231:VAL:HG23	1:E:235:HIS:NE2	2.34	0.42
1:A:146:PRO:HB3	1:A:179:LEU:HD11	2.02	0.42
1:C:115:ARG:NH2	3:C:303:SO4:O2	2.45	0.41
1:D:92:GLN:OE1	1:F:73:SER:HB3	2.20	0.41
1:B:207:LEU:O	1:B:208:LEU:HD12	2.19	0.41
1:F:122[B]:GLU:OE1	6:F:402:HOH:O	2.21	0.41
1:G:234:VAL:HA	1:G:246:VAL:O	2.20	0.41
1:G:179:LEU:CD2	1:G:183:THR:OG1	2.69	0.41
1:C:120:MET:HE2	1:C:124:TYR:CZ	2.55	0.41
1:G:146:PRO:HD2	1:G:207:LEU:HD22	2.02	0.41
1:E:154:GLU:HG2	1:E:154:GLU:H	1.74	0.41
1:F:85:ASN:OD1	1:F:88[A]:ARG:NH1	2.54	0.41
1:F:115:ARG:HA	1:F:116:PRO:C	2.45	0.41
2:B:304[B]:ABU:CD	1:C:129[B]:ARG:HD3	2.51	0.41
1:D:93:PRO:HG3	1:E:153:GLY:CA	2.51	0.41
1:G:197:ALA:HA	1:G:262:ALA:O	2.20	0.41
1:D:65:MET:O	1:D:69:GLU:HG3	2.21	0.41
1:D:219:LEU:HD23	1:D:219:LEU:HA	1.93	0.41
1:G:62:GLU:HG2	1:G:65:MET:HE3	2.03	0.40
1:D:103:TYR:HB3	1:D:114[A]:MET:HG3	2.03	0.40
1:G:68:VAL:HG12	1:G:161:LEU:HD22	2.03	0.40
1:A:181:THR:O	1:A:185:ILE:HG12	2.22	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)
6:A:424:HOH:O	6:D:475:HOH:O[1_556]	1.69	0.51
6:A:484:HOH:O	6:B:463:HOH:O[5_555]	2.04	0.16

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	214/273 (78%)	211 (99%)	3 (1%)	0	100	100
1	B	207/273 (76%)	204 (99%)	3 (1%)	0	100	100
1	C	225/273 (82%)	223 (99%)	2 (1%)	0	100	100
1	D	233/273 (85%)	230 (99%)	3 (1%)	0	100	100
1	E	223/273 (82%)	221 (99%)	2 (1%)	0	100	100
1	F	219/273 (80%)	217 (99%)	2 (1%)	0	100	100
1	G	199/273 (73%)	192 (96%)	7 (4%)	0	100	100
All	All	1520/1911 (80%)	1498 (99%)	22 (1%)	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	179/220 (81%)	175 (98%)	4 (2%)	45	63
1	B	170/220 (77%)	168 (99%)	2 (1%)	63	78
1	C	183/220 (83%)	183 (100%)	0	100	100
1	D	188/220 (86%)	182 (97%)	6 (3%)	34	50
1	E	181/220 (82%)	180 (99%)	1 (1%)	78	88
1	F	182/220 (83%)	180 (99%)	2 (1%)	65	80
1	G	166/220 (76%)	163 (98%)	3 (2%)	51	69
All	All	1249/1540 (81%)	1231 (99%)	18 (1%)	68	75

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	161	LEU
1	A	177	MET

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Mol	Chain	Res	Type
1	A	236[A]	GLU
1	A	236[B]	GLU
1	B	212[A]	SER
1	B	212[B]	SER
1	D	96[A]	SER
1	D	96[B]	SER
1	D	216	LEU
1	D	217[A]	LYS
1	D	217[B]	LYS
1	D	266	ASP
1	E	161	LEU
1	F	180[A]	GLU
1	F	180[B]	GLU
1	G	140[A]	ARG
1	G	140[B]	ARG
1	G	179	LEU

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

Mol	Chain	Res	Type
1	A	56	ASN
1	A	89	GLN
1	A	235	HIS
1	B	44	ASN
1	B	56	ASN
1	B	89	GLN
1	C	56	ASN
1	C	74	GLN
1	C	89	GLN
1	C	92	GLN
1	D	168	GLN
1	F	80	GLN
1	F	168	GLN
1	F	187	ASN
1	G	56	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 ⓘ

30 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	$\# Z > 2$
5	ACT	E	302	-	3,3,3	0.82	0	3,3,3	1.45	0
2	ABU	E	301[A]	-	6,6,6	0.84	0	6,6,6	0.97	0
2	ABU	B	304[B]	-	6,6,6	0.79	0	6,6,6	0.94	0
3	SO4	F	302	-	4,4,4	0.28	0	6,6,6	0.28	0
5	ACT	B	306	-	3,3,3	0.82	0	3,3,3	1.33	0
3	SO4	C	302	-	4,4,4	0.17	0	6,6,6	0.60	0
3	SO4	B	303	-	4,4,4	0.23	0	6,6,6	0.59	0
2	ABU	E	301[B]	-	6,6,6	0.82	0	6,6,6	1.13	0
3	SO4	A	304	-	4,4,4	0.24	0	6,6,6	0.20	0
3	SO4	A	302	-	4,4,4	0.24	0	6,6,6	0.25	0
3	SO4	G	302	-	4,4,4	0.18	0	6,6,6	0.19	0
3	SO4	E	304	-	4,4,4	0.25	0	6,6,6	0.21	0
2	ABU	B	301	-	6,6,6	0.82	0	6,6,6	0.84	0
5	ACT	B	305	-	3,3,3	0.81	0	3,3,3	1.52	0
4	GOL	G	303	-	5,5,5	0.42	0	5,5,5	0.34	0
5	ACT	B	307	-	3,3,3	0.84	0	3,3,3	1.52	0
3	SO4	B	302	-	4,4,4	0.22	0	6,6,6	0.30	0
4	GOL	A	305	-	5,5,5	0.39	0	5,5,5	0.27	0
2	ABU	A	301	-	6,6,6	0.79	0	6,6,6	1.29	1 (16%)
2	ABU	D	301[A]	-	6,6,6	0.92	0	6,6,6	0.86	0
3	SO4	C	303	-	4,4,4	0.22	0	6,6,6	0.17	0
3	SO4	D	302	-	4,4,4	0.26	0	6,6,6	0.59	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	G	301	-	4,4,4	0.27	0	6,6,6	0.72	0
5	ACT	C	301	-	3,3,3	0.78	0	3,3,3	1.36	0
2	ABU	B	304[A]	-	6,6,6	0.86	0	6,6,6	0.78	0
5	ACT	F	301	-	3,3,3	0.91	0	3,3,3	1.22	0
3	SO4	A	303	-	4,4,4	0.37	0	6,6,6	0.32	0
2	ABU	D	301[B]	-	6,6,6	0.79	0	6,6,6	1.76	2 (33%)
3	SO4	E	303	-	4,4,4	0.20	0	6,6,6	0.30	0
4	GOL	F	303	-	5,5,5	0.33	0	5,5,5	0.60	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
2	ABU	A	301	-	-	3/4/4/4	-
2	ABU	E	301[A]	-	-	2/4/4/4	-
2	ABU	B	304[B]	-	-	3/4/4/4	-
4	GOL	A	305	-	-	1/4/4/4	-
2	ABU	D	301[A]	-	-	3/4/4/4	-
2	ABU	E	301[B]	-	-	0/4/4/4	-
2	ABU	D	301[B]	-	-	3/4/4/4	-
2	ABU	B	301	-	-	0/4/4/4	-
4	GOL	G	303	-	-	2/4/4/4	-
4	GOL	F	303	-	-	2/4/4/4	-
2	ABU	B	304[A]	-	-	1/4/4/4	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	301[B]	ABU	CB-CG-C	-2.94	106.85	114.51
2	A	301	ABU	CB-CG-C	2.51	121.06	114.51
2	D	301[B]	ABU	O-C-CG	-2.00	116.75	123.09

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	ABU	CD-CB-CG-C
4	G	303	GOL	O1-C1-C2-C3
2	D	301[B]	ABU	CD-CB-CG-C
4	F	303	GOL	O1-C1-C2-C3
4	F	303	GOL	O1-C1-C2-O2
4	G	303	GOL	O1-C1-C2-O2
2	B	304[A]	ABU	CD-CB-CG-C
2	D	301[A]	ABU	CG-CB-CD-N
2	B	304[B]	ABU	OXT-C-CG-CB
2	B	304[B]	ABU	O-C-CG-CB
2	E	301[A]	ABU	OXT-C-CG-CB
2	E	301[A]	ABU	O-C-CG-CB
4	A	305	GOL	O2-C2-C3-O3
2	D	301[B]	ABU	OXT-C-CG-CB
2	A	301	ABU	OXT-C-CG-CB
2	D	301[A]	ABU	OXT-C-CG-CB
2	A	301	ABU	O-C-CG-CB
2	D	301[B]	ABU	O-C-CG-CB
2	D	301[A]	ABU	O-C-CG-CB
2	B	304[B]	ABU	CD-CB-CG-C

There are no ring outliers.

6 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	304[B]	ABU	3	0
3	C	302	SO4	1	0
2	E	301[B]	ABU	2	0
3	C	303	SO4	1	0
3	G	301	SO4	1	0
4	F	303	GOL	2	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	215/273 (78%)	-0.19	9 (4%)	40	43	15, 34, 84, 102	7 (3%)
1	B	209/273 (76%)	-0.27	5 (2%)	59	62	16, 36, 87, 118	4 (1%)
1	C	223/273 (81%)	-0.05	5 (2%)	62	65	16, 42, 98, 131	6 (2%)
1	D	226/273 (82%)	-0.33	4 (1%)	67	70	14, 34, 77, 105	9 (3%)
1	E	224/273 (82%)	-0.20	9 (4%)	42	45	19, 38, 89, 111	3 (1%)
1	F	219/273 (80%)	-0.16	10 (4%)	37	40	18, 36, 83, 129	6 (2%)
1	G	200/273 (73%)	0.22	23 (11%)	9	11	14, 41, 92, 113	8 (4%)
All	All	1516/1911 (79%)	-0.15	65 (4%)	40	42	14, 37, 88, 131	43 (2%)

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	148	VAL	5.2
1	F	239	LEU	4.9
1	G	147	PHE	4.7
1	F	235[A]	HIS	4.3
1	G	179	LEU	4.2
1	G	245	PHE	3.9
1	G	234	VAL	3.8
1	G	264	VAL	3.6
1	A	189	LEU	3.5
1	C	239	LEU	3.4
1	D	97[A]	ARG	3.4
1	A	223	TYR	3.3
1	E	42	THR	3.3
1	G	196	TYR	3.2
1	E	166	ALA	3.2
1	A	232	PRO	3.1
1	F	122[A]	GLU	3.1

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Mol	Chain	Res	Type	RSRZ
1	G	156	ILE	3.0
1	G	164[A]	ARG	2.9
1	G	195	GLY	2.9
1	A	237	VAL	2.9
1	D	166	ALA	2.8
1	B	243	SER	2.8
1	A	234	VAL	2.8
1	B	234	VAL	2.8
1	C	226	GLY	2.7
1	A	222	ALA	2.7
1	B	189	LEU	2.7
1	C	166	ALA	2.7
1	D	167	GLY	2.6
1	C	242	SER	2.6
1	F	237	VAL	2.5
1	B	266	ASP	2.5
1	G	186	LEU	2.5
1	G	180	GLU	2.5
1	F	129[A]	ARG	2.4
1	G	81	PRO	2.4
1	A	231	VAL	2.4
1	G	213	GLY	2.4
1	G	212	SER	2.3
1	F	42	THR	2.3
1	G	197	ALA	2.3
1	G	42	THR	2.3
1	F	41	ASP	2.2
1	G	210	PRO	2.2
1	A	42	THR	2.2
1	F	245	PHE	2.2
1	E	229	ASN	2.1
1	E	245	PHE	2.1
1	F	194	ALA	2.1
1	G	166	ALA	2.1
1	F	238	GLU	2.1
1	G	178	LYS	2.1
1	G	185	ILE	2.1
1	E	224	PRO	2.1
1	A	233	GLY	2.1
1	D	241	GLY	2.1
1	G	167	GLY	2.1
1	E	266	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	G	188	SER	2.0
1	C	193	GLY	2.0
1	E	241	GLY	2.0
1	B	245	PHE	2.0
1	E	48	GLU	2.0
1	E	240	ASP	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
5	ACT	B	306	4/4	0.71	0.29	111,111,112,112	0
5	ACT	E	302	4/4	0.73	0.20	69,69,69,69	0
5	ACT	F	301	4/4	0.76	0.20	67,69,69,71	0
5	ACT	C	301	4/4	0.79	0.18	87,88,89,90	0
3	SO4	A	304	5/5	0.80	0.09	109,109,110,110	0
5	ACT	B	305	4/4	0.80	0.17	68,71,71,72	0
4	GOL	A	305	6/6	0.82	0.23	95,98,99,100	0
3	SO4	C	303	5/5	0.85	0.16	111,111,111,111	5
4	GOL	F	303	6/6	0.86	0.22	63,69,76,87	0
3	SO4	G	302	5/5	0.87	0.13	109,110,111,113	0
3	SO4	A	303	5/5	0.87	0.15	65,66,67,67	0
5	ACT	B	307	4/4	0.90	0.10	63,63,63,64	0
4	GOL	G	303	6/6	0.92	0.11	73,73,76,77	0
3	SO4	B	302	5/5	0.93	0.10	68,68,70,74	0
2	ABU	D	301[A]	7/7	0.94	0.16	22,24,39,41	7
2	ABU	D	301[B]	7/7	0.94	0.16	19,21,23,27	7
2	ABU	E	301[A]	7/7	0.94	0.12	19,21,32,39	7

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	ABU	E	301[B]	7/7	0.94	0.12	15,19,21,23	7
2	ABU	B	304[A]	7/7	0.94	0.14	32,34,49,50	7
2	ABU	B	304[B]	7/7	0.94	0.14	27,33,35,36	7
2	ABU	A	301	7/7	0.95	0.08	24,31,34,35	0
3	SO4	E	304	5/5	0.96	0.07	73,76,77,78	0
3	SO4	G	301	5/5	0.96	0.07	42,47,48,52	0
2	ABU	B	301	7/7	0.97	0.05	27,28,29,31	0
3	SO4	A	302	5/5	0.97	0.13	39,40,45,46	0
3	SO4	E	303	5/5	0.97	0.06	44,45,48,50	0
3	SO4	B	303	5/5	0.98	0.09	41,44,48,49	0
3	SO4	D	302	5/5	0.98	0.05	32,37,41,43	0
3	SO4	C	302	5/5	0.98	0.05	47,49,52,53	0
3	SO4	F	302	5/5	0.99	0.05	37,40,41,47	0

6.5 Other polymers [i](#)

There are no such residues in this entry.