



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 12, 2017 – 08:49 AM EST

PDB ID : 4ONX  
Title : 2.8 Angstrom Crystal Structure of Sensor Domain of Histidine Kinase from Clostridium perfringens.  
Authors : Minasov, G.; Halavaty, A.; Shuvalova, L.; Dubrovskaya, I.; Winsor, J.; Kwon, K.; Shatsman, S.; Anderson, W.F.; Center for Structural Genomics of Infectious Diseases (CSGID)  
Deposited on : unknown  
Resolution : 2.80 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

---

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

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20030345  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20030345

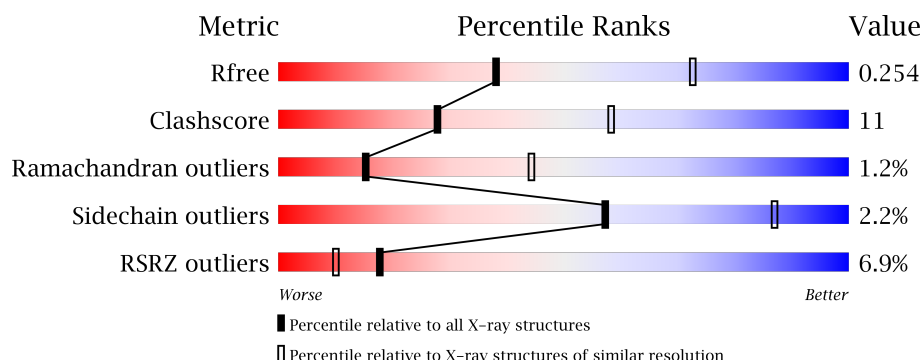
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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))
$R_{free}$	100719	2583 (2.80-2.80)
Clashscore	112137	3033 (2.80-2.80)
Ramachandran outliers	110173	2983 (2.80-2.80)
Sidechain outliers	110143	2985 (2.80-2.80)
RSRZ outliers	101464	2610 (2.80-2.80)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	162	<div> <div>15%</div> <div>65%</div> <div>12%</div> <div>•</div> <div>21%</div> </div>
1	B	162	<div> <div>65%</div> <div>10%</div> <div>•</div> <div>23%</div> </div>
1	C	162	<div> <div>61%</div> <div>17%</div> <div>•</div> <div>21%</div> </div>
1	D	162	<div> <div>60%</div> <div>16%</div> <div>•</div> <div>22%</div> </div>
1	E	162	<div> <div>15%</div> <div>57%</div> <div>22%</div> <div>•</div> <div>20%</div> </div>

*Continued on next page...*

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	162	<div><div></div><div>13%</div><div>60%</div><div>17%</div><div>20%</div><div>••</div></div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6328 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 Sensor histidine kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	128	Total	C	N	O	Se	0	1	0
			1052	670	170	206	6			
1	B	125	Total	C	N	O	Se	0	1	0
			1026	653	166	200	7			
1	C	128	Total	C	N	O	Se	0	1	0
			1052	670	170	206	6			
1	D	126	Total	C	N	O	Se	0	0	0
			1027	653	166	202	6			
1	E	129	Total	C	N	O	Se	0	0	0
			1049	667	170	206	6			
1	F	129	Total	C	N	O	Se	0	0	0
			1049	667	170	206	6			

There are 144 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-23	MSE	-	EXPRESSION TAG	UNP Q0TTS5
A	-22	HIS	-	EXPRESSION TAG	UNP Q0TTS5
A	-21	HIS	-	EXPRESSION TAG	UNP Q0TTS5
A	-20	HIS	-	EXPRESSION TAG	UNP Q0TTS5
A	-19	HIS	-	EXPRESSION TAG	UNP Q0TTS5
A	-18	HIS	-	EXPRESSION TAG	UNP Q0TTS5
A	-17	HIS	-	EXPRESSION TAG	UNP Q0TTS5
A	-16	SER	-	EXPRESSION TAG	UNP Q0TTS5
A	-15	SER	-	EXPRESSION TAG	UNP Q0TTS5
A	-14	GLY	-	EXPRESSION TAG	UNP Q0TTS5
A	-13	VAL	-	EXPRESSION TAG	UNP Q0TTS5
A	-12	ASP	-	EXPRESSION TAG	UNP Q0TTS5
A	-11	LEU	-	EXPRESSION TAG	UNP Q0TTS5
A	-10	GLY	-	EXPRESSION TAG	UNP Q0TTS5
A	-9	THR	-	EXPRESSION TAG	UNP Q0TTS5
A	-8	GLU	-	EXPRESSION TAG	UNP Q0TTS5
A	-7	ASN	-	EXPRESSION TAG	UNP Q0TTS5

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	LEU	-	EXPRESSION TAG	UNP Q0TTS5
A	-5	TYR	-	EXPRESSION TAG	UNP Q0TTS5
A	-4	PHE	-	EXPRESSION TAG	UNP Q0TTS5
A	-3	GLN	-	EXPRESSION TAG	UNP Q0TTS5
A	-2	SER	-	EXPRESSION TAG	UNP Q0TTS5
A	-1	ASN	-	EXPRESSION TAG	UNP Q0TTS5
A	0	ALA	-	EXPRESSION TAG	UNP Q0TTS5
B	-23	MSE	-	EXPRESSION TAG	UNP Q0TTS5
B	-22	HIS	-	EXPRESSION TAG	UNP Q0TTS5
B	-21	HIS	-	EXPRESSION TAG	UNP Q0TTS5
B	-20	HIS	-	EXPRESSION TAG	UNP Q0TTS5
B	-19	HIS	-	EXPRESSION TAG	UNP Q0TTS5
B	-18	HIS	-	EXPRESSION TAG	UNP Q0TTS5
B	-17	HIS	-	EXPRESSION TAG	UNP Q0TTS5
B	-16	SER	-	EXPRESSION TAG	UNP Q0TTS5
B	-15	SER	-	EXPRESSION TAG	UNP Q0TTS5
B	-14	GLY	-	EXPRESSION TAG	UNP Q0TTS5
B	-13	VAL	-	EXPRESSION TAG	UNP Q0TTS5
B	-12	ASP	-	EXPRESSION TAG	UNP Q0TTS5
B	-11	LEU	-	EXPRESSION TAG	UNP Q0TTS5
B	-10	GLY	-	EXPRESSION TAG	UNP Q0TTS5
B	-9	THR	-	EXPRESSION TAG	UNP Q0TTS5
B	-8	GLU	-	EXPRESSION TAG	UNP Q0TTS5
B	-7	ASN	-	EXPRESSION TAG	UNP Q0TTS5
B	-6	LEU	-	EXPRESSION TAG	UNP Q0TTS5
B	-5	TYR	-	EXPRESSION TAG	UNP Q0TTS5
B	-4	PHE	-	EXPRESSION TAG	UNP Q0TTS5
B	-3	GLN	-	EXPRESSION TAG	UNP Q0TTS5
B	-2	SER	-	EXPRESSION TAG	UNP Q0TTS5
B	-1	ASN	-	EXPRESSION TAG	UNP Q0TTS5
B	0	ALA	-	EXPRESSION TAG	UNP Q0TTS5
C	-23	MSE	-	EXPRESSION TAG	UNP Q0TTS5
C	-22	HIS	-	EXPRESSION TAG	UNP Q0TTS5
C	-21	HIS	-	EXPRESSION TAG	UNP Q0TTS5
C	-20	HIS	-	EXPRESSION TAG	UNP Q0TTS5
C	-19	HIS	-	EXPRESSION TAG	UNP Q0TTS5
C	-18	HIS	-	EXPRESSION TAG	UNP Q0TTS5
C	-17	HIS	-	EXPRESSION TAG	UNP Q0TTS5
C	-16	SER	-	EXPRESSION TAG	UNP Q0TTS5
C	-15	SER	-	EXPRESSION TAG	UNP Q0TTS5
C	-14	GLY	-	EXPRESSION TAG	UNP Q0TTS5
C	-13	VAL	-	EXPRESSION TAG	UNP Q0TTS5

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
C	-12	ASP	-	EXPRESSION TAG	UNP Q0TTS5
C	-11	LEU	-	EXPRESSION TAG	UNP Q0TTS5
C	-10	GLY	-	EXPRESSION TAG	UNP Q0TTS5
C	-9	THR	-	EXPRESSION TAG	UNP Q0TTS5
C	-8	GLU	-	EXPRESSION TAG	UNP Q0TTS5
C	-7	ASN	-	EXPRESSION TAG	UNP Q0TTS5
C	-6	LEU	-	EXPRESSION TAG	UNP Q0TTS5
C	-5	TYR	-	EXPRESSION TAG	UNP Q0TTS5
C	-4	PHE	-	EXPRESSION TAG	UNP Q0TTS5
C	-3	GLN	-	EXPRESSION TAG	UNP Q0TTS5
C	-2	SER	-	EXPRESSION TAG	UNP Q0TTS5
C	-1	ASN	-	EXPRESSION TAG	UNP Q0TTS5
C	0	ALA	-	EXPRESSION TAG	UNP Q0TTS5
D	-23	MSE	-	EXPRESSION TAG	UNP Q0TTS5
D	-22	HIS	-	EXPRESSION TAG	UNP Q0TTS5
D	-21	HIS	-	EXPRESSION TAG	UNP Q0TTS5
D	-20	HIS	-	EXPRESSION TAG	UNP Q0TTS5
D	-19	HIS	-	EXPRESSION TAG	UNP Q0TTS5
D	-18	HIS	-	EXPRESSION TAG	UNP Q0TTS5
D	-17	HIS	-	EXPRESSION TAG	UNP Q0TTS5
D	-16	SER	-	EXPRESSION TAG	UNP Q0TTS5
D	-15	SER	-	EXPRESSION TAG	UNP Q0TTS5
D	-14	GLY	-	EXPRESSION TAG	UNP Q0TTS5
D	-13	VAL	-	EXPRESSION TAG	UNP Q0TTS5
D	-12	ASP	-	EXPRESSION TAG	UNP Q0TTS5
D	-11	LEU	-	EXPRESSION TAG	UNP Q0TTS5
D	-10	GLY	-	EXPRESSION TAG	UNP Q0TTS5
D	-9	THR	-	EXPRESSION TAG	UNP Q0TTS5
D	-8	GLU	-	EXPRESSION TAG	UNP Q0TTS5
D	-7	ASN	-	EXPRESSION TAG	UNP Q0TTS5
D	-6	LEU	-	EXPRESSION TAG	UNP Q0TTS5
D	-5	TYR	-	EXPRESSION TAG	UNP Q0TTS5
D	-4	PHE	-	EXPRESSION TAG	UNP Q0TTS5
D	-3	GLN	-	EXPRESSION TAG	UNP Q0TTS5
D	-2	SER	-	EXPRESSION TAG	UNP Q0TTS5
D	-1	ASN	-	EXPRESSION TAG	UNP Q0TTS5
D	0	ALA	-	EXPRESSION TAG	UNP Q0TTS5
E	-23	MSE	-	EXPRESSION TAG	UNP Q0TTS5
E	-22	HIS	-	EXPRESSION TAG	UNP Q0TTS5
E	-21	HIS	-	EXPRESSION TAG	UNP Q0TTS5
E	-20	HIS	-	EXPRESSION TAG	UNP Q0TTS5
E	-19	HIS	-	EXPRESSION TAG	UNP Q0TTS5

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
E	-18	HIS	-	EXPRESSION TAG	UNP Q0TTS5
E	-17	HIS	-	EXPRESSION TAG	UNP Q0TTS5
E	-16	SER	-	EXPRESSION TAG	UNP Q0TTS5
E	-15	SER	-	EXPRESSION TAG	UNP Q0TTS5
E	-14	GLY	-	EXPRESSION TAG	UNP Q0TTS5
E	-13	VAL	-	EXPRESSION TAG	UNP Q0TTS5
E	-12	ASP	-	EXPRESSION TAG	UNP Q0TTS5
E	-11	LEU	-	EXPRESSION TAG	UNP Q0TTS5
E	-10	GLY	-	EXPRESSION TAG	UNP Q0TTS5
E	-9	THR	-	EXPRESSION TAG	UNP Q0TTS5
E	-8	GLU	-	EXPRESSION TAG	UNP Q0TTS5
E	-7	ASN	-	EXPRESSION TAG	UNP Q0TTS5
E	-6	LEU	-	EXPRESSION TAG	UNP Q0TTS5
E	-5	TYR	-	EXPRESSION TAG	UNP Q0TTS5
E	-4	PHE	-	EXPRESSION TAG	UNP Q0TTS5
E	-3	GLN	-	EXPRESSION TAG	UNP Q0TTS5
E	-2	SER	-	EXPRESSION TAG	UNP Q0TTS5
E	-1	ASN	-	EXPRESSION TAG	UNP Q0TTS5
E	0	ALA	-	EXPRESSION TAG	UNP Q0TTS5
F	-23	MSE	-	EXPRESSION TAG	UNP Q0TTS5
F	-22	HIS	-	EXPRESSION TAG	UNP Q0TTS5
F	-21	HIS	-	EXPRESSION TAG	UNP Q0TTS5
F	-20	HIS	-	EXPRESSION TAG	UNP Q0TTS5
F	-19	HIS	-	EXPRESSION TAG	UNP Q0TTS5
F	-18	HIS	-	EXPRESSION TAG	UNP Q0TTS5
F	-17	HIS	-	EXPRESSION TAG	UNP Q0TTS5
F	-16	SER	-	EXPRESSION TAG	UNP Q0TTS5
F	-15	SER	-	EXPRESSION TAG	UNP Q0TTS5
F	-14	GLY	-	EXPRESSION TAG	UNP Q0TTS5
F	-13	VAL	-	EXPRESSION TAG	UNP Q0TTS5
F	-12	ASP	-	EXPRESSION TAG	UNP Q0TTS5
F	-11	LEU	-	EXPRESSION TAG	UNP Q0TTS5
F	-10	GLY	-	EXPRESSION TAG	UNP Q0TTS5
F	-9	THR	-	EXPRESSION TAG	UNP Q0TTS5
F	-8	GLU	-	EXPRESSION TAG	UNP Q0TTS5
F	-7	ASN	-	EXPRESSION TAG	UNP Q0TTS5
F	-6	LEU	-	EXPRESSION TAG	UNP Q0TTS5
F	-5	TYR	-	EXPRESSION TAG	UNP Q0TTS5
F	-4	PHE	-	EXPRESSION TAG	UNP Q0TTS5
F	-3	GLN	-	EXPRESSION TAG	UNP Q0TTS5
F	-2	SER	-	EXPRESSION TAG	UNP Q0TTS5
F	-1	ASN	-	EXPRESSION TAG	UNP Q0TTS5

*Continued on next page...*

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
F	0	ALA	-	EXPRESSION TAG	UNP Q0TTS5

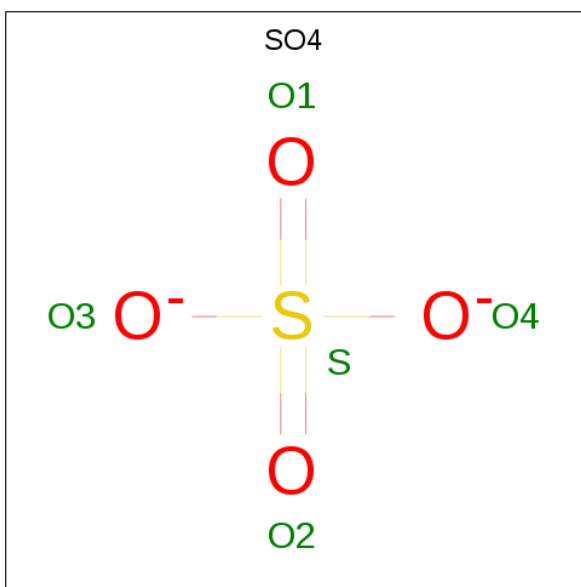
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Zn 1 1	0	0
2	A	1	Total Zn 1 1	0	0
2	D	1	Total Zn 1 1	0	0

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Cl 1 1	0	0
3	A	1	Total Cl 1 1	0	0
3	C	1	Total Cl 1 1	0	0

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).





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

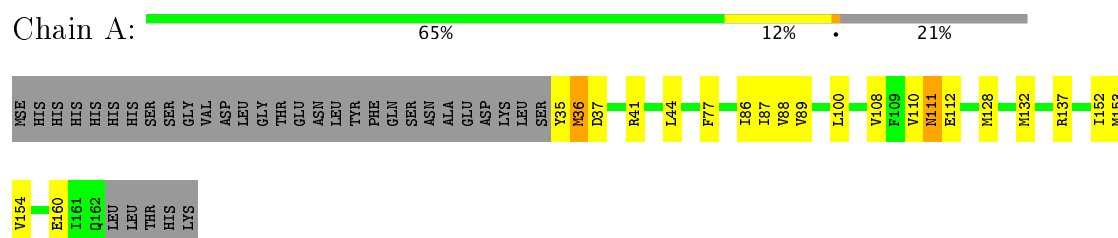
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	13	Total O 13 13	0	0
5	B	6	Total O 6 6	0	0
5	C	5	Total O 5 5	0	0
5	D	7	Total O 7 7	0	0
5	E	3	Total O 3 3	0	0
5	F	8	Total O 8 8	0	0

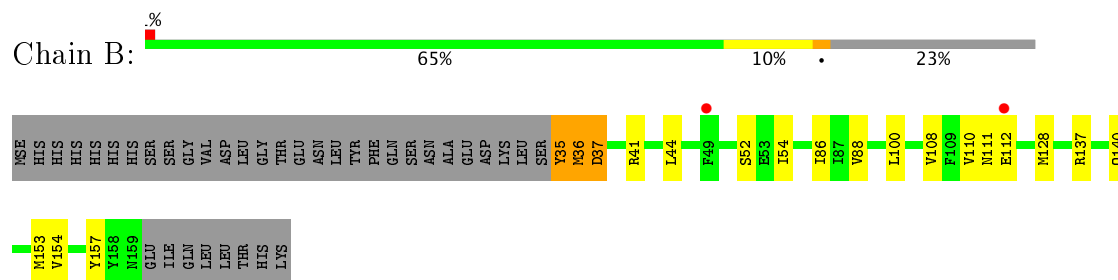
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

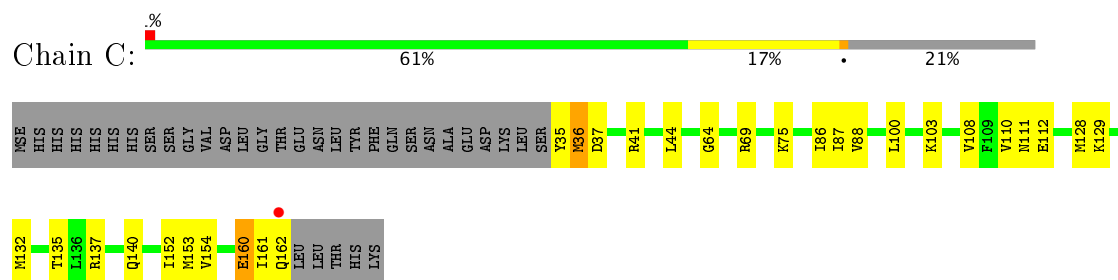
- Molecule 1: Sensor histidine kinase



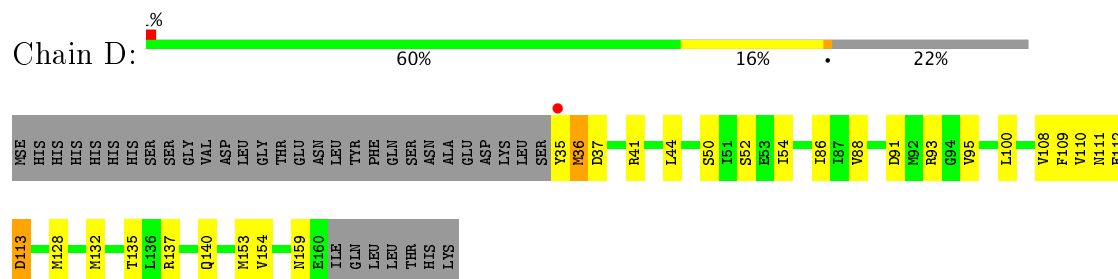
- Molecule 1: Sensor histidine kinase



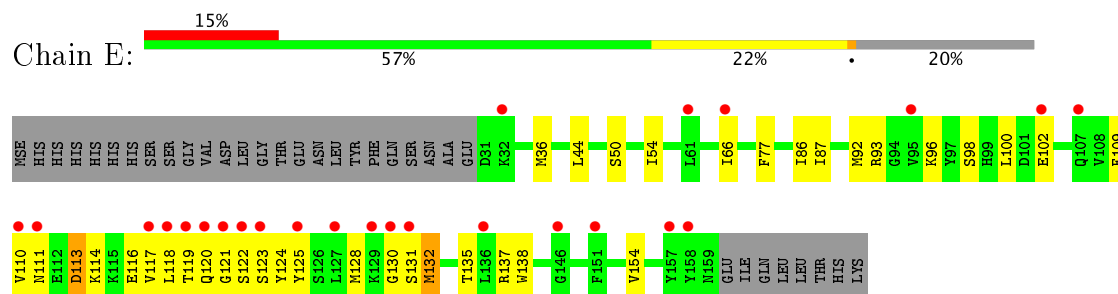
- Molecule 1: Sensor histidine kinase



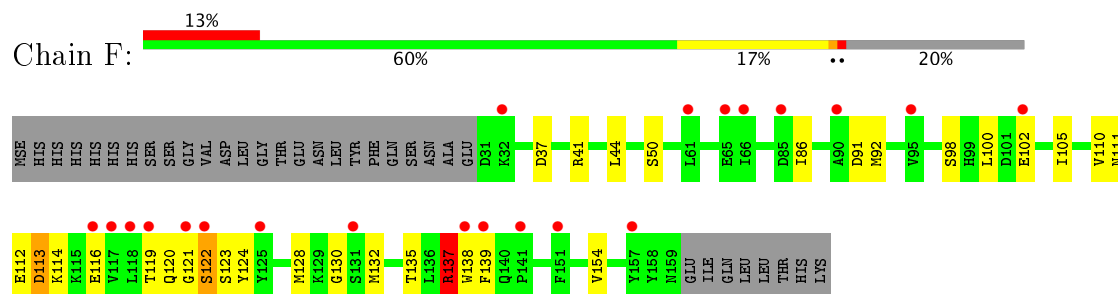
- Molecule 1: Sensor histidine kinase



- Molecule 1: Sensor histidine kinase



- Molecule 1: Sensor histidine kinase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	73.90 Å 82.74 Å 73.95 Å 90.00° 105.92° 90.00°	Depositor
Resolution (Å)	29.51 – 2.80 29.51 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.9 (29.51-2.80) 99.9 (29.51-2.80)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.99 (at 2.80 Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, $R_{free}$	0.197 , 0.250 0.201 , 0.254	Depositor DCC
$R_{free}$ test set	1088 reflections (5.39%)	DCC
Wilson B-factor (Å <sup>2</sup> )	73.6	Xtriage
Anisotropy	0.121	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 72.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.477 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	6328	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	95.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.49% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: ZN, SO4, CL

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	0.51	0/1065	0.74	0/1423
1	B	0.48	0/1039	0.73	0/1387
1	C	0.52	0/1064	0.75	0/1420
1	D	0.48	0/1040	0.72	0/1389
1	E	0.48	0/1062	0.80	3/1418 (0.2%)
1	F	0.45	0/1062	0.78	1/1418 (0.1%)
All	All	0.49	0/6332	0.75	4/8455 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	132	MSE	CB-CA-C	6.80	124.00	110.40
1	E	36	MSE	N-CA-CB	-6.32	99.22	110.60
1	E	132	MSE	CA-CB-CG	5.80	123.16	113.30
1	F	137	ARG	CG-CD-NE	5.17	122.67	111.80

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1052	0	1025	23	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1026	0	998	19	0
1	C	1052	0	1025	24	0
1	D	1027	0	996	21	0
1	E	1049	0	1023	48	0
1	F	1049	0	1023	41	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	D	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
4	A	10	0	0	0	0
4	C	5	0	0	0	0
4	D	5	0	0	1	0
4	E	5	0	0	0	0
5	A	13	0	0	0	0
5	B	6	0	0	0	0
5	C	5	0	0	1	0
5	D	7	0	0	0	0
5	E	3	0	0	0	0
5	F	8	0	0	0	0
All	All	6328	0	6090	138	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 11.

All (138) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:100:LEU:HD12	1:F:100:LEU:HD12	1.13	1.12
1:F:100:LEU:HD13	1:F:105:ILE:HD13	1.43	1.00
1:F:121:GLY:H	1:F:122:SER:HB2	1.26	0.98
1:F:91:ASP:OD1	1:F:92:MSE:N	1.96	0.98
1:E:100:LEU:CD1	1:F:100:LEU:HD12	1.96	0.95
1:E:100:LEU:HD12	1:F:100:LEU:CD1	2.01	0.91
1:F:121:GLY:N	1:F:122:SER:HB2	1.96	0.81
1:E:110:VAL:HG12	1:E:114:LYS:HB3	1.64	0.80
1:F:92:MSE:HE3	1:F:92:MSE:HA	1.62	0.79
1:E:92:MSE:HA	1:E:92:MSE:HE3	1.65	0.79
1:E:117:VAL:HG11	1:F:139:PHE:HB3	1.67	0.75
1:C:86:ILE:HG13	1:C:100:LEU:CD2	2.18	0.74

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:86:ILE:HG13	1:A:100:LEU:HD23	1.70	0.73
1:A:86:ILE:HG13	1:A:100:LEU:CD2	2.18	0.73
1:C:86:ILE:HG13	1:C:100:LEU:HD23	1.69	0.73
1:F:110:VAL:HG12	1:F:114:LYS:HB2	1.69	0.73
1:E:98:SER:HB3	1:F:102:GLU:HB3	1.73	0.71
1:E:102:GLU:HB3	1:F:98:SER:HB3	1.75	0.69
1:E:100:LEU:CD1	1:F:100:LEU:CD1	2.66	0.66
1:E:131:SER:OG	1:E:132:MSE:O	2.12	0.66
1:F:119:THR:OG1	1:F:120:GLN:OE1	2.13	0.65
1:F:116:GLU:HG3	1:F:124:TYR:CE2	2.32	0.65
1:F:137:ARG:HG2	1:F:137:ARG:HH21	1.62	0.64
1:F:116:GLU:HG3	1:F:124:TYR:CZ	2.33	0.64
1:E:135:THR:CG2	1:F:128:MSE:HE2	2.28	0.63
1:E:117:VAL:CG1	1:E:124:TYR:CE2	2.82	0.63
1:E:123:SER:OG	1:F:138:TRP:CZ2	2.52	0.63
1:E:117:VAL:HG13	1:E:124:TYR:OH	1.99	0.62
1:E:117:VAL:HG13	1:E:124:TYR:CZ	2.35	0.62
1:E:110:VAL:CG1	1:E:114:LYS:HB3	2.30	0.61
1:E:117:VAL:HG12	1:E:122:SER:O	2.00	0.60
1:A:137:ARG:NH1	1:B:112:GLU:O	2.33	0.60
1:A:37:ASP:OD1	1:A:37:ASP:N	2.35	0.60
1:C:37:ASP:OD1	1:C:37:ASP:N	2.34	0.59
1:E:128:MSE:HE3	1:E:130:GLY:O	2.03	0.58
1:D:50:SER:OG	1:E:54:ILE:HD11	2.02	0.58
1:E:117:VAL:HG13	1:E:124:TYR:CE2	2.39	0.58
1:E:77:PHE:HB2	1:E:87:ILE:CD1	2.34	0.57
1:E:110:VAL:HG12	1:E:114:LYS:CB	2.34	0.56
1:E:109:PHE:O	1:F:137:ARG:NH2	2.39	0.56
1:E:117:VAL:HG11	1:F:139:PHE:CB	2.36	0.56
1:A:77:PHE:HB2	1:A:87[B]:ILE:CD1	2.35	0.56
1:E:117:VAL:HG12	1:E:124:TYR:CE2	2.41	0.56
1:C:140:GLN:HB3	1:C:152[A]:ILE:CG2	2.36	0.56
1:C:108:VAL:O	1:C:128:MSE:HE1	2.07	0.55
1:C:110:VAL:HG21	1:D:88:VAL:HG11	1.87	0.55
1:A:108:VAL:O	1:A:128:MSE:HE1	2.07	0.55
1:A:110:VAL:HG21	1:B:88:VAL:HG11	1.89	0.55
1:E:77:PHE:HB2	1:E:87:ILE:HD11	1.88	0.54
1:D:112:GLU:OE2	1:D:132:MSE:HG3	2.08	0.54
1:A:77:PHE:HB2	1:A:87[B]:ILE:HD11	1.90	0.54
1:E:137:ARG:NH2	1:F:128:MSE:HB2	2.22	0.53
1:F:128:MSE:HE3	1:F:130:GLY:O	2.08	0.53

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:112:GLU:OE2	1:F:132:MSE:HG3	2.09	0.52
1:F:121:GLY:CA	1:F:122:SER:HB2	2.39	0.52
1:E:120:GLN:O	1:E:120:GLN:HG3	2.09	0.52
1:E:128:MSE:HE2	1:F:135:THR:CG2	2.39	0.52
1:B:108:VAL:O	1:B:128:MSE:HE1	2.09	0.52
1:D:108:VAL:O	1:D:128:MSE:HE1	2.09	0.51
1:D:35:TYR:CE2	1:D:36:MSE:O	2.63	0.51
1:E:116:GLU:O	1:E:121:GLY:CA	2.58	0.51
1:B:54:ILE:HD11	1:F:50:SER:OG	2.10	0.51
1:C:35:TYR:HD1	1:C:162:GLN:HG2	1.77	0.49
1:E:86:ILE:HG23	1:E:100:LEU:CD2	2.43	0.49
1:B:110:VAL:O	1:B:112:GLU:N	2.46	0.49
1:A:110:VAL:CG2	1:B:88:VAL:HG21	2.43	0.48
1:C:140:GLN:HB3	1:C:152[A]:ILE:HG23	1.95	0.48
1:D:50:SER:OG	1:E:54:ILE:CD1	2.61	0.48
1:E:138:TRP:CZ2	1:F:123:SER:HB3	2.49	0.48
1:F:86:ILE:HG23	1:F:100:LEU:CD2	2.43	0.48
1:C:110:VAL:CG2	1:D:88:VAL:HG21	2.44	0.48
1:B:35:TYR:CD1	1:B:35:TYR:C	2.87	0.48
1:E:116:GLU:O	1:E:121:GLY:N	2.47	0.48
1:A:110:VAL:O	1:A:112:GLU:N	2.47	0.47
1:B:86:ILE:HG23	1:B:100:LEU:CD2	2.44	0.47
1:C:137:ARG:NH2	1:D:128:MSE:HB2	2.29	0.47
1:D:91:ASP:OD1	1:D:93:ARG:HG2	2.15	0.47
1:D:86:ILE:HG23	1:D:100:LEU:CD2	2.44	0.47
1:E:77:PHE:CB	1:E:87:ILE:HD11	2.45	0.46
1:F:92:MSE:HA	1:F:92:MSE:CE	2.39	0.46
1:A:89:VAL:HG13	1:A:152:ILE:HD13	1.97	0.45
1:D:54:ILE:HD11	1:E:50:SER:OG	2.15	0.45
1:F:112:GLU:HA	1:F:112:GLU:OE1	2.17	0.45
1:C:110:VAL:O	1:C:112:GLU:N	2.49	0.45
1:A:77:PHE:CB	1:A:87[B]:ILE:HD11	2.46	0.44
1:E:92:MSE:HA	1:E:92:MSE:CE	2.41	0.44
1:E:98:SER:O	1:F:102:GLU:CD	2.55	0.44
1:E:102:GLU:CD	1:F:98:SER:O	2.56	0.44
1:A:88:VAL:HG11	1:B:110:VAL:HG21	2.00	0.44
1:C:135:THR:HG21	1:D:109:PHE:HD1	1.82	0.44
1:C:103:LYS:HE3	1:D:95:VAL:HG12	2.00	0.44
1:C:88:VAL:HG11	1:D:110:VAL:HG21	1.98	0.43
1:A:35:TYR:O	1:A:36:MSE:SE	2.87	0.43
1:F:37:ASP:O	1:F:41:ARG:HG3	2.18	0.43

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:35:TYR:O	1:C:36:MSE:SE	2.87	0.43
1:B:37:ASP:O	1:B:41:ARG:HG3	2.19	0.43
1:B:54:ILE:CD1	1:F:50:SER:OG	2.66	0.43
1:C:153:MSE:HE3	1:D:110:VAL:HG22	2.01	0.43
1:D:37:ASP:O	1:D:41:ARG:HG3	2.18	0.43
1:E:113:ASP:N	1:E:113:ASP:OD1	2.52	0.43
1:A:112:GLU:OE2	1:A:132:MSE:HG3	2.18	0.43
1:A:153:MSE:HE3	1:B:110:VAL:HG22	2.01	0.42
1:B:36:MSE:HB3	1:B:41:ARG:HH11	1.84	0.42
1:C:64:GLY:HA2	5:C:303:HOH:O	2.19	0.42
1:F:121:GLY:H	1:F:122:SER:CB	2.13	0.42
1:B:137:ARG:HG2	1:B:153:MSE:SE	2.69	0.42
1:B:35:TYR:HD1	1:B:35:TYR:C	2.22	0.42
1:A:37:ASP:O	1:A:41:ARG:HG3	2.18	0.42
1:E:118:LEU:HD12	1:F:92:MSE:HE1	2.00	0.42
1:C:75:LYS:NZ	4:D:202:SO4:O1	2.48	0.42
1:D:137:ARG:HG2	1:D:153:MSE:SE	2.69	0.42
1:F:113:ASP:OD1	1:F:113:ASP:N	2.53	0.42
1:B:44:LEU:HD22	1:B:154:VAL:HG12	2.02	0.42
1:C:37:ASP:O	1:C:41:ARG:HG3	2.20	0.42
1:D:44:LEU:HD22	1:D:154:VAL:HG12	2.02	0.42
1:E:110:VAL:HG12	1:E:114:LYS:HD3	2.01	0.42
1:D:113:ASP:OD1	1:D:113:ASP:N	2.53	0.41
1:E:125:TYR:CE2	1:F:138:TRP:CZ3	3.08	0.41
1:E:66:ILE:HA	1:E:96:LYS:NZ	2.35	0.41
1:B:52:SER:OG	1:B:140:GLN:HG2	2.20	0.41
1:E:131:SER:HB3	1:F:130:GLY:HA2	2.02	0.41
1:C:86:ILE:HG12	1:C:87:ILE:N	2.36	0.41
1:D:52:SER:OG	1:D:140:GLN:HG2	2.20	0.41
1:F:44:LEU:HD22	1:F:154:VAL:HG12	2.02	0.41
1:E:44:LEU:HD22	1:E:154:VAL:HG12	2.02	0.41
1:A:44:LEU:HD22	1:A:154:VAL:HG12	2.03	0.41
1:C:86:ILE:HD13	1:C:153:MSE:HE1	2.03	0.41
1:A:86:ILE:HG12	1:A:87[A]:ILE:N	2.35	0.41
1:A:110:VAL:O	1:A:111:ASN:C	2.59	0.41
1:A:137:ARG:NH2	1:B:128:MSE:HB2	2.36	0.41
1:C:128:MSE:HB3	1:D:135:THR:HG23	2.02	0.41
1:E:117:VAL:HG23	1:E:118:LEU:N	2.36	0.41
1:C:44:LEU:HD22	1:C:154:VAL:HG12	2.03	0.40
1:A:86:ILE:HD13	1:A:153:MSE:HE1	2.03	0.40
1:E:119:THR:O	1:E:120:GLN:C	2.59	0.40

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:86:ILE:HG12	1:A:87[B]:ILE:N	2.36	0.40
1:B:108:VAL:HG22	1:B:157:TYR:CZ	2.57	0.40
1:C:160:GLU:HB3	1:C:161:ILE:H	1.69	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	127/162 (78%)	121 (95%)	5 (4%)	1 (1%)	22	55
1	B	124/162 (76%)	120 (97%)	2 (2%)	2 (2%)	11	36
1	C	127/162 (78%)	119 (94%)	7 (6%)	1 (1%)	22	55
1	D	124/162 (76%)	121 (98%)	1 (1%)	2 (2%)	11	36
1	E	127/162 (78%)	118 (93%)	8 (6%)	1 (1%)	22	55
1	F	127/162 (78%)	121 (95%)	4 (3%)	2 (2%)	11	36
All	All	756/972 (78%)	720 (95%)	27 (4%)	9 (1%)	15	44

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	111	ASN
1	B	37	ASP
1	B	111	ASN
1	C	111	ASN
1	D	111	ASN
1	D	36	MSE
1	F	111	ASN
1	E	111	ASN
1	F	122	SER

### 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	117/140 (84%)	115 (98%)	2 (2%)	66	90
1	B	114/140 (81%)	112 (98%)	2 (2%)	64	90
1	C	117/140 (84%)	112 (96%)	5 (4%)	33	67
1	D	114/140 (81%)	112 (98%)	2 (2%)	64	90
1	E	117/140 (84%)	115 (98%)	2 (2%)	66	90
1	F	117/140 (84%)	115 (98%)	2 (2%)	66	90
All	All	696/840 (83%)	681 (98%)	15 (2%)	57	87

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	MSE
1	A	160	GLU
1	B	35	TYR
1	B	36	MSE
1	C	36	MSE
1	C	69	ARG
1	C	129	LYS
1	C	132	MSE
1	C	160	GLU
1	D	113	ASP
1	D	159	ASN
1	E	93	ARG
1	E	113	ASP
1	F	113	ASP
1	F	137	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 6 are monoatomic - leaving 5 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	$\# Z  > 2$
4	SO4	A	203	-	4,4,4	0.49	0	6,6,6	0.19	0
4	SO4	A	204	-	4,4,4	0.44	0	6,6,6	0.14	0
4	SO4	C	202	-	4,4,4	0.46	0	6,6,6	0.18	0
4	SO4	D	202	-	4,4,4	0.51	0	6,6,6	0.17	0
4	SO4	E	201	-	4,4,4	0.47	0	6,6,6	0.16	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	SO4	A	203	-	-	0/0/0/0	0/0/0/0
4	SO4	A	204	-	-	0/0/0/0	0/0/0/0
4	SO4	C	202	-	-	0/0/0/0	0/0/0/0
4	SO4	D	202	-	-	0/0/0/0	0/0/0/0
4	SO4	E	201	-	-	0/0/0/0	0/0/0/0

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
4	D	202	SO4	1	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	122/162 (75%)	0.09	0 100 100	47, 65, 119, 143	0
1	B	119/162 (73%)	0.19	2 (1%) 70 63	58, 82, 118, 154	0
1	C	122/162 (75%)	0.06	1 (0%) 86 81	46, 68, 124, 160	0
1	D	120/162 (74%)	0.14	1 (0%) 86 81	63, 87, 130, 170	0
1	E	123/162 (75%)	0.99	25 (20%) 1 1	79, 114, 180, 222	0
1	F	123/162 (75%)	0.97	21 (17%) 2 1	79, 117, 177, 203	0
All	All	729/972 (75%)	0.41	50 (6%) 18 10	46, 91, 160, 222	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	102	GLU	7.7
1	E	129	LYS	6.4
1	E	119	THR	5.3
1	F	118	LEU	5.0
1	E	131	SER	4.6
1	E	125	TYR	4.2
1	F	66	ILE	4.1
1	F	119	THR	3.8
1	C	162	GLN	3.7
1	E	32	LYS	3.5
1	E	130	GLY	3.4
1	E	136	LEU	3.4
1	F	61	LEU	3.4
1	E	118	LEU	3.3
1	F	116	GLU	3.3
1	E	102	GLU	3.3
1	F	65	GLU	3.2
1	E	120	GLN	3.2
1	F	90	ALA	3.1

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	F	138	TRP	3.1
1	E	107	GLN	3.1
1	F	151	PHE	3.0
1	E	95	VAL	2.9
1	E	158	TYR	2.9
1	E	121	GLY	2.9
1	E	111	ASN	2.8
1	F	121	GLY	2.8
1	E	122	SER	2.8
1	B	112	GLU	2.7
1	F	122	SER	2.7
1	E	110	VAL	2.6
1	E	151	PHE	2.5
1	E	157	TYR	2.5
1	F	125	TYR	2.4
1	F	131	SER	2.4
1	E	117	VAL	2.4
1	E	123	SER	2.4
1	E	61	LEU	2.3
1	F	117	VAL	2.2
1	F	95	VAL	2.2
1	F	85	ASP	2.2
1	F	139	PHE	2.1
1	E	66	ILE	2.1
1	D	35	TYR	2.1
1	F	141	PRO	2.1
1	B	49	PHE	2.0
1	F	157	TYR	2.0
1	E	146	GLY	2.0
1	E	127	LEU	2.0
1	F	32	LYS	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	ZN	A	201	1/1	0.99	0.17	-0.54	52,52,52,52	0
2	ZN	D	201	1/1	0.97	0.13	-0.85	84,84,84,84	0
2	ZN	B	201	1/1	0.98	0.13	-1.43	81,81,81,81	0
4	SO4	E	201	5/5	0.73	0.35	-	73,77,87,96	5
3	CL	A	202	1/1	0.73	0.40	-	91,91,91,91	1
3	CL	B	202	1/1	0.69	0.47	-	77,77,77,77	1
4	SO4	D	202	5/5	0.84	0.25	-	58,66,79,86	5
3	CL	C	201	1/1	0.80	0.38	-	94,94,94,94	1
4	SO4	A	203	5/5	0.94	0.17	-	49,54,74,76	5
4	SO4	C	202	5/5	0.82	0.30	-	56,66,85,86	5
4	SO4	A	204	5/5	0.78	0.29	-	66,70,78,82	5

## 6.5 Other polymers [i](#)

There are no such residues in this entry.