



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 16, 2024 – 08:00 PM EDT

PDB ID : 3S6J
Title : The crystal structure of a hydrolase from *Pseudomonas syringae*
Authors : Zhang, Z.; Syed Ibrahim, B.; Burley, S.K.; Swaminathan, S.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2011-05-25
Resolution : 2.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

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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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

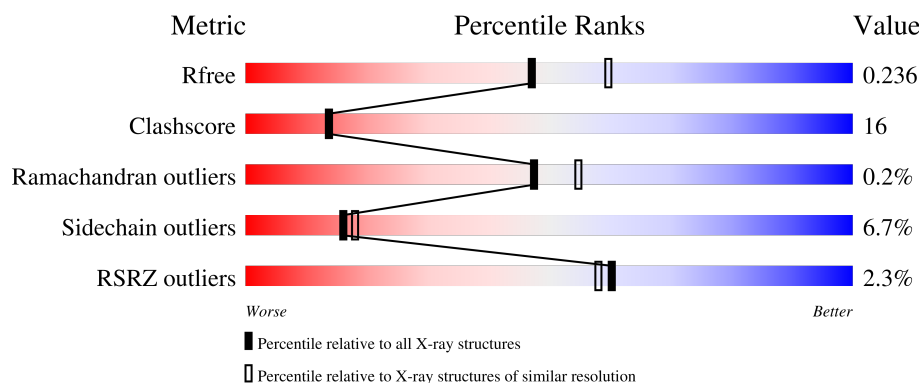
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	233	<div> <div>2%</div> <div>68% 22% 7%</div> </div>
1	B	233	<div> <div>0%</div> <div>65% 22% 10%</div> </div>
1	C	233	<div> <div>3%</div> <div>64% 24% 9%</div> </div>
1	D	233	<div> <div>3%</div> <div>70% 20% 7%</div> </div>
1	E	233	<div> <div>3%</div> <div>68% 22% 6%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	233	<div><div><div>%</div><div><div></div></div><div>71%</div><div>21%</div><div>• 6%</div></div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10211 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 Hydrolase, haloacid dehalogenase-like family.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	216	Total	C	N	O	S	Se	0	0	0
			1666	1053	284	322	3	4			
1	B	209	Total	C	N	O	S	Se	0	0	0
			1610	1019	273	311	3	4			
1	C	212	Total	C	N	O	S	Se	0	0	0
			1627	1027	276	316	3	5			
1	D	216	Total	C	N	O	S	Se	0	0	0
			1666	1052	284	323	3	4			
1	E	220	Total	C	N	O	S	Se	0	0	0
			1691	1067	288	328	3	5			
1	F	219	Total	C	N	O	S	Se	0	0	0
			1684	1062	287	327	3	5			

There are 66 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	102	MSE	-	expression tag	UNP Q88AV7
A	103	SER	-	expression tag	UNP Q88AV7
A	104	LEU	-	expression tag	UNP Q88AV7
A	327	GLU	-	expression tag	UNP Q88AV7
A	328	GLY	-	expression tag	UNP Q88AV7
A	329	HIS	-	expression tag	UNP Q88AV7
A	330	HIS	-	expression tag	UNP Q88AV7
A	331	HIS	-	expression tag	UNP Q88AV7
A	332	HIS	-	expression tag	UNP Q88AV7
A	333	HIS	-	expression tag	UNP Q88AV7
A	334	HIS	-	expression tag	UNP Q88AV7
B	102	MSE	-	expression tag	UNP Q88AV7
B	103	SER	-	expression tag	UNP Q88AV7
B	104	LEU	-	expression tag	UNP Q88AV7
B	327	GLU	-	expression tag	UNP Q88AV7
B	328	GLY	-	expression tag	UNP Q88AV7
B	329	HIS	-	expression tag	UNP Q88AV7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	330	HIS	-	expression tag	UNP Q88AV7
B	331	HIS	-	expression tag	UNP Q88AV7
B	332	HIS	-	expression tag	UNP Q88AV7
B	333	HIS	-	expression tag	UNP Q88AV7
B	334	HIS	-	expression tag	UNP Q88AV7
C	102	MSE	-	expression tag	UNP Q88AV7
C	103	SER	-	expression tag	UNP Q88AV7
C	104	LEU	-	expression tag	UNP Q88AV7
C	327	GLU	-	expression tag	UNP Q88AV7
C	328	GLY	-	expression tag	UNP Q88AV7
C	329	HIS	-	expression tag	UNP Q88AV7
C	330	HIS	-	expression tag	UNP Q88AV7
C	331	HIS	-	expression tag	UNP Q88AV7
C	332	HIS	-	expression tag	UNP Q88AV7
C	333	HIS	-	expression tag	UNP Q88AV7
C	334	HIS	-	expression tag	UNP Q88AV7
D	102	MSE	-	expression tag	UNP Q88AV7
D	103	SER	-	expression tag	UNP Q88AV7
D	104	LEU	-	expression tag	UNP Q88AV7
D	327	GLU	-	expression tag	UNP Q88AV7
D	328	GLY	-	expression tag	UNP Q88AV7
D	329	HIS	-	expression tag	UNP Q88AV7
D	330	HIS	-	expression tag	UNP Q88AV7
D	331	HIS	-	expression tag	UNP Q88AV7
D	332	HIS	-	expression tag	UNP Q88AV7
D	333	HIS	-	expression tag	UNP Q88AV7
D	334	HIS	-	expression tag	UNP Q88AV7
E	102	MSE	-	expression tag	UNP Q88AV7
E	103	SER	-	expression tag	UNP Q88AV7
E	104	LEU	-	expression tag	UNP Q88AV7
E	327	GLU	-	expression tag	UNP Q88AV7
E	328	GLY	-	expression tag	UNP Q88AV7
E	329	HIS	-	expression tag	UNP Q88AV7
E	330	HIS	-	expression tag	UNP Q88AV7
E	331	HIS	-	expression tag	UNP Q88AV7
E	332	HIS	-	expression tag	UNP Q88AV7
E	333	HIS	-	expression tag	UNP Q88AV7
E	334	HIS	-	expression tag	UNP Q88AV7
F	102	MSE	-	expression tag	UNP Q88AV7
F	103	SER	-	expression tag	UNP Q88AV7
F	104	LEU	-	expression tag	UNP Q88AV7
F	327	GLU	-	expression tag	UNP Q88AV7

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Chain	Residue	Modelled	Actual	Comment	Reference
F	328	GLY	-	expression tag	UNP Q88AV7
F	329	HIS	-	expression tag	UNP Q88AV7
F	330	HIS	-	expression tag	UNP Q88AV7
F	331	HIS	-	expression tag	UNP Q88AV7
F	332	HIS	-	expression tag	UNP Q88AV7
F	333	HIS	-	expression tag	UNP Q88AV7
F	334	HIS	-	expression tag	UNP Q88AV7

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Ca 1 1	0	0
2	B	2	Total Ca 2 2	0	0
2	C	2	Total Ca 2 2	0	0
2	D	1	Total Ca 1 1	0	0
2	E	2	Total Ca 2 2	0	0
2	F	1	Total Ca 1 1	0	0

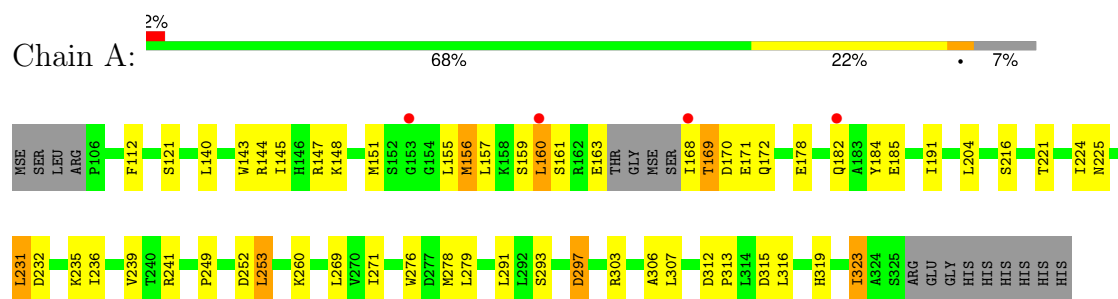
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	46	Total O 46 46	0	0
3	B	40	Total O 40 40	0	0
3	C	45	Total O 45 45	0	0
3	D	34	Total O 34 34	0	0
3	E	49	Total O 49 49	0	0
3	F	44	Total O 44 44	0	0

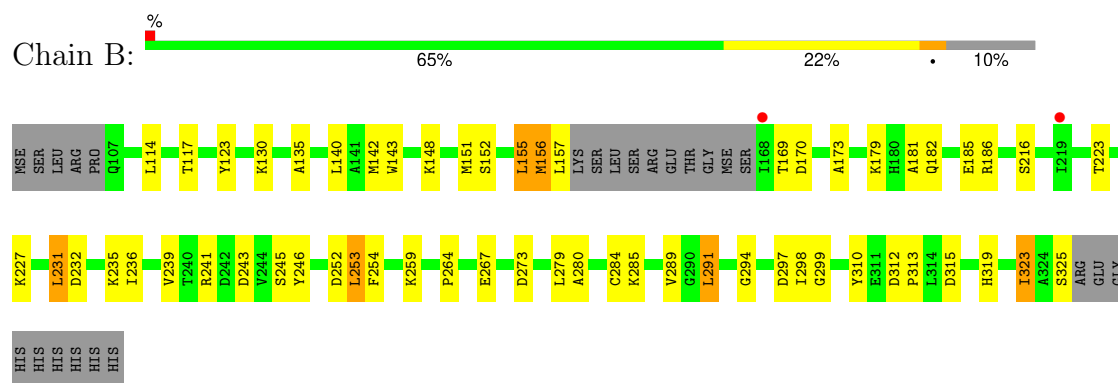
3 Residue-property plots [i](#)

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.

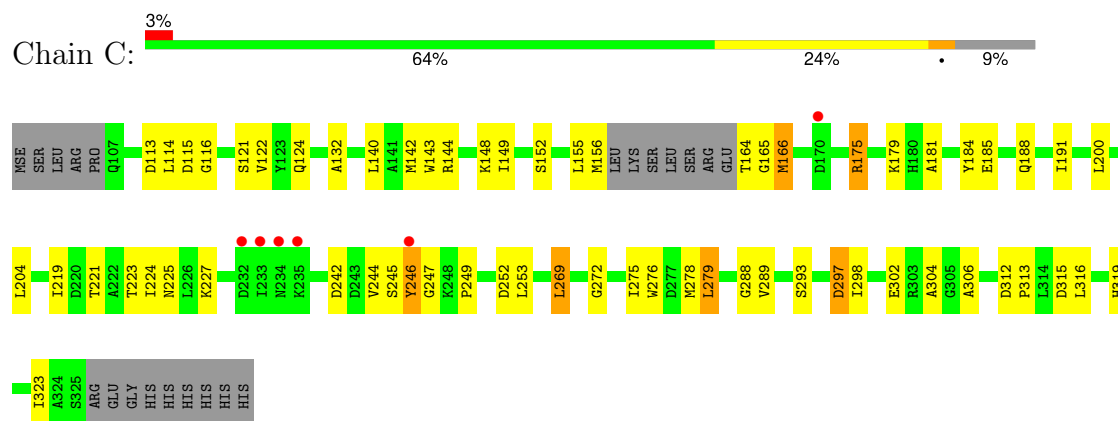
- Molecule 1: Hydrolase, haloacid dehalogenase-like family



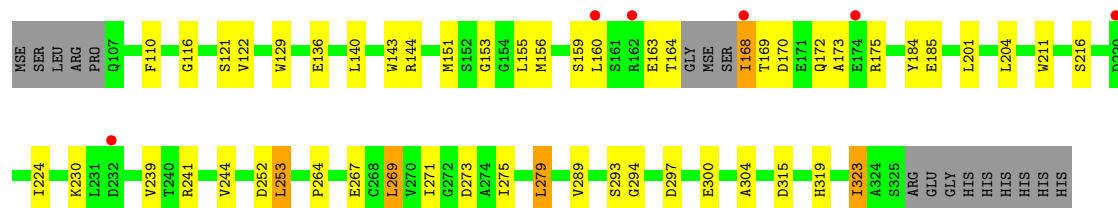
- Molecule 1: Hydrolase, haloacid dehalogenase-like family



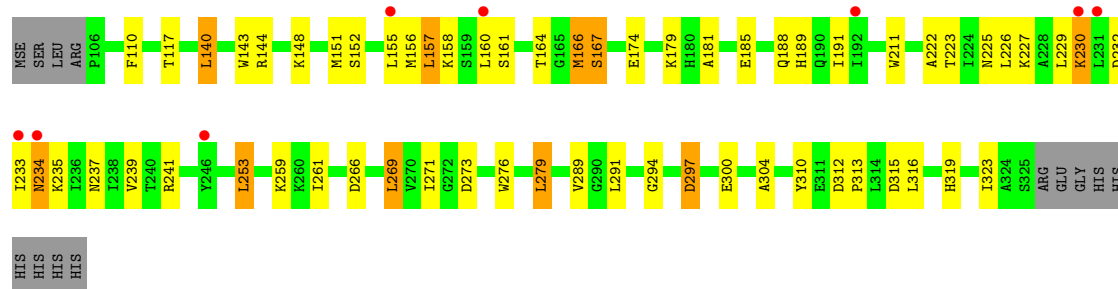
- Molecule 1: Hydrolase, haloacid dehalogenase-like family



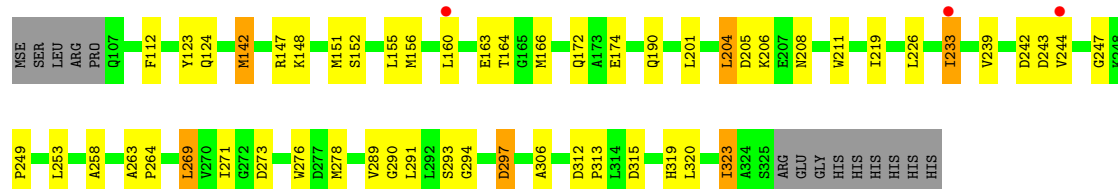
- Molecule 1: Hydrolase, haloacid dehalogenase-like family



- Molecule 1: Hydrolase, haloacid dehalogenase-like family



- Molecule 1: Hydrolase, haloacid dehalogenase-like family



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	69.53Å 74.89Å 75.11Å 59.77° 67.49° 88.00°	Depositor
Resolution (Å)	49.89 – 2.20 49.89 – 2.20	Depositor EDS
% Data completeness (in resolution range)	92.3 (49.89-2.20) 94.7 (49.89-2.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.11 (at 2.20Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, R_{free}	0.195 , 0.243 0.191 , 0.236	Depositor DCC
R_{free} test set	2889 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	32.3	Xtriage
Anisotropy	0.299	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 57.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.015 for -h,k,k-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10211	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.21% 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:
CA

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	0.47	0/1687	0.63	0/2276
1	B	0.43	0/1630	0.62	0/2201
1	C	0.45	0/1646	0.63	0/2220
1	D	0.44	0/1686	0.59	0/2275
1	E	0.44	0/1712	0.61	0/2309
1	F	0.45	0/1704	0.62	0/2298
All	All	0.45	0/10065	0.62	0/13579

There are no bond length outliers.

There are no bond angle outliers.

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	1666	0	1682	56	0
1	B	1610	0	1621	39	0
1	C	1627	0	1634	63	0
1	D	1666	0	1681	50	0
1	E	1691	0	1707	61	0
1	F	1684	0	1699	61	0
2	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	1	0	0	0	0
2	E	2	0	0	0	0
2	F	1	0	0	0	0
3	A	46	0	0	0	0
3	B	40	0	0	3	0
3	C	45	0	0	1	0
3	D	34	0	0	1	0
3	E	49	0	0	1	0
3	F	44	0	0	3	0
All	All	10211	0	10024	317	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 16.

The worst 5 of 317 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:F:278:MSE:HE3	1:F:306:ALA:CB	1.72	1.18
1:C:278:MSE:HE1	1:C:288:GLY:HA3	1.17	1.11
1:F:278:MSE:HE3	1:F:306:ALA:HB2	1.17	1.11
1:C:164:THR:N	1:C:165:GLY:HA2	1.76	0.98
1:A:151:MSE:HE3	1:A:156:MSE:HA	1.45	0.96

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	212/233 (91%)	208 (98%)	4 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	205/233 (88%)	191 (93%)	13 (6%)	1 (0%)	29	31
1	C	208/233 (89%)	200 (96%)	8 (4%)	0	100	100
1	D	212/233 (91%)	206 (97%)	6 (3%)	0	100	100
1	E	218/233 (94%)	206 (94%)	11 (5%)	1 (0%)	29	31
1	F	217/233 (93%)	213 (98%)	4 (2%)	0	100	100
All	All	1272/1398 (91%)	1224 (96%)	46 (4%)	2 (0%)	47	55

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	167	SER
1	B	156	MSE

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	176/185 (95%)	161 (92%)	15 (8%)	10	10
1	B	169/185 (91%)	158 (94%)	11 (6%)	17	19
1	C	171/185 (92%)	162 (95%)	9 (5%)	22	27
1	D	176/185 (95%)	166 (94%)	10 (6%)	20	24
1	E	179/185 (97%)	166 (93%)	13 (7%)	14	15
1	F	178/185 (96%)	166 (93%)	12 (7%)	16	18
All	All	1049/1110 (94%)	979 (93%)	70 (7%)	16	18

5 of 70 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	297	ASP
1	F	155	LEU
1	F	233	ILE
1	B	323	ILE

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Mol	Chain	Res	Type
1	B	291	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	172	GLN
1	F	319	HIS
1	D	234	ASN
1	D	319	HIS
1	E	189	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 9 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	212/233 (90%)	0.11	4 (1%) 66 65	25, 35, 53, 57	0
1	B	205/233 (87%)	0.06	2 (0%) 82 81	25, 37, 57, 72	0
1	C	207/233 (88%)	0.07	6 (2%) 51 49	27, 37, 54, 61	0
1	D	212/233 (90%)	0.06	6 (2%) 53 51	26, 39, 56, 65	0
1	E	215/233 (92%)	0.07	8 (3%) 41 39	26, 38, 53, 64	0
1	F	214/233 (91%)	-0.05	3 (1%) 75 73	26, 35, 50, 56	0
All	All	1265/1398 (90%)	0.05	29 (2%) 60 58	25, 37, 54, 72	0

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	160	LEU	5.3
1	B	168	ILE	4.5
1	D	168	ILE	4.1
1	C	235	LYS	3.4
1	E	234	ASN	3.3

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 monosaccharides 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
2	CA	B	7	1/1	0.93	0.13	42,42,42,42	0
2	CA	C	9	1/1	0.94	0.04	46,46,46,46	0
2	CA	E	8	1/1	0.96	0.15	43,43,43,43	0
2	CA	C	5	1/1	0.99	0.08	38,38,38,38	0
2	CA	B	2	1/1	0.99	0.12	33,33,33,33	0
2	CA	E	1	1/1	0.99	0.13	34,34,34,34	0
2	CA	A	4	1/1	0.99	0.06	32,32,32,32	0
2	CA	F	3	1/1	0.99	0.07	32,32,32,32	0
2	CA	D	6	1/1	1.00	0.11	31,31,31,31	0

6.5 Other polymers [i](#)

There are no such residues in this entry.