wwPDB X-ray Structure Validation Summary Report (i)

Aug 21, 2023 – 07:21 PM EDT

PDB ID	:	2Q4I
Title	:	Ensemble refinement of the protein crystal structure of allene oxide cyclase from Arabidopsis thaliana At3g25770
Authors	:	Levin, E.J.; Kondrashov, D.A.; Wesenberg, G.E.; Phillips Jr., G.N.; Center for Eukaryotic Structural Genomics (CESG)
Deposited on	:	2007-05-31
Resolution	:	1.71 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (i) 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 (1)) were used in the production of this report:

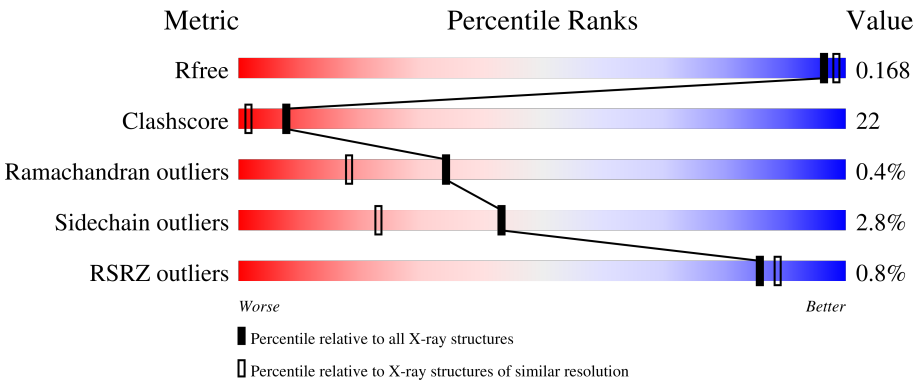
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.71 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	5722 (1.74-1.70)
Clashscore	141614	6152 (1.74-1.70)
Ramachandran outliers	138981	6051 (1.74-1.70)
Sidechain outliers	138945	6051 (1.74-1.70)
RSRZ outliers	127900	5629 (1.74-1.70)

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 <=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	1-A	193	67% 22% • 10%
1	1-B	193	% 57% 32% •• 10%
1	1-C	193	% 63% 25% •• 10%
1	2-A	193	55% 33% • 10%
1	2-B	193	% 51% 38% • 10%

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Mol	Chain	Length	Quality of chain
1	2-C	193	% 55% 33% • 10%
1	3-A	193	54% 32% • • 10%
1	3-B	193	% 60% 27% • 10%
1	3-C	193	% 59% 30% • • 10%
1	4-A	193	64% 24% • 10%
1	4-B	193	% 53% 35% • • 10%
1	4-C	193	% 54% 33% • 10%
1	5-A	193	67% 21% • 10%
1	5-B	193	% 60% 28% • • 10%
1	5-C	193	% 61% 26% • 10%
1	6-A	193	59% 28% • 10%
1	6-B	193	% 60% 28% • 10%
1	6-C	193	% 66% 21% • 10%
1	7-A	193	68% 21% • 10%
1	7-B	193	% 71% 18% • 10%
1	7-C	193	% 55% 33% • 10%
1	8-A	193	54% 34% • 10%
1	8-B	193	% 64% 24% • 10%
1	8-C	193	% 63% 26% • 10%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 38664 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 Allene oxide cyclase 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	1-A	174	1364	891	213	258	1	1	0	0	0
1	2-A	174	1364	891	213	258	1	1	0	0	0
1	3-A	174	1364	891	213	258	1	1	0	0	0
1	4-A	174	1364	891	213	258	1	1	0	0	0
1	5-A	174	1364	891	213	258	1	1	0	0	0
1	6-A	174	1364	891	213	258	1	1	0	0	0
1	7-A	174	1364	891	213	258	1	1	0	0	0
1	8-A	174	1364	891	213	258	1	1	0	0	0
1	1-B	174	1364	891	213	258	1	1	0	0	0
1	2-B	174	1364	891	213	258	1	1	0	0	0
1	3-B	174	1364	891	213	258	1	1	0	0	0
1	4-B	174	1364	891	213	258	1	1	0	0	0
1	5-B	174	1364	891	213	258	1	1	0	0	0
1	6-B	174	1364	891	213	258	1	1	0	0	0
1	7-B	174	1364	891	213	258	1	1	0	0	0
1	8-B	174	1364	891	213	258	1	1	0	0	0

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	1-C	174	1364	891	213	258	1	1	0	0	0
1	2-C	174	1364	891	213	258	1	1	0	0	0
1	3-C	174	1364	891	213	258	1	1	0	0	0
1	4-C	174	1364	891	213	258	1	1	0	0	0
1	5-C	174	1364	891	213	258	1	1	0	0	0
1	6-C	174	1364	891	213	258	1	1	0	0	0
1	7-C	174	1364	891	213	258	1	1	0	0	0
1	8-C	174	1364	891	213	258	1	1	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	SER	-	expression tag	UNP Q9LS02
A	47	MSE	MET	modified residue	UNP Q9LS02
B	1	SER	-	expression tag	UNP Q9LS02
B	47	MSE	MET	modified residue	UNP Q9LS02
C	1	SER	-	expression tag	UNP Q9LS02
C	47	MSE	MET	modified residue	UNP Q9LS02

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	1-A	248	248	248	0	0
2	2-A	250	250	250	0	0
2	3-A	246	246	246	0	0
2	4-A	244	244	244	0	0
2	5-A	243	243	243	0	0
2	6-A	247	247	247	0	0

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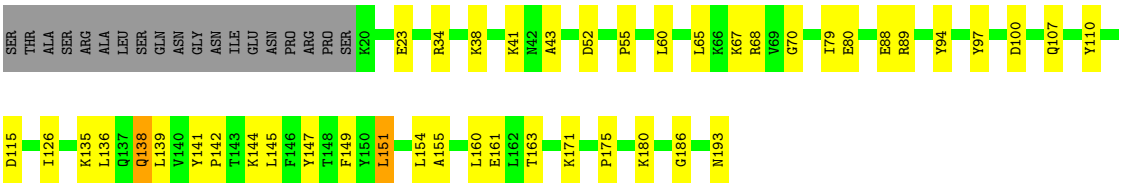
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	7-A	241	Total O 241 241	0	0
2	8-A	251	Total O 251 251	0	0
2	1-B	247	Total O 247 247	0	0
2	2-B	248	Total O 248 248	0	0
2	3-B	249	Total O 249 249	0	0
2	4-B	254	Total O 254 254	0	0
2	5-B	251	Total O 251 251	0	0
2	6-B	250	Total O 250 250	0	0
2	7-B	251	Total O 251 251	0	0
2	8-B	249	Total O 249 249	0	0
2	1-C	246	Total O 246 246	0	0
2	2-C	243	Total O 243 243	0	0
2	3-C	246	Total O 246 246	0	0
2	4-C	243	Total O 243 243	0	0
2	5-C	247	Total O 247 247	0	0
2	6-C	244	Total O 244 244	0	0
2	7-C	249	Total O 249 249	0	0
2	8-C	241	Total O 241 241	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.

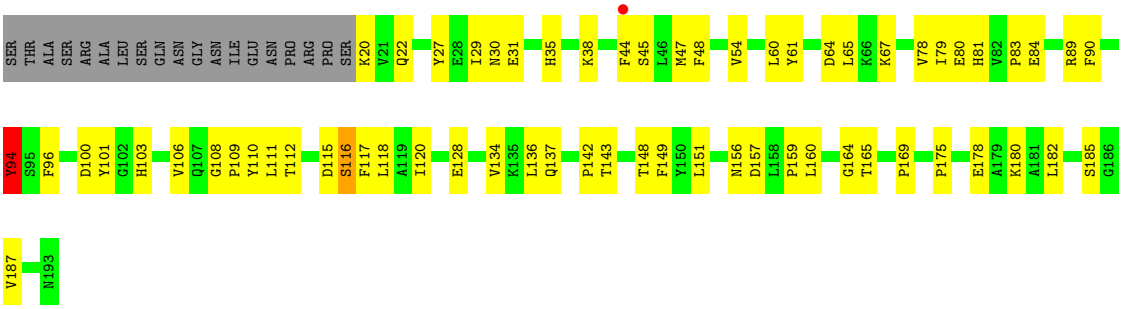
• Molecule 1: Allene oxide cyclase 2

Chain 1-A:



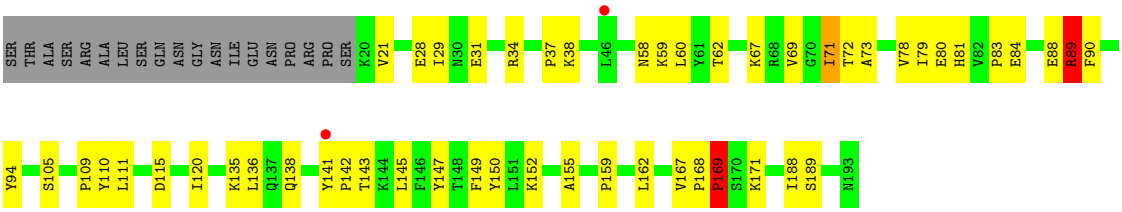
• Molecule 1: Allene oxide cyclase 2

Chain 1-B:



• Molecule 1: Allene oxide cyclase 2

Chain 1-C:

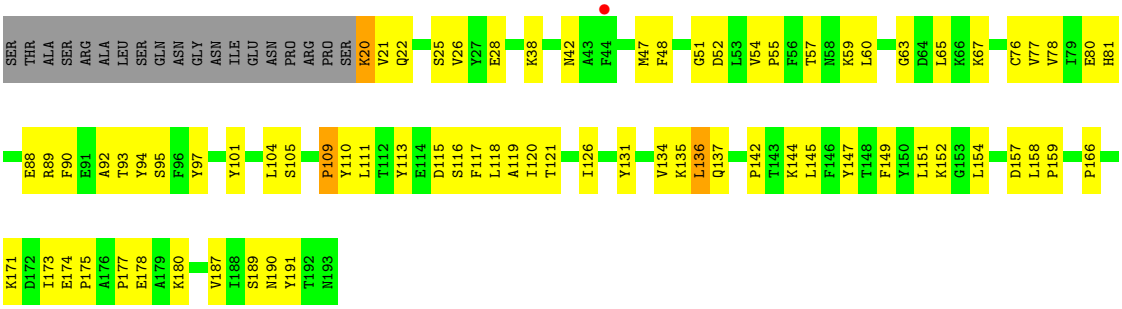


• Molecule 1: Allene oxide cyclase 2

Chain 2-A:

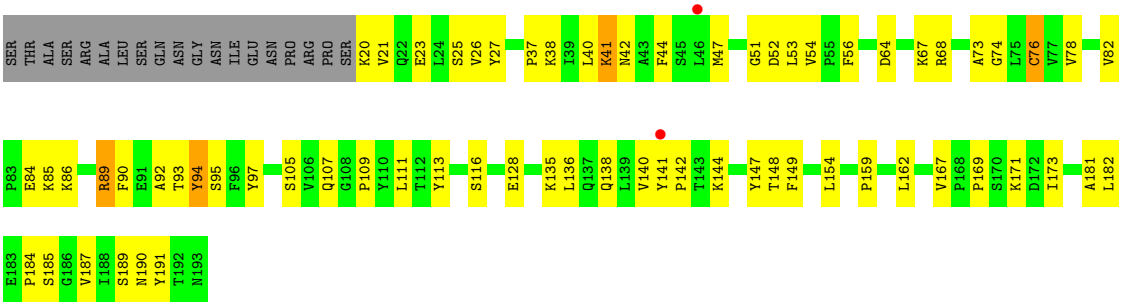
• Molecule 1: Allene oxide cyclase 2

Chain 2-B:



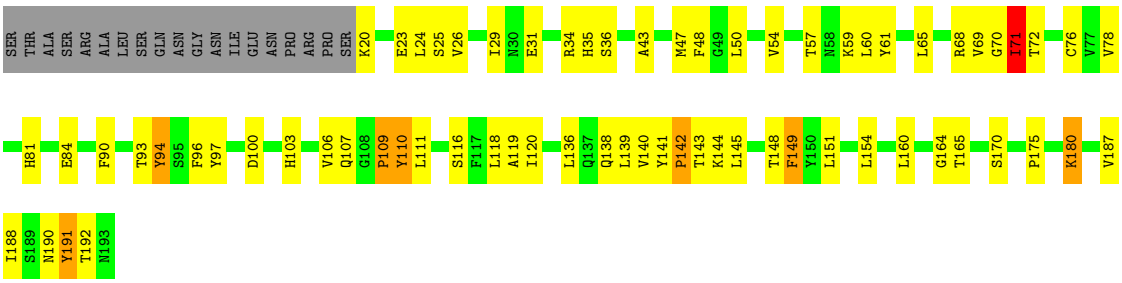
• Molecule 1: Allene oxide cyclase 2

Chain 2-C:



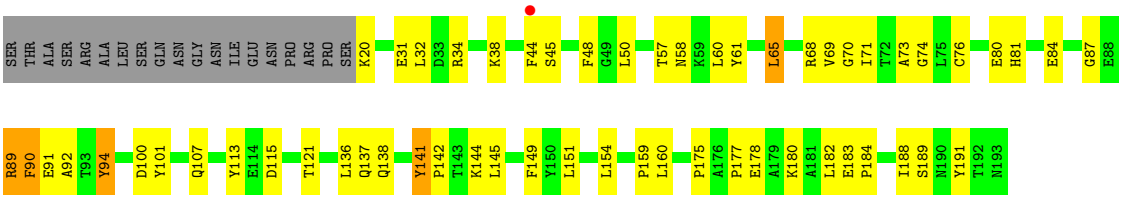
• Molecule 1: Allene oxide cyclase 2

Chain 3-A:



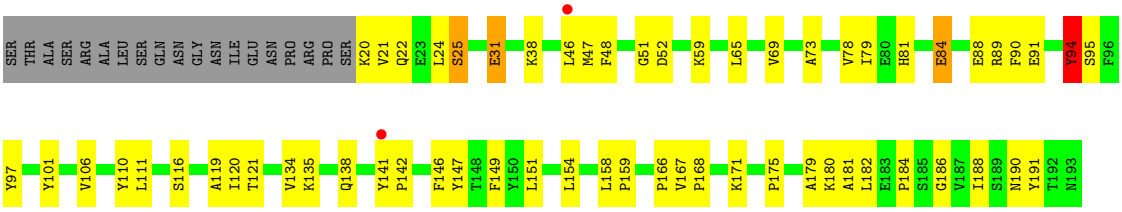
• Molecule 1: Allene oxide cyclase 2

Chain 3-B:



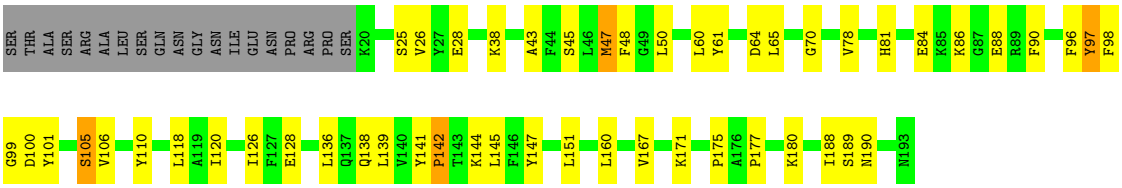
- Molecule 1: Allene oxide cyclase 2

Chain 3-C:



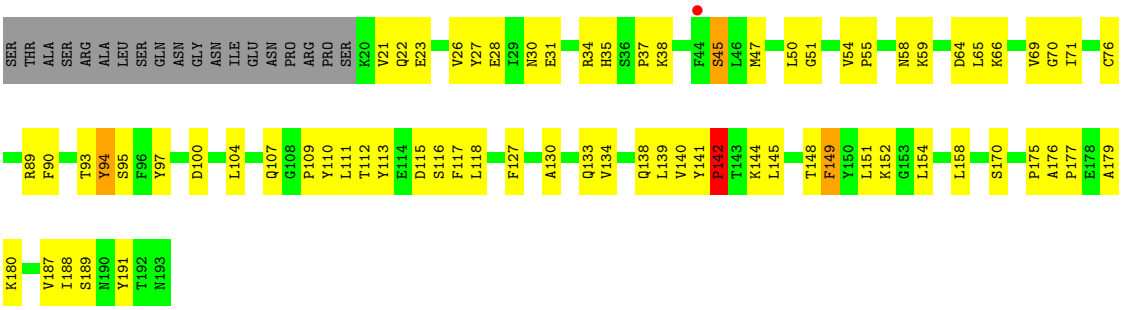
- Molecule 1: Allene oxide cyclase 2

Chain 4-A:



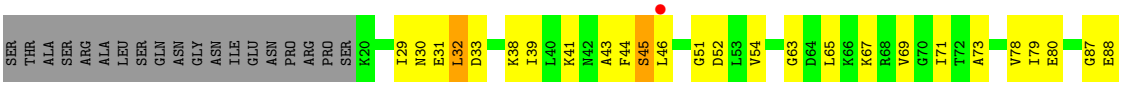
- Molecule 1: Allene oxide cyclase 2

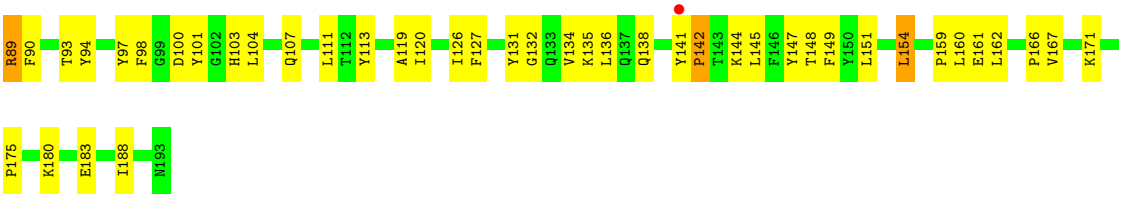
Chain 4-B:



- Molecule 1: Allene oxide cyclase 2

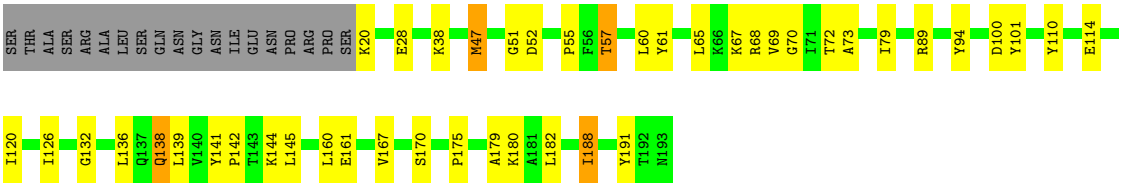
Chain 4-C:





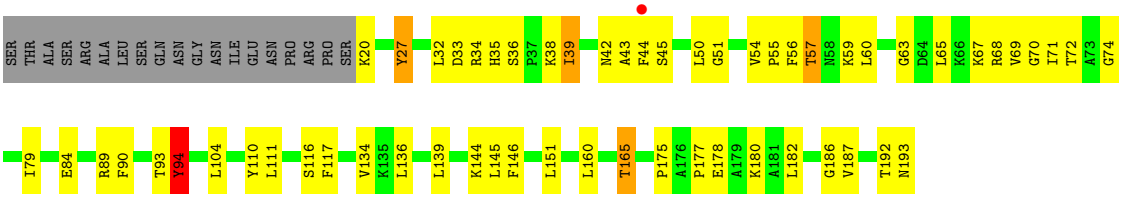
• Molecule 1: Allene oxide cyclase 2

Chain 5-A:



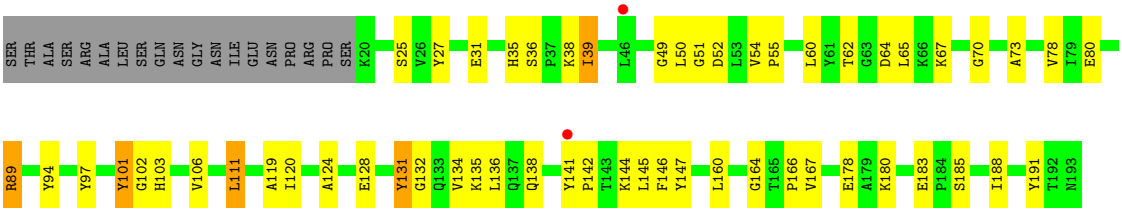
• Molecule 1: Allene oxide cyclase 2

Chain 5-B:



• Molecule 1: Allene oxide cyclase 2

Chain 5-C:

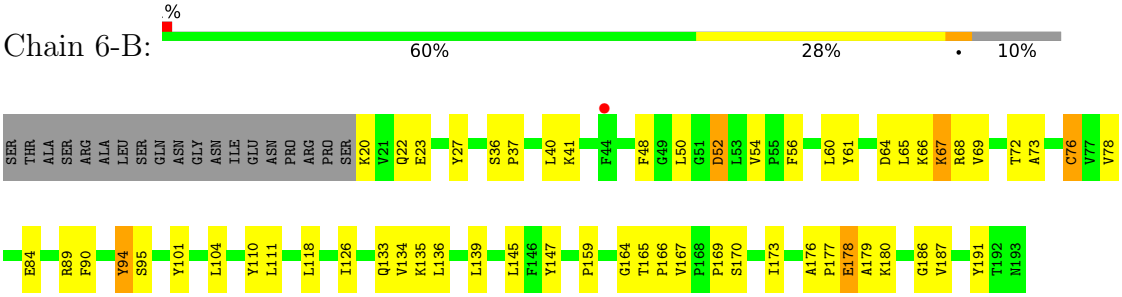


• Molecule 1: Allene oxide cyclase 2

Chain 6-A:

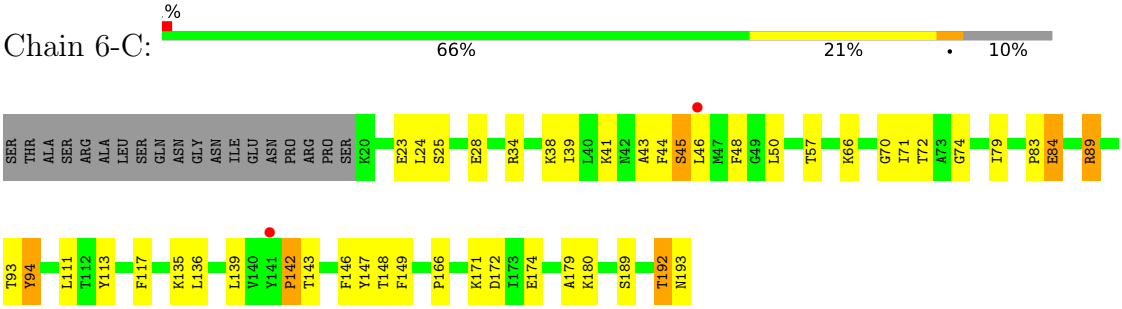
• Molecule 1: Allene oxide cyclase 2

Chain 6-B:



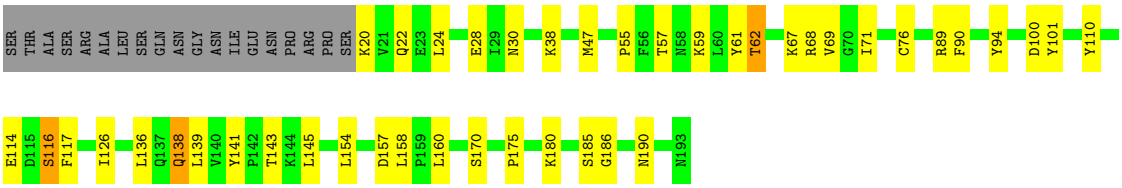
• Molecule 1: Allene oxide cyclase 2

Chain 6-C:



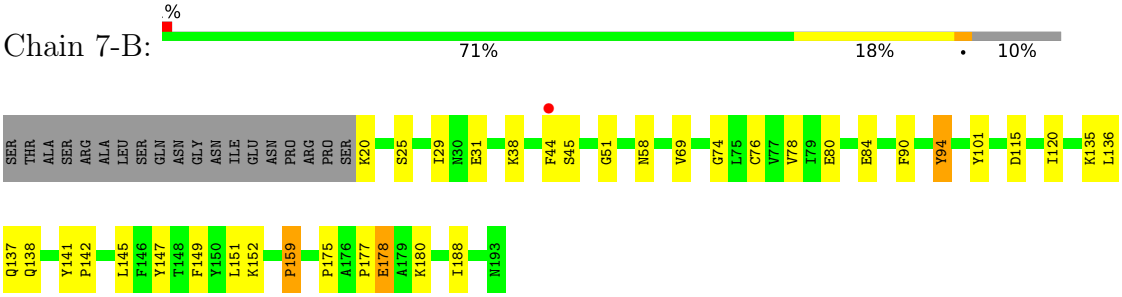
• Molecule 1: Allene oxide cyclase 2

Chain 7-A:



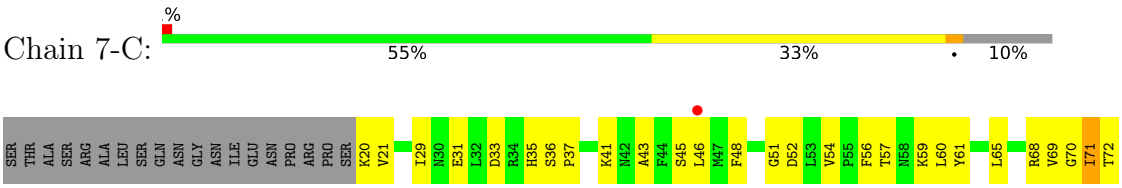
• Molecule 1: Allene oxide cyclase 2

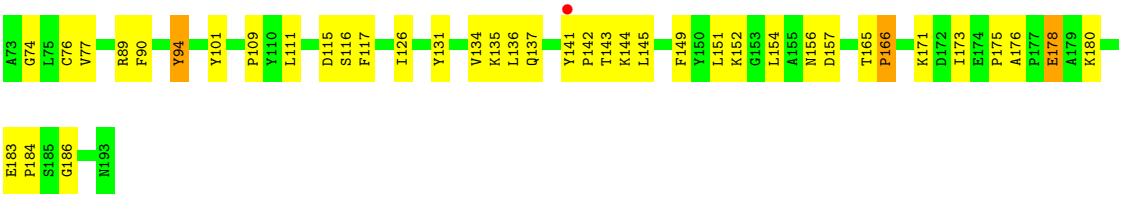
Chain 7-B:



• Molecule 1: Allene oxide cyclase 2

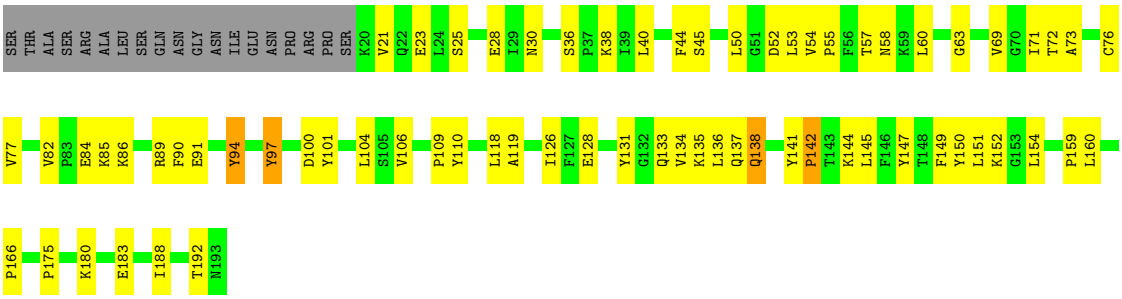
Chain 7-C:





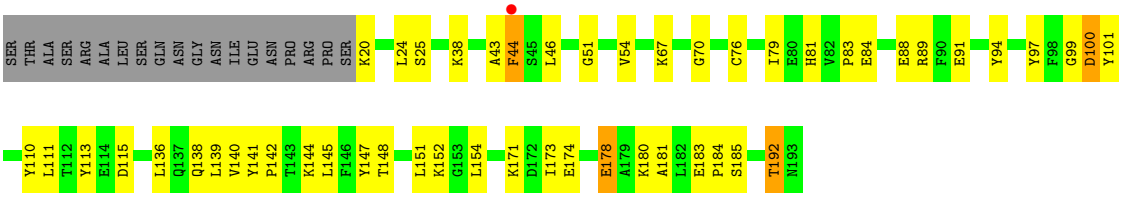
• Molecule 1: Allene oxide cyclase 2

Chain 8-A:



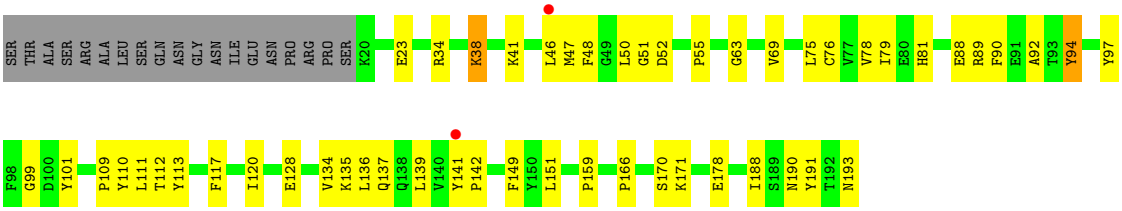
• Molecule 1: Allene oxide cyclase 2

Chain 8-B:



• Molecule 1: Allene oxide cyclase 2

Chain 8-C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	64.41Å 100.01Å 105.39Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.17 – 1.71 48.17 – 1.71	Depositor EDS
% Data completeness (in resolution range)	99.7 (48.17-1.71) 99.9 (48.17-1.71)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	5.53 (at 1.71Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.132 , 0.172 0.130 , 0.168	Depositor DCC
R_{free} test set	3725 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	11.3	Xtriage
Anisotropy	0.023	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 40.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	38664	wwPDB-VP
Average B, all atoms (Å^2)	12.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.00% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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)

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	1-A	0.95	0/1399	0.93	1/1897 (0.1%)
1	1-B	0.92	0/1399	0.96	1/1897 (0.1%)
1	1-C	0.96	0/1399	0.93	1/1897 (0.1%)
1	2-A	0.96	1/1399 (0.1%)	0.94	1/1897 (0.1%)
1	2-B	0.96	0/1399	1.00	1/1897 (0.1%)
1	2-C	0.97	0/1399	1.00	3/1897 (0.2%)
1	3-A	0.98	0/1399	0.95	1/1897 (0.1%)
1	3-B	0.97	0/1399	0.97	4/1897 (0.2%)
1	3-C	0.96	1/1399 (0.1%)	0.98	3/1897 (0.2%)
1	4-A	0.91	0/1399	0.92	0/1897
1	4-B	0.98	0/1399	0.99	0/1897
1	4-C	0.97	1/1399 (0.1%)	0.91	0/1897
1	5-A	1.04	0/1399	1.01	2/1897 (0.1%)
1	5-B	1.02	1/1399 (0.1%)	1.03	1/1897 (0.1%)
1	5-C	1.03	0/1399	1.01	1/1897 (0.1%)
1	6-A	1.05	0/1399	0.99	1/1897 (0.1%)
1	6-B	1.01	0/1399	1.00	0/1897
1	6-C	1.02	0/1399	0.99	1/1897 (0.1%)
1	7-A	1.00	0/1399	0.98	3/1897 (0.2%)
1	7-B	1.03	0/1399	0.99	0/1897
1	7-C	1.04	2/1399 (0.1%)	1.04	2/1897 (0.1%)
1	8-A	1.01	0/1399	1.03	2/1897 (0.1%)
1	8-B	1.04	1/1399 (0.1%)	1.04	0/1897
1	8-C	0.99	0/1399	1.02	2/1897 (0.1%)
All	All	0.99	7/33576 (0.0%)	0.98	31/45528 (0.1%)

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	1-A	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	1-B	0	1
1	1-C	0	1
1	2-A	0	1
1	2-B	0	1
1	2-C	0	1
1	3-A	0	2
1	3-B	0	1
1	3-C	0	1
1	4-A	0	1
1	4-B	0	1
1	4-C	0	1
1	5-A	0	1
1	5-B	0	1
1	5-C	0	2
1	6-A	0	2
1	6-B	0	1
1	6-C	0	1
1	7-A	0	1
1	7-B	0	1
1	7-C	0	1
1	8-A	0	3
1	8-B	0	2
All	All	0	29

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	3-C	31	GLU	CD-OE1	5.58	1.31	1.25
1	5-B	27	TYR	CD2-CE2	5.48	1.47	1.39
1	8-B	178	GLU	CD-OE2	-5.32	1.19	1.25
1	4-C	131	TYR	CD2-CE2	5.26	1.47	1.39
1	7-C	71	ILE	CA-CB	5.22	1.66	1.54

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	7-C	89	ARG	NE-CZ-NH2	-13.18	113.71	120.30
1	3-C	89	ARG	NE-CZ-NH2	-11.09	114.76	120.30
1	8-C	89	ARG	NE-CZ-NH2	-11.06	114.77	120.30
1	3-C	89	ARG	NE-CZ-NH1	9.85	125.22	120.30
1	2-C	89	ARG	NE-CZ-NH1	9.56	125.08	120.30

There are no chirality outliers.

5 of 29 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1-A	94	TYR	Sidechain
1	1-B	94	TYR	Sidechain
1	1-C	94	TYR	Sidechain
1	2-A	94	TYR	Sidechain
1	2-B	94	TYR	Sidechain

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	1-A	1364	0	1356	48	0
1	1-B	1364	0	1356	57	0
1	1-C	1364	0	1356	62	0
1	2-A	1364	0	1356	91	0
1	2-B	1364	0	1356	79	0
1	2-C	1364	0	1356	66	0
1	3-A	1364	0	1356	84	0
1	3-B	1364	0	1356	53	0
1	3-C	1364	0	1356	59	0
1	4-A	1364	0	1356	62	0
1	4-B	1364	0	1356	80	0
1	4-C	1364	0	1356	68	0
1	5-A	1364	0	1356	59	0
1	5-B	1364	0	1356	50	0
1	5-C	1364	0	1356	66	0
1	6-A	1364	0	1356	69	0
1	6-B	1364	0	1356	56	0
1	6-C	1364	0	1356	52	0
1	7-A	1364	0	1356	44	0
1	7-B	1364	0	1356	34	0
1	7-C	1364	0	1356	59	0
1	8-A	1364	0	1356	74	0
1	8-B	1364	0	1356	52	0
1	8-C	1364	0	1356	51	0
2	1-A	248	0	0	17	0
2	1-B	247	0	0	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	1-C	246	0	0	13	0
2	2-A	250	0	0	30	0
2	2-B	248	0	0	10	0
2	2-C	243	0	0	15	0
2	3-A	246	0	0	20	0
2	3-B	249	0	0	12	0
2	3-C	246	0	0	15	0
2	4-A	244	0	0	20	0
2	4-B	254	0	0	25	0
2	4-C	243	0	0	18	0
2	5-A	243	0	0	25	0
2	5-B	251	0	0	15	0
2	5-C	247	0	0	18	0
2	6-A	247	0	0	34	0
2	6-B	250	0	0	7	0
2	6-C	244	0	0	17	0
2	7-A	241	0	0	19	0
2	7-B	251	0	0	10	0
2	7-C	249	0	0	12	0
2	8-A	251	0	0	25	0
2	8-B	249	0	0	18	0
2	8-C	241	0	0	14	0
All	All	38664	0	32544	1409	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 22.

The worst 5 of 1409 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:80:GLU:OE1	2:B:283:HOH:O	1.55	1.24
1:A:110:TYR:CE1	2:A:375:HOH:O	1.90	1.19
1:C:38:LYS:HD3	2:C:334:HOH:O	1.48	1.13
1:A:138:GLN:HB2	2:A:274:HOH:O	1.49	1.09
1:C:151:LEU:HD13	1:C:154:LEU:HD21	1.35	1.08

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	1-A	172/193 (89%)	166 (96%)	6 (4%)	0	100	100
1	1-B	172/193 (89%)	165 (96%)	7 (4%)	0	100	100
1	1-C	172/193 (89%)	162 (94%)	9 (5%)	1 (1%)	25	10
1	2-A	172/193 (89%)	157 (91%)	13 (8%)	2 (1%)	13	3
1	2-B	172/193 (89%)	161 (94%)	11 (6%)	0	100	100
1	2-C	172/193 (89%)	161 (94%)	11 (6%)	0	100	100
1	3-A	172/193 (89%)	154 (90%)	15 (9%)	3 (2%)	9	1
1	3-B	172/193 (89%)	158 (92%)	13 (8%)	1 (1%)	25	10
1	3-C	172/193 (89%)	164 (95%)	8 (5%)	0	100	100
1	4-A	172/193 (89%)	165 (96%)	7 (4%)	0	100	100
1	4-B	172/193 (89%)	166 (96%)	4 (2%)	2 (1%)	13	3
1	4-C	172/193 (89%)	159 (92%)	11 (6%)	2 (1%)	13	3
1	5-A	172/193 (89%)	165 (96%)	7 (4%)	0	100	100
1	5-B	172/193 (89%)	162 (94%)	9 (5%)	1 (1%)	25	10
1	5-C	172/193 (89%)	167 (97%)	5 (3%)	0	100	100
1	6-A	172/193 (89%)	168 (98%)	4 (2%)	0	100	100
1	6-B	172/193 (89%)	162 (94%)	10 (6%)	0	100	100
1	6-C	172/193 (89%)	168 (98%)	3 (2%)	1 (1%)	25	10
1	7-A	172/193 (89%)	165 (96%)	7 (4%)	0	100	100
1	7-B	172/193 (89%)	167 (97%)	5 (3%)	0	100	100
1	7-C	172/193 (89%)	163 (95%)	8 (5%)	1 (1%)	25	10
1	8-A	172/193 (89%)	161 (94%)	11 (6%)	0	100	100
1	8-B	172/193 (89%)	165 (96%)	6 (4%)	1 (1%)	25	10
1	8-C	172/193 (89%)	162 (94%)	10 (6%)	0	100	100
All	All	4128/4632 (89%)	3913 (95%)	200 (5%)	15 (0%)	34	18

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	2-A	32	LEU
1	3-A	191	TYR
1	3-B	65	LEU
1	4-C	32	LEU
1	4-C	45	SER

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	1-A	147/162 (91%)	145 (99%)	2 (1%)	67	52
1	1-B	147/162 (91%)	144 (98%)	3 (2%)	55	37
1	1-C	147/162 (91%)	143 (97%)	4 (3%)	44	25
1	2-A	147/162 (91%)	142 (97%)	5 (3%)	37	16
1	2-B	147/162 (91%)	141 (96%)	6 (4%)	30	11
1	2-C	147/162 (91%)	142 (97%)	5 (3%)	37	16
1	3-A	147/162 (91%)	142 (97%)	5 (3%)	37	16
1	3-B	147/162 (91%)	146 (99%)	1 (1%)	84	76
1	3-C	147/162 (91%)	143 (97%)	4 (3%)	44	25
1	4-A	147/162 (91%)	142 (97%)	5 (3%)	37	16
1	4-B	147/162 (91%)	142 (97%)	5 (3%)	37	16
1	4-C	147/162 (91%)	144 (98%)	3 (2%)	55	37
1	5-A	147/162 (91%)	141 (96%)	6 (4%)	30	11
1	5-B	147/162 (91%)	144 (98%)	3 (2%)	55	37
1	5-C	147/162 (91%)	143 (97%)	4 (3%)	44	25
1	6-A	147/162 (91%)	141 (96%)	6 (4%)	30	11
1	6-B	147/162 (91%)	141 (96%)	6 (4%)	30	11
1	6-C	147/162 (91%)	144 (98%)	3 (2%)	55	37
1	7-A	147/162 (91%)	143 (97%)	4 (3%)	44	25

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	7-B	147/162 (91%)	143 (97%)	4 (3%)	44	25
1	7-C	147/162 (91%)	143 (97%)	4 (3%)	44	25
1	8-A	147/162 (91%)	144 (98%)	3 (2%)	55	37
1	8-B	147/162 (91%)	143 (97%)	4 (3%)	44	25
1	8-C	147/162 (91%)	144 (98%)	3 (2%)	55	37
All	All	3528/3888 (91%)	3430 (97%)	98 (3%)	43	23

5 of 98 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	5-C	39	ILE
1	6-B	94	TYR
1	5-C	131	TYR
1	6-A	170	SER
1	6-C	192	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	5-B	138	GLN
1	6-A	137	GLN
1	7-B	190	ASN
1	5-C	42	ASN
1	6-A	138	GLN

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)

There are no ligands in this entry.

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	1-A	173/193 (89%)	-0.45	0 100 100	2, 7, 21, 34	173 (100%)
1	1-B	173/193 (89%)	-0.38	1 (0%) 89 91	2, 7, 16, 32	173 (100%)
1	1-C	173/193 (89%)	-0.31	2 (1%) 79 83	3, 8, 19, 32	173 (100%)
1	2-A	173/193 (89%)	-0.45	0 100 100	2, 7, 21, 34	173 (100%)
1	2-B	173/193 (89%)	-0.38	1 (0%) 89 91	2, 7, 16, 32	173 (100%)
1	2-C	173/193 (89%)	-0.31	2 (1%) 79 83	3, 8, 19, 32	173 (100%)
1	3-A	173/193 (89%)	-0.45	0 100 100	2, 7, 21, 34	173 (100%)
1	3-B	173/193 (89%)	-0.38	1 (0%) 89 91	2, 7, 16, 32	173 (100%)
1	3-C	173/193 (89%)	-0.31	2 (1%) 79 83	3, 8, 19, 32	173 (100%)
1	4-A	173/193 (89%)	-0.45	0 100 100	2, 7, 21, 34	173 (100%)
1	4-B	173/193 (89%)	-0.38	1 (0%) 89 91	2, 7, 16, 32	173 (100%)
1	4-C	173/193 (89%)	-0.31	2 (1%) 79 83	3, 8, 19, 32	173 (100%)
1	5-A	173/193 (89%)	-0.45	0 100 100	2, 7, 21, 34	173 (100%)
1	5-B	173/193 (89%)	-0.38	1 (0%) 89 91	2, 7, 16, 32	173 (100%)
1	5-C	173/193 (89%)	-0.31	2 (1%) 79 83	3, 8, 19, 32	173 (100%)
1	6-A	173/193 (89%)	-0.45	0 100 100	2, 7, 21, 34	173 (100%)
1	6-B	173/193 (89%)	-0.38	1 (0%) 89 91	2, 7, 16, 32	173 (100%)
1	6-C	173/193 (89%)	-0.31	2 (1%) 79 83	3, 8, 19, 32	173 (100%)
1	7-A	173/193 (89%)	-0.45	0 100 100	2, 7, 21, 34	173 (100%)
1	7-B	173/193 (89%)	-0.38	1 (0%) 89 91	2, 7, 16, 32	173 (100%)
1	7-C	173/193 (89%)	-0.31	2 (1%) 79 83	3, 8, 19, 32	173 (100%)
1	8-A	173/193 (89%)	-0.45	0 100 100	2, 7, 21, 34	173 (100%)
1	8-B	173/193 (89%)	-0.38	1 (0%) 89 91	2, 7, 16, 32	173 (100%)
1	8-C	173/193 (89%)	-0.31	2 (1%) 79 83	3, 8, 19, 32	173 (100%)

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
All	All	4152/4632 (89%)	-0.38	24 (0%) 86 91	2, 8, 19, 34	4152 (100%)

The worst 5 of 24 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	1-C	46	LEU	3.2
1	2-C	46	LEU	3.2
1	3-C	46	LEU	3.2
1	4-C	46	LEU	3.2
1	5-C	46	LEU	3.2

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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.