Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 04:28 PM GMT

PDB ID	:	4F21
Title	:	Crystal structure of carboxylesterase/phospholipase family protein from Francisella tularensis
Authors	:	Filippova, E.V.; Minasov, G.; Kuhn M.; Wawrzak, Z.; Shuvalova L.; Dubrovska, I.; Winsor, J.R.; Kiryukhina, O.; Becker, D.P.; Armoush, N.; Anderson, W.F.; Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on	:	2012-05-07
Resolution	:	2.50 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

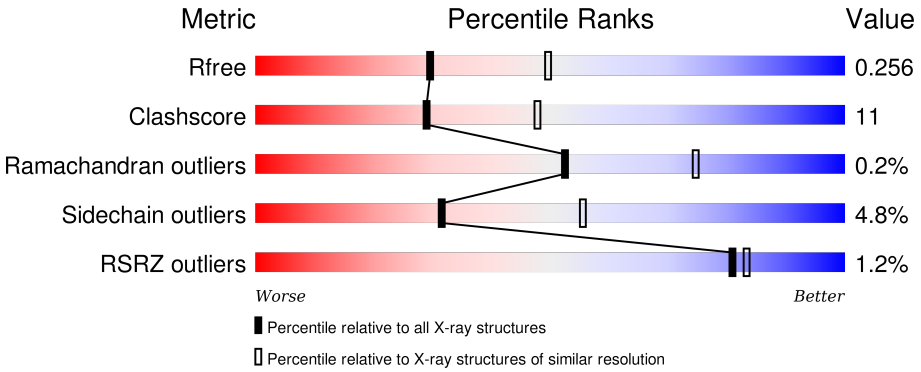
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 2.50 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}	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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 >=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 <=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	246	% 65% 22% • 12%
1	B	246	% 67% 22% • 11%
1	C	246	63% 24% • 11%
1	D	246	64% 24% • 11%
1	E	246	58% 25% 16%

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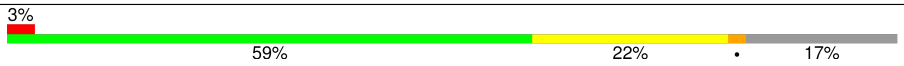
Mol	Chain	Length	Quality of chain
1	F	246	
1	G	246	
1	H	246	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13732 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 Carboxylesterase/phospholipase family protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	217	Total	C	N	O	S	0	0	0
			1701	1091	283	317	10			
1	B	220	Total	C	N	O	S	0	0	0
			1718	1101	285	321	11			
1	C	220	Total	C	N	O	S	0	0	0
			1718	1100	285	322	11			
1	D	220	Total	C	N	O	S	0	0	0
			1720	1101	286	322	11			
1	E	206	Total	C	N	O	S	0	0	0
			1607	1033	265	300	9			
1	F	205	Total	C	N	O	S	0	1	0
			1605	1030	267	298	10			
1	G	204	Total	C	N	O	S	0	0	0
			1598	1028	264	297	9			
1	H	204	Total	C	N	O	S	0	0	0
			1601	1032	264	296	9			

There are 192 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-23	MET	-	EXPRESSION TAG	UNP Q5NI32
A	-22	HIS	-	EXPRESSION TAG	UNP Q5NI32
A	-21	HIS	-	EXPRESSION TAG	UNP Q5NI32
A	-20	HIS	-	EXPRESSION TAG	UNP Q5NI32
A	-19	HIS	-	EXPRESSION TAG	UNP Q5NI32
A	-18	HIS	-	EXPRESSION TAG	UNP Q5NI32
A	-17	HIS	-	EXPRESSION TAG	UNP Q5NI32
A	-16	SER	-	EXPRESSION TAG	UNP Q5NI32
A	-15	SER	-	EXPRESSION TAG	UNP Q5NI32
A	-14	GLY	-	EXPRESSION TAG	UNP Q5NI32
A	-13	VAL	-	EXPRESSION TAG	UNP Q5NI32
A	-12	ASP	-	EXPRESSION TAG	UNP Q5NI32
A	-11	LEU	-	EXPRESSION TAG	UNP Q5NI32

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	GLY	-	EXPRESSION TAG	UNP Q5NI32
A	-9	THR	-	EXPRESSION TAG	UNP Q5NI32
A	-8	GLU	-	EXPRESSION TAG	UNP Q5NI32
A	-7	ASN	-	EXPRESSION TAG	UNP Q5NI32
A	-6	LEU	-	EXPRESSION TAG	UNP Q5NI32
A	-5	TYR	-	EXPRESSION TAG	UNP Q5NI32
A	-4	PHE	-	EXPRESSION TAG	UNP Q5NI32
A	-3	GLN	-	EXPRESSION TAG	UNP Q5NI32
A	-2	SER	-	EXPRESSION TAG	UNP Q5NI32
A	-1	ASN	-	EXPRESSION TAG	UNP Q5NI32
A	0	ALA	-	EXPRESSION TAG	UNP Q5NI32
B	-23	MET	-	EXPRESSION TAG	UNP Q5NI32
B	-22	HIS	-	EXPRESSION TAG	UNP Q5NI32
B	-21	HIS	-	EXPRESSION TAG	UNP Q5NI32
B	-20	HIS	-	EXPRESSION TAG	UNP Q5NI32
B	-19	HIS	-	EXPRESSION TAG	UNP Q5NI32
B	-18	HIS	-	EXPRESSION TAG	UNP Q5NI32
B	-17	HIS	-	EXPRESSION TAG	UNP Q5NI32
B	-16	SER	-	EXPRESSION TAG	UNP Q5NI32
B	-15	SER	-	EXPRESSION TAG	UNP Q5NI32
B	-14	GLY	-	EXPRESSION TAG	UNP Q5NI32
B	-13	VAL	-	EXPRESSION TAG	UNP Q5NI32
B	-12	ASP	-	EXPRESSION TAG	UNP Q5NI32
B	-11	LEU	-	EXPRESSION TAG	UNP Q5NI32
B	-10	GLY	-	EXPRESSION TAG	UNP Q5NI32
B	-9	THR	-	EXPRESSION TAG	UNP Q5NI32
B	-8	GLU	-	EXPRESSION TAG	UNP Q5NI32
B	-7	ASN	-	EXPRESSION TAG	UNP Q5NI32
B	-6	LEU	-	EXPRESSION TAG	UNP Q5NI32
B	-5	TYR	-	EXPRESSION TAG	UNP Q5NI32
B	-4	PHE	-	EXPRESSION TAG	UNP Q5NI32
B	-3	GLN	-	EXPRESSION TAG	UNP Q5NI32
B	-2	SER	-	EXPRESSION TAG	UNP Q5NI32
B	-1	ASN	-	EXPRESSION TAG	UNP Q5NI32
B	0	ALA	-	EXPRESSION TAG	UNP Q5NI32
C	-23	MET	-	EXPRESSION TAG	UNP Q5NI32
C	-22	HIS	-	EXPRESSION TAG	UNP Q5NI32
C	-21	HIS	-	EXPRESSION TAG	UNP Q5NI32
C	-20	HIS	-	EXPRESSION TAG	UNP Q5NI32
C	-19	HIS	-	EXPRESSION TAG	UNP Q5NI32
C	-18	HIS	-	EXPRESSION TAG	UNP Q5NI32
C	-17	HIS	-	EXPRESSION TAG	UNP Q5NI32

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-16	SER	-	EXPRESSION TAG	UNP Q5NI32
C	-15	SER	-	EXPRESSION TAG	UNP Q5NI32
C	-14	GLY	-	EXPRESSION TAG	UNP Q5NI32
C	-13	VAL	-	EXPRESSION TAG	UNP Q5NI32
C	-12	ASP	-	EXPRESSION TAG	UNP Q5NI32
C	-11	LEU	-	EXPRESSION TAG	UNP Q5NI32
C	-10	GLY	-	EXPRESSION TAG	UNP Q5NI32
C	-9	THR	-	EXPRESSION TAG	UNP Q5NI32
C	-8	GLU	-	EXPRESSION TAG	UNP Q5NI32
C	-7	ASN	-	EXPRESSION TAG	UNP Q5NI32
C	-6	LEU	-	EXPRESSION TAG	UNP Q5NI32
C	-5	TYR	-	EXPRESSION TAG	UNP Q5NI32
C	-4	PHE	-	EXPRESSION TAG	UNP Q5NI32
C	-3	GLN	-	EXPRESSION TAG	UNP Q5NI32
C	-2	SER	-	EXPRESSION TAG	UNP Q5NI32
C	-1	ASN	-	EXPRESSION TAG	UNP Q5NI32
C	0	ALA	-	EXPRESSION TAG	UNP Q5NI32
D	-23	MET	-	EXPRESSION TAG	UNP Q5NI32
D	-22	HIS	-	EXPRESSION TAG	UNP Q5NI32
D	-21	HIS	-	EXPRESSION TAG	UNP Q5NI32
D	-20	HIS	-	EXPRESSION TAG	UNP Q5NI32
D	-19	HIS	-	EXPRESSION TAG	UNP Q5NI32
D	-18	HIS	-	EXPRESSION TAG	UNP Q5NI32
D	-17	HIS	-	EXPRESSION TAG	UNP Q5NI32
D	-16	SER	-	EXPRESSION TAG	UNP Q5NI32
D	-15	SER	-	EXPRESSION TAG	UNP Q5NI32
D	-14	GLY	-	EXPRESSION TAG	UNP Q5NI32
D	-13	VAL	-	EXPRESSION TAG	UNP Q5NI32
D	-12	ASP	-	EXPRESSION TAG	UNP Q5NI32
D	-11	LEU	-	EXPRESSION TAG	UNP Q5NI32
D	-10	GLY	-	EXPRESSION TAG	UNP Q5NI32
D	-9	THR	-	EXPRESSION TAG	UNP Q5NI32
D	-8	GLU	-	EXPRESSION TAG	UNP Q5NI32
D	-7	ASN	-	EXPRESSION TAG	UNP Q5NI32
D	-6	LEU	-	EXPRESSION TAG	UNP Q5NI32
D	-5	TYR	-	EXPRESSION TAG	UNP Q5NI32
D	-4	PHE	-	EXPRESSION TAG	UNP Q5NI32
D	-3	GLN	-	EXPRESSION TAG	UNP Q5NI32
D	-2	SER	-	EXPRESSION TAG	UNP Q5NI32
D	-1	ASN	-	EXPRESSION TAG	UNP Q5NI32
D	0	ALA	-	EXPRESSION TAG	UNP Q5NI32
E	-23	MET	-	EXPRESSION TAG	UNP Q5NI32

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-22	HIS	-	EXPRESSION TAG	UNP Q5NI32
E	-21	HIS	-	EXPRESSION TAG	UNP Q5NI32
E	-20	HIS	-	EXPRESSION TAG	UNP Q5NI32
E	-19	HIS	-	EXPRESSION TAG	UNP Q5NI32
E	-18	HIS	-	EXPRESSION TAG	UNP Q5NI32
E	-17	HIS	-	EXPRESSION TAG	UNP Q5NI32
E	-16	SER	-	EXPRESSION TAG	UNP Q5NI32
E	-15	SER	-	EXPRESSION TAG	UNP Q5NI32
E	-14	GLY	-	EXPRESSION TAG	UNP Q5NI32
E	-13	VAL	-	EXPRESSION TAG	UNP Q5NI32
E	-12	ASP	-	EXPRESSION TAG	UNP Q5NI32
E	-11	LEU	-	EXPRESSION TAG	UNP Q5NI32
E	-10	GLY	-	EXPRESSION TAG	UNP Q5NI32
E	-9	THR	-	EXPRESSION TAG	UNP Q5NI32
E	-8	GLU	-	EXPRESSION TAG	UNP Q5NI32
E	-7	ASN	-	EXPRESSION TAG	UNP Q5NI32
E	-6	LEU	-	EXPRESSION TAG	UNP Q5NI32
E	-5	TYR	-	EXPRESSION TAG	UNP Q5NI32
E	-4	PHE	-	EXPRESSION TAG	UNP Q5NI32
E	-3	GLN	-	EXPRESSION TAG	UNP Q5NI32
E	-2	SER	-	EXPRESSION TAG	UNP Q5NI32
E	-1	ASN	-	EXPRESSION TAG	UNP Q5NI32
E	0	ALA	-	EXPRESSION TAG	UNP Q5NI32
F	-23	MET	-	EXPRESSION TAG	UNP Q5NI32
F	-22	HIS	-	EXPRESSION TAG	UNP Q5NI32
F	-21	HIS	-	EXPRESSION TAG	UNP Q5NI32
F	-20	HIS	-	EXPRESSION TAG	UNP Q5NI32
F	-19	HIS	-	EXPRESSION TAG	UNP Q5NI32
F	-18	HIS	-	EXPRESSION TAG	UNP Q5NI32
F	-17	HIS	-	EXPRESSION TAG	UNP Q5NI32
F	-16	SER	-	EXPRESSION TAG	UNP Q5NI32
F	-15	SER	-	EXPRESSION TAG	UNP Q5NI32
F	-14	GLY	-	EXPRESSION TAG	UNP Q5NI32
F	-13	VAL	-	EXPRESSION TAG	UNP Q5NI32
F	-12	ASP	-	EXPRESSION TAG	UNP Q5NI32
F	-11	LEU	-	EXPRESSION TAG	UNP Q5NI32
F	-10	GLY	-	EXPRESSION TAG	UNP Q5NI32
F	-9	THR	-	EXPRESSION TAG	UNP Q5NI32
F	-8	GLU	-	EXPRESSION TAG	UNP Q5NI32
F	-7	ASN	-	EXPRESSION TAG	UNP Q5NI32
F	-6	LEU	-	EXPRESSION TAG	UNP Q5NI32
F	-5	TYR	-	EXPRESSION TAG	UNP Q5NI32

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-4	PHE	-	EXPRESSION TAG	UNP Q5NI32
F	-3	GLN	-	EXPRESSION TAG	UNP Q5NI32
F	-2	SER	-	EXPRESSION TAG	UNP Q5NI32
F	-1	ASN	-	EXPRESSION TAG	UNP Q5NI32
F	0	ALA	-	EXPRESSION TAG	UNP Q5NI32
G	-23	MET	-	EXPRESSION TAG	UNP Q5NI32
G	-22	HIS	-	EXPRESSION TAG	UNP Q5NI32
G	-21	HIS	-	EXPRESSION TAG	UNP Q5NI32
G	-20	HIS	-	EXPRESSION TAG	UNP Q5NI32
G	-19	HIS	-	EXPRESSION TAG	UNP Q5NI32
G	-18	HIS	-	EXPRESSION TAG	UNP Q5NI32
G	-17	HIS	-	EXPRESSION TAG	UNP Q5NI32
G	-16	SER	-	EXPRESSION TAG	UNP Q5NI32
G	-15	SER	-	EXPRESSION TAG	UNP Q5NI32
G	-14	GLY	-	EXPRESSION TAG	UNP Q5NI32
G	-13	VAL	-	EXPRESSION TAG	UNP Q5NI32
G	-12	ASP	-	EXPRESSION TAG	UNP Q5NI32
G	-11	LEU	-	EXPRESSION TAG	UNP Q5NI32
G	-10	GLY	-	EXPRESSION TAG	UNP Q5NI32
G	-9	THR	-	EXPRESSION TAG	UNP Q5NI32
G	-8	GLU	-	EXPRESSION TAG	UNP Q5NI32
G	-7	ASN	-	EXPRESSION TAG	UNP Q5NI32
G	-6	LEU	-	EXPRESSION TAG	UNP Q5NI32
G	-5	TYR	-	EXPRESSION TAG	UNP Q5NI32
G	-4	PHE	-	EXPRESSION TAG	UNP Q5NI32
G	-3	GLN	-	EXPRESSION TAG	UNP Q5NI32
G	-2	SER	-	EXPRESSION TAG	UNP Q5NI32
G	-1	ASN	-	EXPRESSION TAG	UNP Q5NI32
G	0	ALA	-	EXPRESSION TAG	UNP Q5NI32
H	-23	MET	-	EXPRESSION TAG	UNP Q5NI32
H	-22	HIS	-	EXPRESSION TAG	UNP Q5NI32
H	-21	HIS	-	EXPRESSION TAG	UNP Q5NI32
H	-20	HIS	-	EXPRESSION TAG	UNP Q5NI32
H	-19	HIS	-	EXPRESSION TAG	UNP Q5NI32
H	-18	HIS	-	EXPRESSION TAG	UNP Q5NI32
H	-17	HIS	-	EXPRESSION TAG	UNP Q5NI32
H	-16	SER	-	EXPRESSION TAG	UNP Q5NI32
H	-15	SER	-	EXPRESSION TAG	UNP Q5NI32
H	-14	GLY	-	EXPRESSION TAG	UNP Q5NI32
H	-13	VAL	-	EXPRESSION TAG	UNP Q5NI32
H	-12	ASP	-	EXPRESSION TAG	UNP Q5NI32
H	-11	LEU	-	EXPRESSION TAG	UNP Q5NI32

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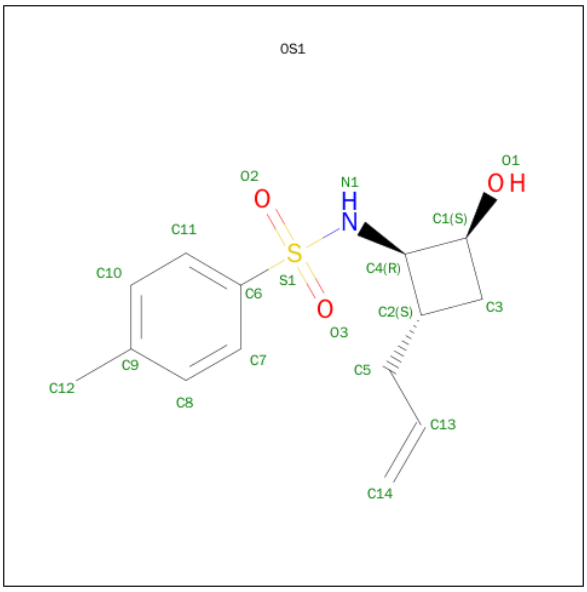
Chain	Residue	Modelled	Actual	Comment	Reference
H	-10	GLY	-	EXPRESSION TAG	UNP Q5NI32
H	-9	THR	-	EXPRESSION TAG	UNP Q5NI32
H	-8	GLU	-	EXPRESSION TAG	UNP Q5NI32
H	-7	ASN	-	EXPRESSION TAG	UNP Q5NI32
H	-6	LEU	-	EXPRESSION TAG	UNP Q5NI32
H	-5	TYR	-	EXPRESSION TAG	UNP Q5NI32
H	-4	PHE	-	EXPRESSION TAG	UNP Q5NI32
H	-3	GLN	-	EXPRESSION TAG	UNP Q5NI32
H	-2	SER	-	EXPRESSION TAG	UNP Q5NI32
H	-1	ASN	-	EXPRESSION TAG	UNP Q5NI32
H	0	ALA	-	EXPRESSION TAG	UNP Q5NI32

- Molecule 2 is N-((1R,2S)-2-ALLYL-4-OXOCYCLOBUTYL)-4-METHYLBENZENESULFONAMIDE, BOUND FORM (three-letter code: 0S1) (formula: $C_{14}H_{19}NO_3S$).



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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	66	Total O 66 66	0	0
3	B	59	Total O 59 59	0	0

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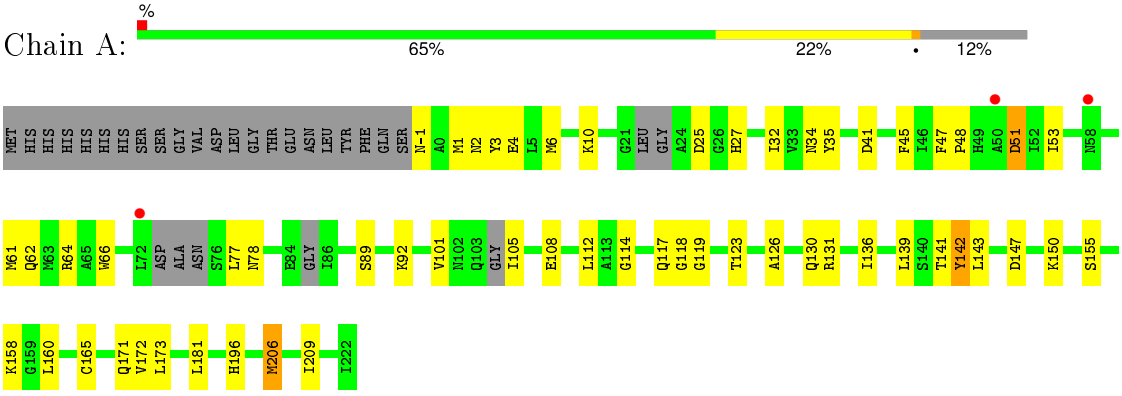
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	87	Total O 87 87	0	0
3	D	87	Total O 87 87	0	0
3	E	47	Total O 47 47	0	0
3	F	42	Total O 42 42	0	0
3	G	37	Total O 37 37	0	0
3	H	33	Total O 34 34	1	1

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 errors 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.

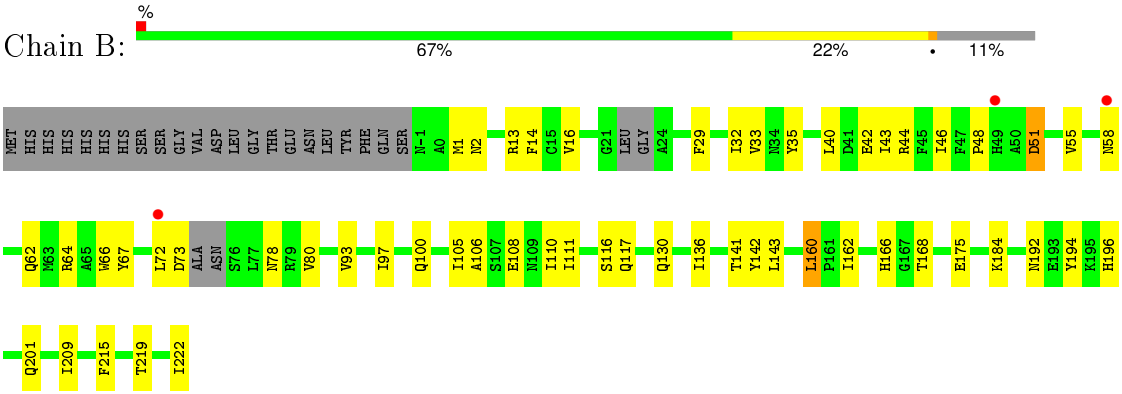
- Molecule 1: Carboxylesterase/phospholipase family protein

Chain A:



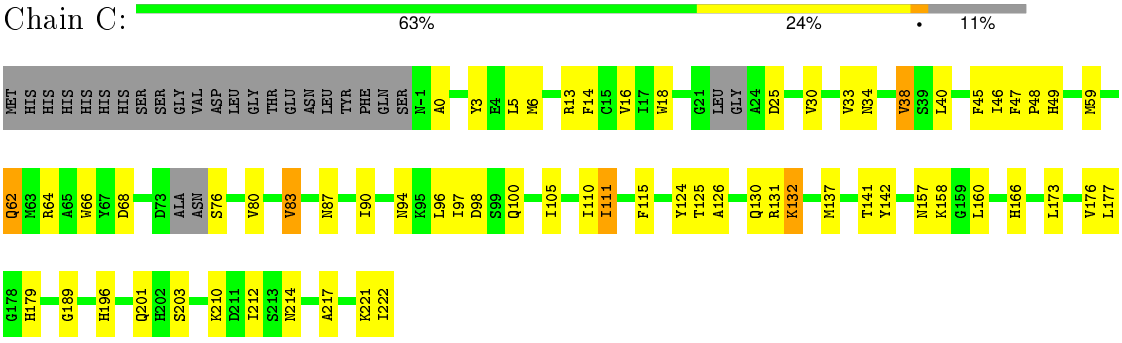
- Molecule 1: Carboxylesterase/phospholipase family protein

Chain B:



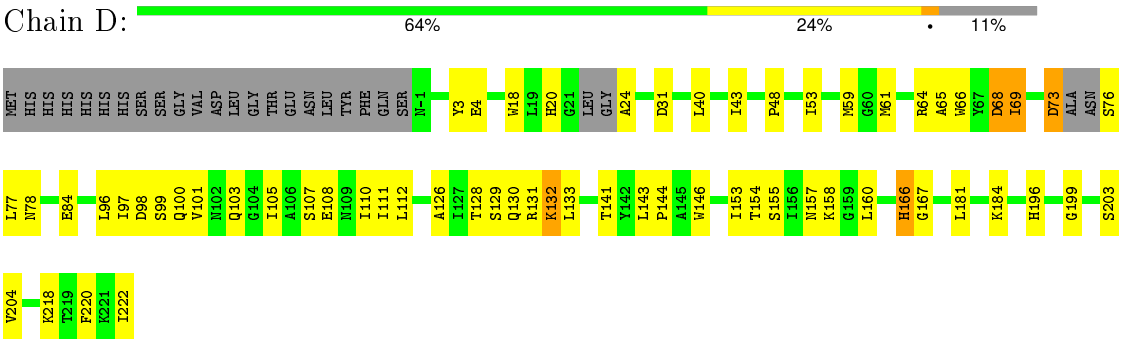
- Molecule 1: Carboxylesterase/phospholipase family protein

Chain C:



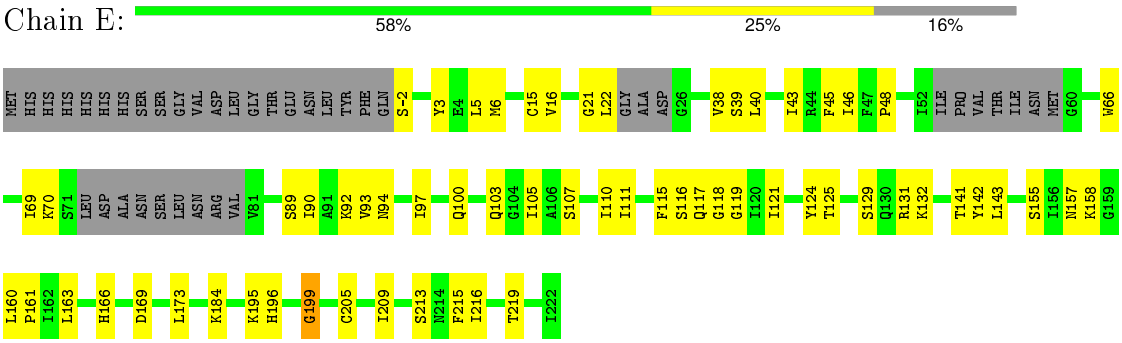
- Molecule 1: Carboxylesterase/phospholipase family protein

Chain D:



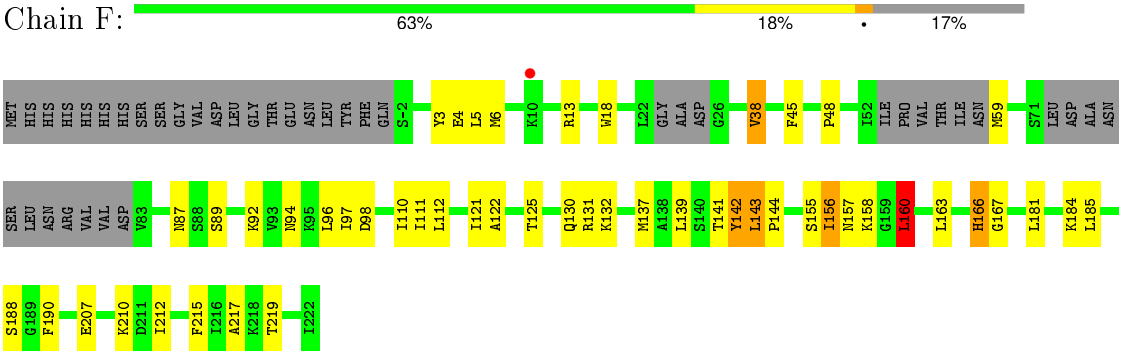
- Molecule 1: Carboxylesterase/phospholipase family protein

Chain E:



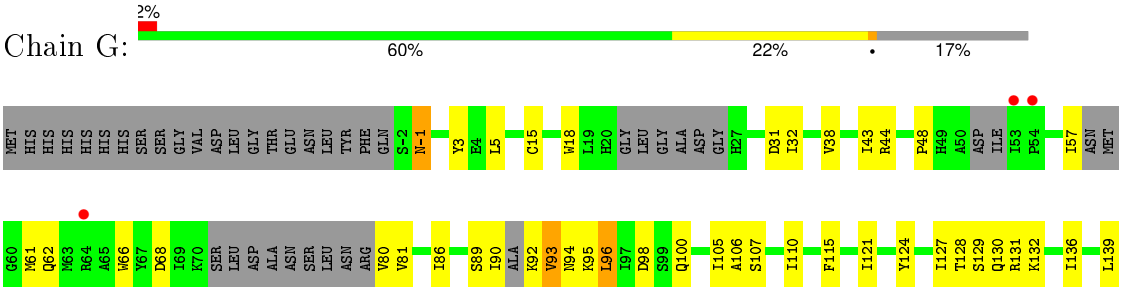
- Molecule 1: Carboxylesterase/phospholipase family protein

Chain F:



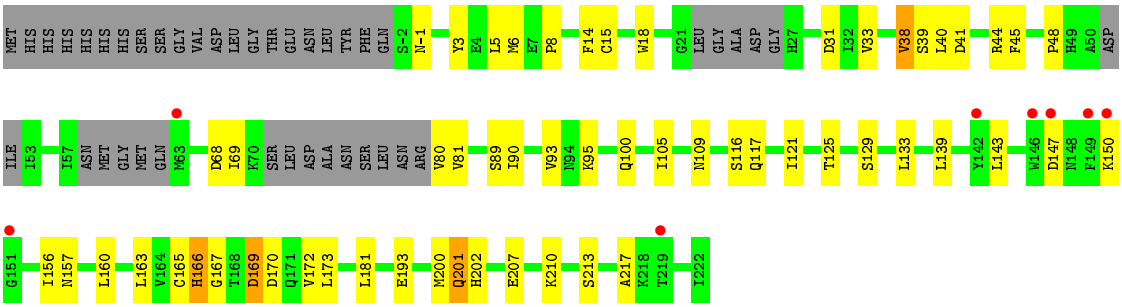
- Molecule 1: Carboxylesterase/phospholipase family protein

Chain G:



• Molecule 1: Carboxylesterase/phospholipase family protein

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	51.00Å 64.42Å 139.04Å 94.89° 90.12° 89.96°	Depositor
Resolution (Å)	29.46 – 2.50 29.46 – 2.49	Depositor EDS
% Data completeness (in resolution range)	94.3 (29.46-2.50) 91.3 (29.46-2.49)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.29 (at 2.48Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.199 , 0.259 0.212 , 0.256	Depositor DCC
R_{free} test set	2905 reflections (5.32%)	DCC
Wilson B-factor (Å^2)	33.0	Xtriage
Anisotropy	0.686	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 31.2	EDS
Estimated twinning fraction	0.418 for h,-k,-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Outliers	0 of 58033 reflections	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	13732	wwPDB-VP
Average B, all atoms (Å^2)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 50.84 % of the origin peak, indicating pseudo translational symmetry.The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 6.1070e-05.The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: 0S1

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	0.24	0/1732	0.42	0/2338
1	B	0.31	1/1751 (0.1%)	0.45	2/2367 (0.1%)
1	C	0.25	0/1751	0.46	0/2366
1	D	0.28	0/1753	0.48	0/2368
1	E	0.30	1/1638 (0.1%)	0.51	3/2210 (0.1%)
1	F	0.27	0/1636	0.46	1/2205 (0.0%)
1	G	0.26	0/1626	0.44	1/2191 (0.0%)
1	H	0.23	0/1632	0.44	0/2203
All	All	0.27	2/13519 (0.0%)	0.46	7/18248 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	201	GLN	C-N	7.37	1.51	1.34
1	E	199	GLY	C-N	-5.59	1.21	1.34

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	119	GLY	O-C-N	6.91	133.76	122.70
1	E	115	PHE	O-C-N	-6.26	112.68	122.70
1	G	93	VAL	N-CA-C	-5.48	96.21	111.00
1	E	119	GLY	CA-C-N	-5.39	105.33	117.20
1	F	160	LEU	CA-CB-CG	5.38	127.69	115.30
1	B	73	ASP	CB-CG-OD2	5.20	122.98	118.30
1	B	160	LEU	CA-CB-CG	5.02	126.85	115.30

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	1701	0	1685	35	0
1	B	1718	0	1705	30	0
1	C	1718	0	1703	42	0
1	D	1720	0	1710	36	0
1	E	1607	0	1578	46	0
1	F	1605	0	1579	35	0
1	G	1598	0	1583	53	0
1	H	1601	0	1596	37	0
2	E	5	0	3	2	0
3	A	66	0	0	6	0
3	B	59	0	0	0	0
3	C	87	0	0	6	0
3	D	87	0	0	3	0
3	E	47	0	0	5	0
3	F	42	0	0	2	0
3	G	37	0	0	0	0
3	H	34	0	0	0	0
All	All	13732	0	13142	301	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 (301) 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:H:80:VAL:HG12	1:H:81:VAL:N	1.65	1.06
1:F:141:THR:HG22	1:F:142:TYR:H	1.08	1.05
1:C:141:THR:HG22	1:C:142:TYR:H	1.18	1.05
1:C:141:THR:HG22	1:C:142:TYR:N	1.71	1.04
1:G:80:VAL:HG12	1:G:81:VAL:H	1.21	1.02
1:H:80:VAL:HG12	1:H:81:VAL:H	0.85	1.00
1:H:80:VAL:CG1	1:H:81:VAL:H	1.69	1.00
1:G:80:VAL:HG12	1:G:81:VAL:N	1.78	0.98
1:F:141:THR:HG22	1:F:142:TYR:N	1.72	0.98
1:C:141:THR:CG2	1:C:142:TYR:H	1.79	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:141:THR:CG2	1:F:142:TYR:H	1.83	0.90
1:G:80:VAL:CG1	1:G:81:VAL:H	1.83	0.90
1:G:154:THR:CG2	1:G:156:ILE:HG13	2.04	0.86
1:G:154:THR:HG21	1:G:156:ILE:HG13	1.65	0.79
1:G:154:THR:HG22	1:G:155:SER:N	1.97	0.78
1:B:100:GLN:HB3	1:B:105:ILE:HD11	1.66	0.78
1:G:90:ILE:HD13	1:G:121:ILE:HG23	1.66	0.78
1:E:38:VAL:HG12	1:E:39:SER:N	1.99	0.77
1:G:154:THR:HG22	1:G:155:SER:H	1.51	0.76
1:D:100:GLN:HB3	1:D:105:ILE:HD11	1.68	0.75
1:G:154:THR:HG22	1:G:156:ILE:HG13	1.72	0.72
1:G:100:GLN:HB3	1:G:105:ILE:HD11	1.73	0.71
1:D:112:LEU:HD12	1:D:126:ALA:HB2	1.74	0.70
1:G:154:THR:HG22	1:G:156:ILE:H	1.57	0.69
1:E:129:SER:OG	1:E:157:ASN:ND2	2.26	0.68
1:C:141:THR:CG2	1:C:142:TYR:N	2.40	0.68
1:D:143:LEU:HD12	1:D:184:LYS:HE3	1.76	0.68
1:C:210:LYS:HE3	1:E:196:HIS:CE1	2.30	0.67
1:F:94:ASN:O	1:F:131:ARG:NH1	2.28	0.67
1:C:221:LYS:NZ	3:C:352:HOH:O	2.28	0.65
1:B:44:ARG:NH1	1:B:100:GLN:OE1	2.29	0.65
1:G:98:ASP:OD1	1:G:131:ARG:NH1	2.30	0.64
1:C:64:ARG:NH1	3:C:353:HOH:O	2.27	0.64
1:E:15:CYS:HB2	1:E:105:ILE:HD12	1.78	0.64
1:H:80:VAL:CG1	1:H:81:VAL:N	2.40	0.64
1:D:78:ASN:ND2	3:D:324:HOH:O	2.30	0.64
1:E:38:VAL:CG1	1:E:39:SER:N	2.60	0.64
1:G:136:ILE:HD12	1:G:162:ILE:HG12	1.80	0.63
1:G:3:TYR:HB3	1:G:48:PRO:HA	1.79	0.63
1:B:162:ILE:HB	1:B:192:ASN:HB3	1.79	0.63
1:B:64:ARG:NE	1:D:199:GLY:O	2.31	0.63
1:C:83:VAL:O	1:C:87:ASN:ND2	2.31	0.63
1:E:46:ILE:HG22	1:E:48:PRO:HD3	1.81	0.63
1:G:154:THR:CG2	1:G:155:SER:H	2.11	0.62
1:C:210:LYS:HE3	1:E:196:HIS:HE1	1.63	0.62
1:F:143:LEU:HD13	1:F:181:LEU:HG	1.80	0.62
1:F:89:SER:HA	1:F:92:LYS:HD2	1.81	0.62
1:G:154:THR:CG2	1:G:155:SER:N	2.63	0.61
1:H:169:ASP:O	1:H:201:GLN:NE2	2.33	0.61
1:A:3:TYR:HB3	1:A:48:PRO:HA	1.83	0.61
1:B:196:HIS:NE2	1:H:207:GLU:OE2	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:154:THR:HG21	1:G:156:ILE:CG1	2.32	0.60
1:A:78:ASN:ND2	3:A:335:HOH:O	2.34	0.60
1:A:-1:ASN:N	3:A:319:HOH:O	2.34	0.59
1:C:25:ASP:HB2	1:C:115:PHE:HE2	1.67	0.59
1:D:129:SER:OG	1:D:157:ASN:ND2	2.34	0.59
1:E:143:LEU:HD23	1:E:184:LYS:HE3	1.84	0.59
1:A:147:ASP:HA	1:A:150:LYS:HD2	1.84	0.59
1:F:98:ASP:OD1	1:F:131:ARG:NH2	2.23	0.58
1:H:-1:ASN:OD1	1:H:95:LYS:NZ	2.33	0.58
1:D:64:ARG:NH1	1:D:76:SER:O	2.36	0.58
1:C:3:TYR:HB3	1:C:48:PRO:HA	1.85	0.58
1:A:206:MET:HE3	1:A:206:MET:HA	1.85	0.58
1:C:76:SER:N	3:C:315:HOH:O	2.36	0.57
1:C:132:LYS:NZ	3:C:301:HOH:O	2.20	0.57
1:C:98:ASP:OD1	1:C:131:ARG:NH2	2.27	0.57
1:F:6:MET:HB2	1:F:45:PHE:HB2	1.85	0.57
1:B:29:PHE:HD2	1:B:32:ILE:HD12	1.69	0.57
1:A:61:MET:HG3	1:A:62:GLN:HG3	1.86	0.57
1:D:3:TYR:HB3	1:D:48:PRO:HA	1.85	0.57
1:E:6:MET:HB2	1:E:45:PHE:HB2	1.86	0.57
1:D:108:GLU:HG3	1:D:132:LYS:HG2	1.85	0.57
1:H:173:LEU:HD23	1:H:202:HIS:CE1	2.40	0.57
1:A:206:MET:HA	1:A:206:MET:CE	2.35	0.57
1:E:90:ILE:HD11	1:E:124:TYR:HB3	1.87	0.56
1:C:62:GLN:HG2	3:C:342:HOH:O	2.06	0.56
1:D:24:ALA:N	3:D:306:HOH:O	2.38	0.56
1:B:14:PHE:HB2	1:B:43:ILE:HG12	1.86	0.55
1:F:139:LEU:HD21	1:F:212:ILE:HD11	1.89	0.55
1:D:203:SER:OG	1:D:204:VAL:N	2.39	0.55
1:C:38:VAL:HG13	1:C:217:ALA:HB2	1.89	0.55
1:A:6:MET:HB2	1:A:45:PHE:HB2	1.87	0.54
1:C:210:LYS:CE	1:E:196:HIS:HE1	2.20	0.54
1:E:94:ASN:O	1:E:131:ARG:NH1	2.41	0.54
1:F:157:ASN:O	1:F:160:LEU:HG	2.08	0.54
1:A:62:GLN:NE2	1:A:172:VAL:O	2.41	0.54
1:C:210:LYS:NZ	1:C:214:ASN:OD1	2.41	0.53
1:D:166:HIS:HD2	1:D:167:GLY:H	1.56	0.53
1:G:115:PHE:HB2	1:G:139:LEU:HD12	1.90	0.53
1:E:16:VAL:HG22	1:E:111:ILE:HB	1.91	0.53
1:B:196:HIS:HE1	1:H:210:LYS:HD2	1.74	0.53
1:E:40:LEU:HD23	1:E:43:ILE:HD12	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:143:LEU:HD22	1:H:181:LEU:HA	1.90	0.53
1:H:89:SER:O	1:H:93:VAL:HG23	2.08	0.53
1:E:70:LYS:O	1:E:117:GLN:NE2	2.34	0.53
1:D:128:THR:HA	1:D:153:ILE:HA	1.91	0.53
1:F:158:LYS:HA	1:F:190:PHE:CE1	2.44	0.53
1:D:66:TRP:HB3	1:D:68:ASP:H	1.73	0.53
1:D:166:HIS:CD2	1:D:167:GLY:H	2.27	0.53
1:B:13:ARG:HB3	1:B:42:GLU:HB3	1.91	0.53
1:G:38:VAL:HG22	1:G:217:ALA:HB2	1.92	0.52
1:E:195:LYS:NZ	3:E:424:HOH:O	2.41	0.52
1:G:15:CYS:HB2	1:G:105:ILE:HD12	1.91	0.52
1:D:132:LYS:NZ	3:D:333:HOH:O	2.33	0.52
1:C:90:ILE:HD11	1:C:124:TYR:HB3	1.91	0.52
1:G:-1:ASN:N	1:G:-1:ASN:OD1	2.42	0.52
1:C:66:TRP:HB3	1:C:68:ASP:H	1.74	0.52
1:F:137:MET:HG2	1:F:163:LEU:HB3	1.92	0.52
1:D:98:ASP:OD1	1:D:131:ARG:NH1	2.43	0.52
1:A:64:ARG:HB2	1:A:77:LEU:HD11	1.92	0.52
1:H:100:GLN:HB3	1:H:105:ILE:HD11	1.92	0.51
1:E:117:GLN:H	2:E:301:0S1:H14	1.75	0.51
1:A:196:HIS:NE2	1:G:207:GLU:OE2	2.44	0.51
1:B:46:ILE:HG22	1:B:48:PRO:HD3	1.91	0.51
1:A:114:GLY:HA3	1:A:119:GLY:HA2	1.93	0.51
1:A:142:TYR:HD1	1:A:142:TYR:H	1.58	0.51
1:G:92:LYS:HE3	1:G:92:LYS:HA	1.92	0.51
1:H:166:HIS:CD2	1:H:167:GLY:H	2.28	0.51
1:E:155:SER:HA	1:E:158:LYS:HG3	1.91	0.51
1:A:155:SER:HA	1:A:158:LYS:HG3	1.93	0.51
1:H:6:MET:HB2	1:H:45:PHE:HB2	1.93	0.51
1:F:156:ILE:HD12	1:F:157:ASN:H	1.75	0.51
1:D:99:SER:O	1:D:103:GLN:HB2	2.11	0.51
1:B:215:PHE:O	1:B:219:THR:HG23	2.11	0.51
1:H:133:LEU:HG	1:H:157:ASN:HD21	1.76	0.51
1:F:38:VAL:HG13	1:F:217:ALA:HB2	1.93	0.50
1:H:3:TYR:HB3	1:H:48:PRO:HA	1.93	0.50
1:D:61:MET:HA	1:D:77:LEU:HD11	1.93	0.50
1:A:139:LEU:HD23	1:A:165:CYS:HB2	1.92	0.50
1:E:103:GLN:NE2	3:E:413:HOH:O	2.42	0.50
1:B:1:MET:HE1	1:B:51:ASP:HB2	1.92	0.50
1:F:111:ILE:HD11	1:F:219:THR:OG1	2.12	0.50
1:E:100:GLN:OE1	1:E:105:ILE:HD11	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:201:GLN:O	1:C:203:SER:N	2.43	0.49
1:G:129:SER:O	1:G:156:ILE:HD11	2.12	0.49
1:G:18:TRP:O	1:G:48:PRO:HD2	2.13	0.49
1:G:92:LYS:CE	1:G:95:LYS:HB2	2.43	0.49
1:H:33:VAL:HG22	1:H:40:LEU:HD13	1.95	0.49
1:C:6:MET:HB2	1:C:45:PHE:HB2	1.95	0.49
1:G:130:GLN:OE1	1:G:130:GLN:N	2.39	0.48
1:F:166:HIS:CD2	1:F:167:GLY:H	2.31	0.48
1:F:143:LEU:HD23	1:F:184:LYS:HE3	1.94	0.48
1:G:66:TRP:HB3	1:G:68:ASP:H	1.78	0.48
1:C:33:VAL:HG22	1:C:40:LEU:HD13	1.94	0.48
1:C:46:ILE:HG21	1:C:96:LEU:HD21	1.95	0.48
1:D:43:ILE:HD11	1:D:222:ILE:HD11	1.94	0.48
1:F:215:PHE:O	1:F:219:THR:HG23	2.13	0.48
1:E:38:VAL:CG1	1:E:39:SER:H	2.25	0.48
1:D:73:ASP:OD1	1:D:73:ASP:N	2.44	0.48
1:B:166:HIS:CD2	1:B:175:GLU:HA	2.49	0.48
1:A:171:GLN:NE2	1:C:34:ASN:O	2.47	0.48
1:G:92:LYS:HE2	1:G:95:LYS:HD3	1.95	0.48
1:F:112:LEU:HB3	1:F:122:ALA:HB1	1.96	0.47
1:G:92:LYS:CE	1:G:92:LYS:HA	2.44	0.47
1:A:27:HIS:N	3:A:347:HOH:O	2.40	0.47
1:C:18:TRP:HB3	1:C:47:PHE:CD1	2.49	0.47
1:E:21:GLY:HA3	1:E:118:GLY:HA2	1.95	0.47
1:E:-2:SER:N	3:E:425:HOH:O	2.37	0.47
1:G:162:ILE:HB	1:G:192:ASN:HB3	1.96	0.47
1:H:8:PRO:HB2	1:H:41:ASP:O	2.15	0.47
1:F:184:LYS:O	1:F:188:SER:OG	2.27	0.47
1:A:101:VAL:HA	1:A:105:ILE:O	2.15	0.46
1:G:90:ILE:HG22	1:G:90:ILE:O	2.15	0.46
1:C:210:LYS:CD	1:E:196:HIS:HE1	2.28	0.46
1:H:166:HIS:HD2	1:H:167:GLY:H	1.63	0.46
1:H:147:ASP:HA	1:H:150:LYS:HG2	1.98	0.46
1:E:125:THR:O	3:E:406:HOH:O	2.20	0.46
1:E:3:TYR:CD2	1:E:46:ILE:HG23	2.51	0.46
1:D:101:VAL:HA	1:D:105:ILE:O	2.15	0.46
1:E:21:GLY:CA	1:E:118:GLY:HA2	2.45	0.46
1:A:4:GLU:HB2	1:A:47:PHE:HB2	1.96	0.46
1:C:137:MET:SD	1:C:212:ILE:HG23	2.56	0.46
1:F:155:SER:HA	1:F:158:LYS:HD2	1.96	0.46
1:H:15:CYS:HB2	1:H:105:ILE:HD12	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:100:GLN:HB3	1:C:105:ILE:HD11	1.97	0.46
1:A:35:TYR:HB3	1:A:209:ILE:HG21	1.97	0.46
1:A:25:ASP:O	3:A:347:HOH:O	2.21	0.46
1:B:58:ASN:ND2	1:B:117:GLN:HG2	2.31	0.45
1:F:142:TYR:CZ	1:F:144:PRO:HB3	2.52	0.45
1:D:20:HIS:O	1:D:53:ILE:HD12	2.16	0.45
1:B:1:MET:HE2	1:B:2:ASN:H	1.81	0.45
1:A:150:LYS:HG3	3:A:331:HOH:O	2.15	0.45
1:F:3:TYR:HE2	1:F:5:LEU:HD12	1.81	0.45
1:F:97:ILE:HG23	1:F:110:ILE:HD12	1.97	0.45
1:C:176:VAL:HG23	1:C:177:LEU:HD23	1.98	0.45
1:H:14:PHE:HD1	1:H:109:ASN:HB3	1.82	0.45
1:G:143:LEU:HD23	1:G:184:LYS:HE3	1.98	0.45
1:F:141:THR:HG22	1:F:142:TYR:O	2.17	0.44
1:B:29:PHE:CD2	1:B:32:ILE:HD12	2.51	0.44
1:C:166:HIS:NE2	1:C:173:LEU:O	2.46	0.44
1:B:16:VAL:HG13	1:B:111:ILE:HG22	1.99	0.44
1:E:100:GLN:HB3	1:E:105:ILE:HG13	1.99	0.44
1:E:205:CYS:O	1:E:209:ILE:HG12	2.17	0.44
1:G:43:ILE:HD11	1:G:222:ILE:HD11	1.99	0.44
1:A:53:ILE:HD12	1:A:118:GLY:HA2	1.99	0.44
1:H:121:ILE:O	1:H:125:THR:OG1	2.29	0.44
1:C:64:ARG:HD2	1:C:80:VAL:HG21	2.00	0.44
1:A:77:LEU:O	3:A:339:HOH:O	2.21	0.44
1:B:116:SER:O	1:B:141:THR:OG1	2.28	0.44
1:B:46:ILE:HD11	1:B:100:GLN:NE2	2.33	0.44
1:C:3:TYR:HE2	1:C:5:LEU:HD12	1.82	0.44
1:G:90:ILE:C	1:G:92:LYS:N	2.71	0.44
1:E:143:LEU:HB3	1:E:184:LYS:NZ	2.33	0.44
1:B:67:TYR:OH	1:D:31:ASP:OD2	2.24	0.44
1:E:66:TRP:HB3	3:E:423:HOH:O	2.18	0.44
1:G:57:ILE:HG22	1:G:61:MET:HB3	2.00	0.44
1:H:116:SER:OG	1:H:117:GLN:N	2.51	0.44
1:G:156:ILE:H	1:G:156:ILE:HG13	1.62	0.43
1:H:38:VAL:HG11	1:H:217:ALA:HA	2.00	0.43
1:E:163:LEU:HB2	1:E:215:PHE:CD1	2.53	0.43
1:B:55:VAL:HG12	1:B:55:VAL:O	2.17	0.43
1:D:111:ILE:HG13	1:D:220:PHE:CZ	2.53	0.43
1:D:61:MET:SD	1:D:77:LEU:HD21	2.58	0.43
1:G:96:LEU:O	1:G:100:GLN:HG2	2.18	0.43
1:E:3:TYR:HE2	1:E:5:LEU:HD12	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:141:THR:HG23	1:D:181:LEU:HD13	2.00	0.43
1:D:154:THR:HB	1:D:155:SER:H	1.71	0.43
1:F:158:LYS:HA	1:F:190:PHE:CD1	2.52	0.43
1:H:129:SER:O	1:H:156:ILE:HD11	2.18	0.43
1:G:129:SER:HB3	1:G:157:ASN:ND2	2.34	0.43
1:D:155:SER:HA	1:D:158:LYS:HG3	2.01	0.43
1:A:123:THR:HA	1:A:136:ILE:HD13	2.01	0.43
1:C:16:VAL:HG13	1:C:111:ILE:HG22	2.01	0.43
1:F:13:ARG:NE	3:F:341:HOH:O	2.50	0.43
1:C:126:ALA:O	1:C:157:ASN:ND2	2.48	0.43
1:B:143:LEU:HD12	1:B:184:LYS:HE3	2.01	0.43
1:B:136:ILE:HB	1:B:162:ILE:HG12	2.00	0.43
1:G:106:ALA:O	1:G:110:ILE:HG13	2.19	0.43
1:G:107:SER:OG	1:G:132:LYS:O	2.28	0.43
1:G:166:HIS:ND1	1:G:178:GLY:HA3	2.34	0.43
1:G:86:ILE:O	1:G:90:ILE:HG12	2.19	0.43
1:F:18:TRP:O	1:F:48:PRO:HD2	2.19	0.43
1:G:80:VAL:CG1	1:G:81:VAL:N	2.46	0.43
1:E:38:VAL:HG21	1:E:216:ILE:HB	2.00	0.43
1:G:124:TYR:O	1:G:128:THR:OG1	2.30	0.43
1:H:172:VAL:HG12	1:H:173:LEU:HD22	2.01	0.42
1:F:137:MET:SD	1:F:212:ILE:HG23	2.59	0.42
1:G:124:TYR:HD1	1:G:127:ILE:HD11	1.84	0.42
1:D:107:SER:O	1:D:133:LEU:HA	2.18	0.42
1:C:13:ARG:HB3	1:C:14:PHE:CD2	2.54	0.42
1:D:65:ALA:HB1	1:D:69:ILE:HD12	2.00	0.42
1:G:31:ASP:OD1	1:G:32:ILE:N	2.52	0.42
1:F:185:LEU:HA	1:F:185:LEU:HD23	1.90	0.42
1:G:89:SER:O	1:G:93:VAL:HG23	2.19	0.42
1:A:143:LEU:HD13	1:A:181:LEU:HD12	2.02	0.42
1:G:92:LYS:HE2	1:G:95:LYS:HB2	2.01	0.42
1:D:40:LEU:HA	1:D:43:ILE:HD12	2.01	0.42
1:A:126:ALA:HB3	1:A:136:ILE:HD11	2.01	0.42
1:E:141:THR:HG22	1:E:142:TYR:H	1.84	0.42
1:G:92:LYS:HD2	1:G:92:LYS:HA	1.77	0.42
1:C:210:LYS:CE	1:E:196:HIS:CE1	2.98	0.42
1:E:97:ILE:HG23	1:E:110:ILE:HD12	2.01	0.42
1:F:207:GLU:O	1:F:210:LYS:HB3	2.20	0.42
1:B:33:VAL:HG22	1:B:40:LEU:HD13	2.01	0.42
1:A:119:GLY:C	1:A:141:THR:HG21	2.40	0.42
1:C:158:LYS:HD3	1:C:189:GLY:HA3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:97:ILE:HG23	1:C:110:ILE:HD12	2.02	0.42
1:B:66:TRP:CZ2	1:D:203:SER:HA	2.55	0.42
1:F:141:THR:CG2	1:F:142:TYR:N	2.45	0.42
1:F:87:ASN:HB3	3:F:338:HOH:O	2.20	0.42
1:B:93:VAL:O	1:B:97:ILE:HG13	2.20	0.42
1:B:194:TYR:CE2	1:B:196:HIS:HB3	2.55	0.41
1:H:163:LEU:HD12	1:H:193:GLU:O	2.20	0.41
1:E:161:PRO:HG2	1:E:219:THR:HG23	2.02	0.41
1:H:139:LEU:HA	1:H:165:CYS:HB2	2.02	0.41
1:G:95:LYS:HD2	1:G:95:LYS:HA	1.92	0.41
1:H:18:TRP:O	1:H:48:PRO:HD2	2.20	0.41
1:A:25:ASP:OD1	1:A:117:GLN:HB2	2.20	0.41
1:E:121:ILE:O	1:E:125:THR:N	2.51	0.41
1:H:90:ILE:HG23	1:H:125:THR:HG23	2.02	0.41
1:H:69:ILE:HA	1:H:69:ILE:HD12	1.96	0.41
1:D:143:LEU:HD13	1:D:146:TRP:CE3	2.54	0.41
1:D:97:ILE:HG23	1:D:110:ILE:HD12	2.03	0.41
1:E:89:SER:HA	1:E:92:LYS:HD2	2.01	0.41
1:F:96:LEU:HD23	1:F:96:LEU:HA	1.92	0.41
1:H:200:MET:HG2	1:H:201:GLN:O	2.20	0.41
1:A:66:TRP:CZ2	1:C:203:SER:HA	2.56	0.41
1:G:5:LEU:HD21	1:G:44:ARG:HG3	2.02	0.41
1:H:170:ASP:OD2	1:H:202:HIS:ND1	2.38	0.41
1:A:1:MET:HE2	1:A:2:ASN:H	1.84	0.41
1:G:92:LYS:HE3	1:G:95:LYS:HB2	2.02	0.41
1:E:38:VAL:CG2	1:E:213:SER:O	2.68	0.41
1:E:89:SER:O	1:E:93:VAL:HG23	2.21	0.41
1:E:116:SER:HB3	2:E:301:0S1:H14	1.55	0.41
1:E:70:LYS:HB2	1:E:70:LYS:HE3	1.89	0.41
1:H:38:VAL:HG12	1:H:39:SER:H	1.85	0.41
1:A:51:ASP:N	1:A:51:ASP:OD1	2.52	0.41
1:B:35:TYR:HB3	1:B:209:ILE:HG21	2.03	0.41
1:B:72:LEU:HD11	1:B:142:TYR:HD2	1.85	0.41
1:B:106:ALA:O	1:B:110:ILE:HG13	2.21	0.41
1:C:83:VAL:HG22	3:C:337:HOH:O	2.21	0.40
1:A:112:LEU:O	1:A:136:ILE:HA	2.21	0.40
1:A:89:SER:HA	1:A:92:LYS:HD2	2.03	0.40
1:E:107:SER:OG	1:E:132:LYS:O	2.24	0.40
1:A:10:LYS:HD2	1:A:41:ASP:HB3	2.04	0.40
1:F:121:ILE:O	1:F:125:THR:N	2.50	0.40
1:E:169:ASP:OD2	1:E:199:GLY:HA2	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:210:LYS:O	1:H:213:SER:HB3	2.22	0.40
1:D:18:TRP:O	1:D:48:PRO:HD2	2.21	0.40
1:H:5:LEU:HD11	1:H:44:ARG:HD3	2.04	0.40
1:C:94:ASN:ND2	1:C:125:THR:HG23	2.36	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	207/246 (84%)	189 (91%)	18 (9%)	0	100	100
1	B	214/246 (87%)	202 (94%)	12 (6%)	0	100	100
1	C	214/246 (87%)	199 (93%)	14 (6%)	1 (0%)	34	55
1	D	214/246 (87%)	199 (93%)	13 (6%)	2 (1%)	21	37
1	E	198/246 (80%)	186 (94%)	11 (6%)	1 (0%)	34	55
1	F	198/246 (80%)	178 (90%)	20 (10%)	0	100	100
1	G	190/246 (77%)	177 (93%)	13 (7%)	0	100	100
1	H	194/246 (79%)	179 (92%)	15 (8%)	0	100	100
All	All	1629/1968 (83%)	1509 (93%)	116 (7%)	4 (0%)	52	75

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	0	ALA
1	D	69	ILE
1	E	69	ILE
1	D	144	PRO

5.3.2 Protein sidechains (i)

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	184/211 (87%)	174 (95%)	10 (5%)	27 49
1	B	187/211 (89%)	178 (95%)	9 (5%)	31 55
1	C	187/211 (89%)	174 (93%)	13 (7%)	19 34
1	D	188/211 (89%)	176 (94%)	12 (6%)	22 39
1	E	171/211 (81%)	167 (98%)	4 (2%)	58 83
1	F	171/211 (81%)	160 (94%)	11 (6%)	22 39
1	G	173/211 (82%)	169 (98%)	4 (2%)	58 83
1	H	175/211 (83%)	168 (96%)	7 (4%)	38 64
All	All	1436/1688 (85%)	1366 (95%)	70 (5%)	31 55

All (70) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	ILE
1	A	34	ASN
1	A	51	ASP
1	A	108	GLU
1	A	130	GLN
1	A	131	ARG
1	A	142	TYR
1	A	160	LEU
1	A	173	LEU
1	A	206	MET
1	B	51	ASP
1	B	62	GLN
1	B	78	ASN
1	B	80	VAL
1	B	108	GLU
1	B	130	GLN
1	B	160	LEU
1	B	168	THR
1	B	222	ILE

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Mol	Chain	Res	Type
1	C	30	VAL
1	C	38	VAL
1	C	49	HIS
1	C	59	MET
1	C	62	GLN
1	C	83	VAL
1	C	111	ILE
1	C	130	GLN
1	C	132	LYS
1	C	160	LEU
1	C	179	HIS
1	C	196	HIS
1	C	222	ILE
1	D	4	GLU
1	D	59	MET
1	D	68	ASP
1	D	73	ASP
1	D	84	GLU
1	D	96	LEU
1	D	130	GLN
1	D	132	LYS
1	D	160	LEU
1	D	166	HIS
1	D	196	HIS
1	D	218	LYS
1	E	22	LEU
1	E	160	LEU
1	E	166	HIS
1	E	173	LEU
1	F	4	GLU
1	F	38	VAL
1	F	59	MET
1	F	130[A]	GLN
1	F	130[B]	GLN
1	F	132	LYS
1	F	142	TYR
1	F	143	LEU
1	F	156	ILE
1	F	160	LEU
1	F	166	HIS
1	G	-1	ASN
1	G	62	GLN

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Mol	Chain	Res	Type
1	G	94	ASN
1	G	96	LEU
1	H	31	ASP
1	H	38	VAL
1	H	68	ASP
1	H	160	LEU
1	H	166	HIS
1	H	169	ASP
1	H	201	GLN

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

Mol	Chain	Res	Type
1	A	62	GLN
1	B	201	GLN
1	D	157	ASN
1	E	196	HIS
1	G	94	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 carbohydrates in this entry.

5.6 Ligand geometry

1 ligand is 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	$\#\|Z\| > 2$
2	0S1	E	301	1	3,5,20	0.28	0	3,6,29	3.60	2 (66%)

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	0S1	E	301	1	-	0/0/6/26	0/1/1/2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	301	0S1	O1-C1-C4	-4.76	110.98	119.39
2	E	301	0S1	O1-C1-C3	-3.98	112.36	119.39

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	301	0S1	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, 95^{th} 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	217/246 (88%)	-0.46	3 (1%) 78 80	17, 45, 79, 131	0
1	B	220/246 (89%)	-0.52	3 (1%) 78 80	16, 43, 85, 162	0
1	C	220/246 (89%)	-0.68	0 100 100	5, 37, 62, 103	0
1	D	220/246 (89%)	-0.70	0 100 100	7, 32, 59, 83	0
1	E	206/246 (83%)	-0.60	0 100 100	15, 43, 75, 126	0
1	F	205/246 (83%)	-0.59	1 (0%) 91 92	12, 42, 73, 111	0
1	G	204/246 (82%)	-0.37	6 (2%) 55 60	24, 50, 88, 113	0
1	H	204/246 (82%)	-0.23	8 (3%) 43 48	20, 56, 103, 163	0
All	All	1696/1968 (86%)	-0.52	21 (1%) 81 83	5, 44, 83, 163	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	151	GLY	5.3
1	B	49	HIS	4.6
1	A	50	ALA	3.8
1	H	219	THR	3.7
1	H	147	ASP	3.6
1	G	53	ILE	3.4
1	A	72	LEU	3.3
1	H	149	PHE	3.0
1	G	150	LYS	3.0
1	H	150	LYS	3.0
1	A	58	ASN	3.0
1	H	63	MET	2.6
1	B	58	ASN	2.6
1	F	10	LYS	2.6
1	H	142	TYR	2.5
1	H	146	TRP	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	72	LEU	2.3
1	G	54	PRO	2.2
1	G	64	ARG	2.2
1	G	142	TYR	2.1
1	G	167	GLY	2.1

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^{th} 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^2)	Q<0.9
2	0S1	E	301	5/19	0.92	0.15	1.55	17,28,38,46	0

6.5 Other polymers (i)

There are no such residues in this entry.