



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 11:13 PM GMT

PDB ID : 2Q4M
Title : Ensemble refinement of the crystal structure of protein from Arabidopsis thaliana At5g01750
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 : 1.70 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

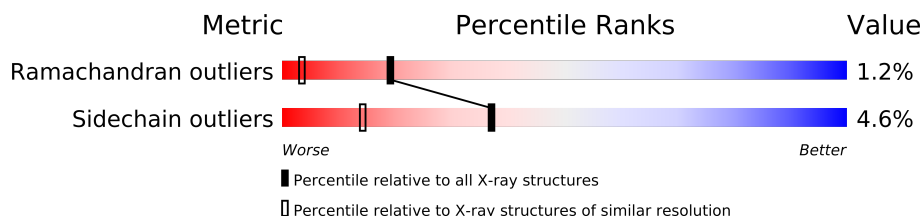
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : **FAILED**
Percentile statistics : 21963
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 1.70 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))
Ramachandran outliers	78287	2878 (1.70-1.70)
Sidechain outliers	78261	2878 (1.70-1.70)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	1-A	217	
1	10-A	217	
1	11-A	217	
1	12-A	217	
1	13-A	217	
1	14-A	217	
1	15-A	217	
1	16-A	217	
1	2-A	217	
1	3-A	217	
1	4-A	217	
1	5-A	217	
1	6-A	217	
1	7-A	217	
1	8-A	217	
1	9-A	217	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 22688 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

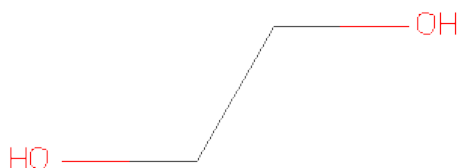
- Molecule 1 is a protein called Protein At5g01750.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	1-A	162	Total	C	N	O	S	Se	0	0	0
			1287	820	228	234	3	2			
1	2-A	162	Total	C	N	O	S	Se	0	0	0
			1287	820	228	234	3	2			
1	3-A	162	Total	C	N	O	S	Se	0	0	0
			1287	820	228	234	3	2			
1	4-A	162	Total	C	N	O	S	Se	0	0	0
			1287	820	228	234	3	2			
1	5-A	162	Total	C	N	O	S	Se	0	0	0
			1287	820	228	234	3	2			
1	6-A	162	Total	C	N	O	S	Se	0	0	0
			1287	820	228	234	3	2			
1	7-A	162	Total	C	N	O	S	Se	0	0	0
			1287	820	228	234	3	2			
1	8-A	162	Total	C	N	O	S	Se	0	0	0
			1287	820	228	234	3	2			
1	9-A	162	Total	C	N	O	S	Se	0	0	0
			1287	820	228	234	3	2			
1	10-A	162	Total	C	N	O	S	Se	0	0	0
			1287	820	228	234	3	2			
1	11-A	162	Total	C	N	O	S	Se	0	0	0
			1287	820	228	234	3	2			
1	12-A	162	Total	C	N	O	S	Se	0	0	0
			1287	820	228	234	3	2			
1	13-A	162	Total	C	N	O	S	Se	0	0	0
			1287	820	228	234	3	2			
1	14-A	162	Total	C	N	O	S	Se	0	0	0
			1287	820	228	234	3	2			
1	15-A	162	Total	C	N	O	S	Se	0	0	0
			1287	820	228	234	3	2			
1	16-A	162	Total	C	N	O	S	Se	0	0	0
			1287	820	228	234	3	2			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	MODIFIED RESIDUE	UNP Q9LZX1
A	40	MSE	MET	MODIFIED RESIDUE	UNP Q9LZX1
A	46	MSE	MET	MODIFIED RESIDUE	UNP Q9LZX1
A	47	MSE	MET	MODIFIED RESIDUE	UNP Q9LZX1
A	95	MSE	MET	MODIFIED RESIDUE	UNP Q9LZX1
A	98	MSE	MET	MODIFIED RESIDUE	UNP Q9LZX1
A	124	MSE	MET	MODIFIED RESIDUE	UNP Q9LZX1
A	171	MSE	MET	MODIFIED RESIDUE	UNP Q9LZX1

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	1-A	1	Total C O 4 2 2	0	0
2	2-A	1	Total C O 4 2 2	0	0
2	3-A	1	Total C O 4 2 2	0	0
2	4-A	1	Total C O 4 2 2	0	0
2	5-A	1	Total C O 4 2 2	0	0
2	6-A	1	Total C O 4 2 2	0	0
2	7-A	1	Total C O 4 2 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	8-A	1	Total C O 4 2 2	0	0
2	9-A	1	Total C O 4 2 2	0	0
2	10-A	1	Total C O 4 2 2	0	0
2	11-A	1	Total C O 4 2 2	0	0
2	12-A	1	Total C O 4 2 2	0	0
2	13-A	1	Total C O 4 2 2	0	0
2	14-A	1	Total C O 4 2 2	0	0
2	15-A	1	Total C O 4 2 2	0	0
2	16-A	1	Total C O 4 2 2	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	1-A	127	Total O 127 127	0	0
3	2-A	127	Total O 127 127	0	0
3	3-A	127	Total O 127 127	0	0
3	4-A	127	Total O 127 127	0	0
3	5-A	127	Total O 127 127	0	0
3	6-A	127	Total O 127 127	0	0
3	7-A	127	Total O 127 127	0	0
3	8-A	127	Total O 127 127	0	0
3	9-A	127	Total O 127 127	0	0
3	10-A	127	Total O 127 127	0	0

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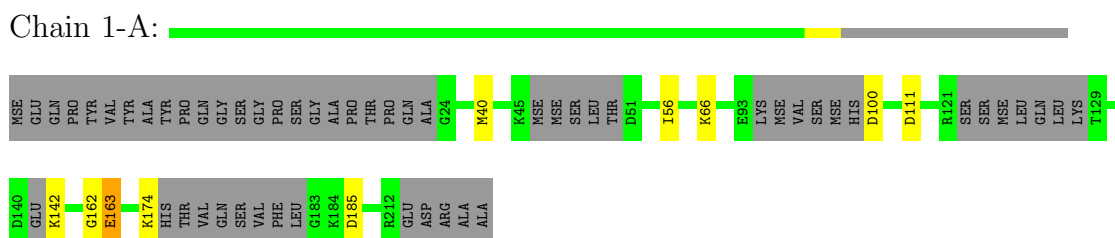
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	11-A	127	Total 127	O 127	0	0
3	12-A	127	Total 127	O 127	0	0
3	13-A	127	Total 127	O 127	0	0
3	14-A	127	Total 127	O 127	0	0
3	15-A	127	Total 127	O 127	0	0
3	16-A	127	Total 127	O 127	0	0

3 Residue-property plots

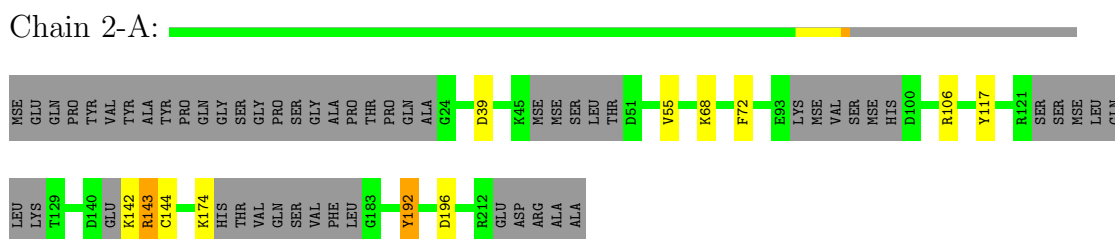
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS failed to run properly.

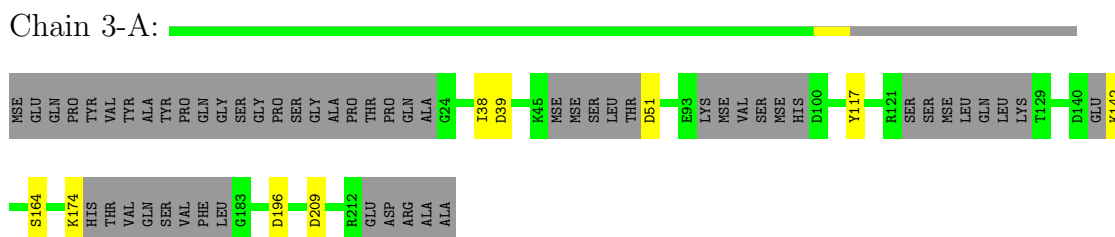
- Molecule 1: Protein At5g01750



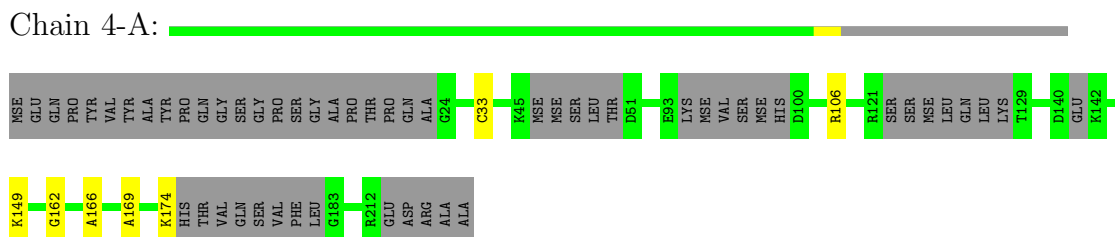
- Molecule 1: Protein At5g01750



- Molecule 1: Protein At5g01750

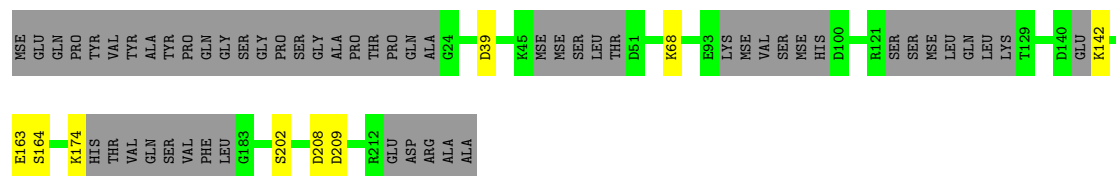


- Molecule 1: Protein At5g01750



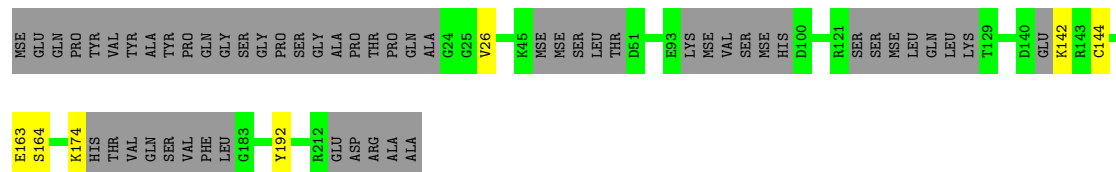
- Molecule 1: Protein At5g01750

Chain 5-A: 



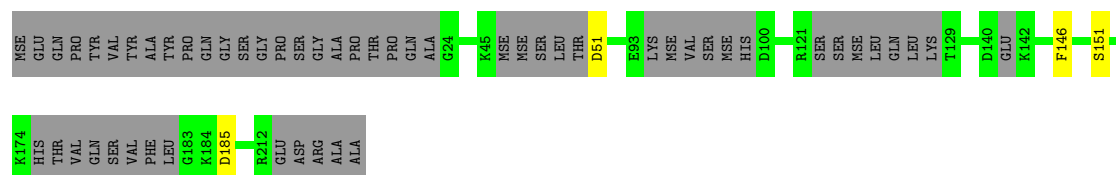
- Molecule 1: Protein At5g01750

Chain 6-A: 



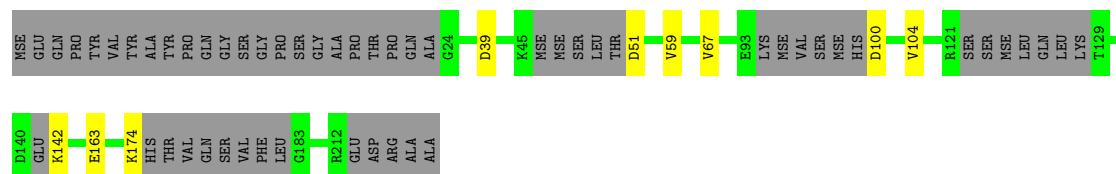
- Molecule 1: Protein At5g01750

Chain 7-A: 



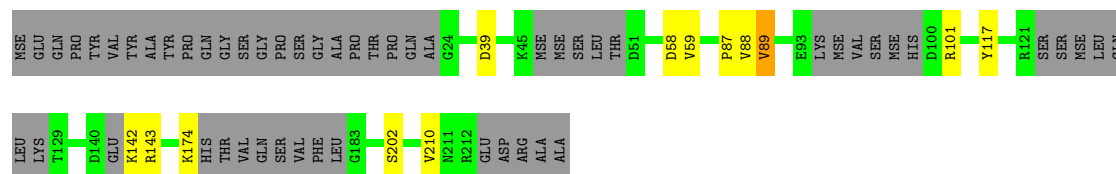
- Molecule 1: Protein At5g01750

Chain 8-A: 



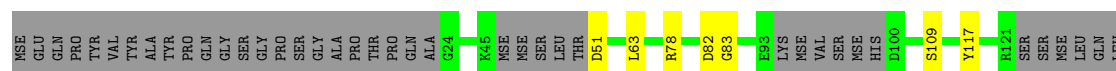
- Molecule 1: Protein At5g01750

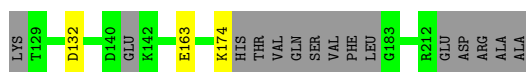
Chain 9-A: 



- Molecule 1: Protein At5g01750

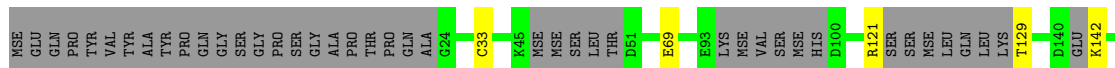
Chain 10-A: 





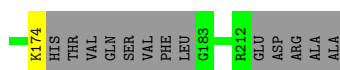
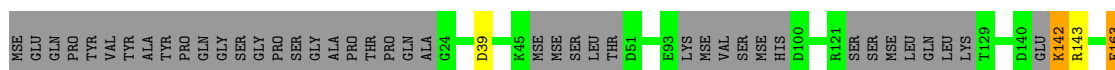
• Molecule 1: Protein At5g01750

Chain 11-A:



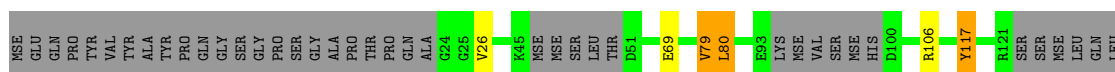
• Molecule 1: Protein At5g01750

Chain 12-A:



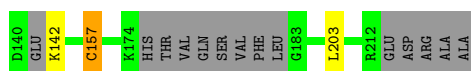
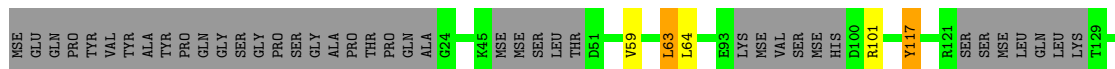
• Molecule 1: Protein At5g01750

Chain 13-A:



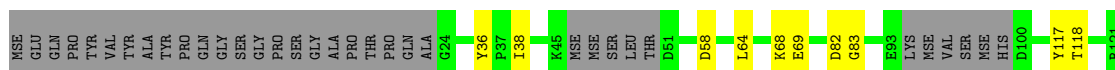
• Molecule 1: Protein At5g01750

Chain 14-A:



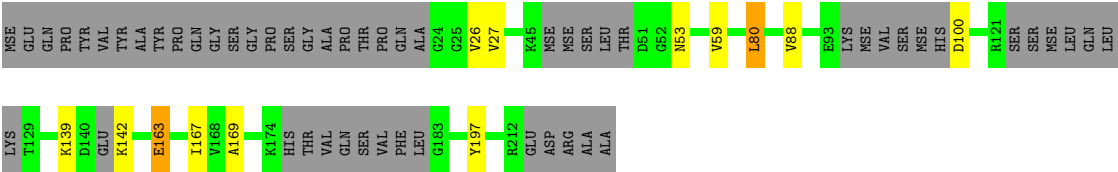
• Molecule 1: Protein At5g01750

Chain 15-A:



• Molecule 1: Protein At5g01750

Chain 16-A: 



4 Data and refinement statistics

EDS failed to run properly - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	41.07Å 57.50Å 75.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.68 – 1.70	Depositor
% Data completeness (in resolution range)	99.7 (37.68-1.70)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.66 (at 1.70Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.158 , 0.207	Depositor
Wilson B-factor (Å ²)	20.1	Xtriage
Anisotropy	0.067	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 20237 reflections	Xtriage
Total number of atoms	22688	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.64% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: EDO

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	0.90	0/1306	0.92	1/1756 (0.1%)
1	2-A	0.93	1/1306 (0.1%)	0.96	2/1756 (0.1%)
1	3-A	0.88	1/1306 (0.1%)	0.96	1/1756 (0.1%)
1	4-A	0.92	0/1306	0.97	0/1756
1	5-A	0.88	0/1306	0.91	0/1756
1	6-A	0.90	0/1306	0.92	0/1756
1	7-A	0.91	0/1306	0.92	0/1756
1	8-A	0.91	2/1306 (0.2%)	0.91	0/1756
1	9-A	0.94	1/1306 (0.1%)	0.97	0/1756
1	10-A	0.90	1/1306 (0.1%)	0.93	2/1756 (0.1%)
1	11-A	0.92	1/1306 (0.1%)	0.92	2/1756 (0.1%)
1	12-A	0.90	0/1306	0.94	0/1756
1	13-A	1.10	3/1306 (0.2%)	1.08	3/1756 (0.2%)
1	14-A	1.16	3/1306 (0.2%)	1.17	4/1756 (0.2%)
1	15-A	1.11	4/1306 (0.3%)	1.23	6/1756 (0.3%)
1	16-A	1.11	2/1306 (0.2%)	1.13	2/1756 (0.1%)
All	All	0.96	19/20896 (0.1%)	1.00	23/28096 (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	2-A	0	2
1	6-A	0	1
1	11-A	0	1
1	15-A	0	2
1	16-A	0	1
All	All	0	7

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	13-A	79	VAL	CA-CB	9.51	1.74	1.54
1	14-A	157	CYS	CB-SG	8.85	1.97	1.82
1	14-A	117	TYR	CD1-CE1	7.77	1.50	1.39
1	15-A	117	TYR	CE1-CZ	6.84	1.47	1.38
1	13-A	117	TYR	CD1-CE1	6.84	1.49	1.39
1	9-A	117	TYR	CD1-CE1	6.55	1.49	1.39
1	8-A	104	VAL	CB-CG2	6.27	1.66	1.52
1	15-A	133	VAL	CB-CG2	6.08	1.65	1.52
1	3-A	117	TYR	CD1-CE1	6.06	1.48	1.39
1	11-A	33	CYS	CB-SG	5.92	1.92	1.82
1	14-A	203	LEU	CG-CD1	5.57	1.72	1.51
1	8-A	67	VAL	CB-CG2	5.42	1.64	1.52
1	10-A	117	TYR	CD1-CE1	5.31	1.47	1.39
1	16-A	88	VAL	CB-CG2	5.26	1.63	1.52
1	15-A	117	TYR	CD2-CE2	-5.19	1.31	1.39
1	13-A	79	VAL	CA-C	5.06	1.66	1.52
1	15-A	117	TYR	CD1-CE1	5.05	1.47	1.39
1	16-A	167	ILE	CB-CG2	5.03	1.68	1.52
1	2-A	117	TYR	CD1-CE1	5.01	1.46	1.39

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	13-A	80	LEU	CA-CB-CG	-10.25	91.73	115.30
1	15-A	117	TYR	CB-CG-CD2	-9.24	115.45	121.00
1	1-A	40	MSE	CB-CG-SE	-8.26	87.93	112.70
1	15-A	117	TYR	OH-CZ-CE2	-7.01	101.18	120.10
1	16-A	80	LEU	CA-CB-CG	-6.82	99.61	115.30
1	14-A	157	CYS	CA-CB-SG	6.81	126.27	114.00
1	3-A	196	ASP	CB-CG-OD1	-6.74	112.24	118.30
1	14-A	117	TYR	CB-CG-CD2	-6.26	117.24	121.00
1	2-A	106	ARG	NE-CZ-NH1	6.06	123.33	120.30
1	2-A	143	ARG	N-CA-C	6.05	127.32	111.00
1	10-A	63	LEU	CA-CB-CG	-6.01	101.47	115.30
1	14-A	63	LEU	CA-CB-CG	-5.95	101.63	115.30
1	15-A	117	TYR	CG-CD1-CE1	-5.83	116.64	121.30
1	13-A	69	GLU	N-CA-C	-5.72	95.55	111.00
1	15-A	69	GLU	N-CA-C	-5.60	95.88	111.00
1	10-A	78	ARG	NE-CZ-NH2	-5.59	117.50	120.30
1	15-A	117	TYR	CE1-CZ-OH	5.51	134.99	120.10
1	16-A	142	LYS	CD-CE-NZ	5.29	123.86	111.70
1	15-A	171	MSE	CB-CG-SE	-5.25	96.95	112.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	13-A	117	TYR	CB-CG-CD2	-5.15	117.91	121.00
1	14-A	117	TYR	CG-CD1-CE1	-5.13	117.20	121.30
1	11-A	161	ALA	N-CA-C	-5.09	97.25	111.00
1	11-A	69	GLU	N-CA-C	-5.05	97.36	111.00

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	11-A	192	TYR	Sidechain
1	15-A	197	TYR	Sidechain
1	15-A	36	TYR	Sidechain
1	16-A	197	TYR	Sidechain
1	2-A	192	TYR	Sidechain
1	2-A	72	PHE	Sidechain
1	6-A	192	TYR	Sidechain

5.2 Close contacts ⓘ

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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1-A	1287	0	1289	0	1
1	2-A	1287	0	1289	0	0
1	3-A	1287	0	1289	0	0
1	4-A	1287	0	1289	0	0
1	5-A	1287	0	1289	0	0
1	6-A	1287	0	1289	0	0
1	7-A	1287	0	1289	0	0
1	8-A	1287	0	1289	0	0
1	9-A	1287	0	1289	0	0
1	10-A	1287	0	1289	0	0
1	11-A	1287	0	1289	0	0
1	12-A	1287	0	1289	0	1
1	13-A	1287	0	1289	0	0
1	14-A	1287	0	1289	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	15-A	1287	0	1289	0	0
1	16-A	1287	0	1289	0	1
2	1-A	4	0	6	0	0
2	2-A	4	0	6	0	0
2	3-A	4	0	6	0	0
2	4-A	4	0	6	0	0
2	5-A	4	0	6	0	0
2	6-A	4	0	6	0	0
2	7-A	4	0	6	0	0
2	8-A	4	0	6	0	0
2	9-A	4	0	6	0	0
2	10-A	4	0	6	0	0
2	11-A	4	0	6	0	0
2	12-A	4	0	6	0	0
2	13-A	4	0	6	0	0
2	14-A	4	0	6	0	0
2	15-A	4	0	6	0	0
2	16-A	4	0	6	0	0
3	1-A	127	0	0	0	1
3	2-A	127	0	0	0	0
3	3-A	127	0	0	0	0
3	4-A	127	0	0	0	0
3	5-A	127	0	0	0	0
3	6-A	127	0	0	0	0
3	7-A	127	0	0	0	0
3	8-A	127	0	0	0	0
3	9-A	127	0	0	0	0
3	10-A	127	0	0	0	0
3	11-A	127	0	0	0	0
3	12-A	127	0	0	0	1
3	13-A	127	0	0	0	0
3	14-A	127	0	0	0	0
3	15-A	127	0	0	0	0
3	16-A	127	0	0	0	1
All	All	22688	0	20720	0	3

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. Clashscore could not be calculated for this entry.

There are no clashes within the asymmetric unit.

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:100:ASP:OD2	3:A:768:HOH:O[4_445]	2.03	0.17
1:A:142:LYS:N	3:A:746:HOH:O[4_445]	2.10	0.10
1:A:100:ASP:OD2	3:A:768:HOH:O[4_445]	2.20	0.00

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	1-A	150/217 (69%)	139 (93%)	9 (6%)	2 (1%)	18	3
1	2-A	150/217 (69%)	140 (93%)	9 (6%)	1 (1%)	30	10
1	3-A	150/217 (69%)	136 (91%)	12 (8%)	2 (1%)	18	3
1	4-A	150/217 (69%)	132 (88%)	15 (10%)	3 (2%)	11	1
1	5-A	150/217 (69%)	139 (93%)	10 (7%)	1 (1%)	30	10
1	6-A	150/217 (69%)	142 (95%)	6 (4%)	2 (1%)	18	3
1	7-A	150/217 (69%)	140 (93%)	9 (6%)	1 (1%)	30	10
1	8-A	150/217 (69%)	141 (94%)	9 (6%)	0	100	100
1	9-A	150/217 (69%)	133 (89%)	14 (9%)	3 (2%)	11	1
1	10-A	150/217 (69%)	141 (94%)	7 (5%)	2 (1%)	18	3
1	11-A	150/217 (69%)	145 (97%)	5 (3%)	0	100	100
1	12-A	150/217 (69%)	137 (91%)	12 (8%)	1 (1%)	30	10
1	13-A	150/217 (69%)	137 (91%)	9 (6%)	4 (3%)	8	1
1	14-A	150/217 (69%)	139 (93%)	11 (7%)	0	100	100
1	15-A	150/217 (69%)	135 (90%)	11 (7%)	4 (3%)	8	1
1	16-A	150/217 (69%)	136 (91%)	11 (7%)	3 (2%)	11	1
All	All	2400/3472 (69%)	2212 (92%)	159 (7%)	29 (1%)	19	3

All (29) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1-A	163	GLU
1	4-A	169	ALA

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Mol	Chain	Res	Type
1	13-A	163	GLU
1	1-A	162	GLY
1	4-A	162	GLY
1	6-A	164	SER
1	7-A	185	ASP
1	10-A	109	SER
1	12-A	163	GLU
1	13-A	162	GLY
1	13-A	164	SER
1	15-A	185	ASP
1	15-A	211	ASN
1	16-A	163	GLU
1	3-A	164	SER
1	4-A	166	ALA
1	9-A	87	PRO
1	10-A	83	GLY
1	15-A	83	GLY
1	15-A	204	VAL
1	16-A	169	ALA
1	5-A	164	SER
1	6-A	144	CYS
1	9-A	88	VAL
1	2-A	192	TYR
1	3-A	38	ILE
1	9-A	89	VAL
1	16-A	27	VAL
1	13-A	79	VAL

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	1-A	142/181 (78%)	135 (95%)	7 (5%)	35	13
1	2-A	142/181 (78%)	134 (94%)	8 (6%)	30	10
1	3-A	142/181 (78%)	137 (96%)	5 (4%)	48	23
1	4-A	142/181 (78%)	138 (97%)	4 (3%)	56	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	5-A	142/181 (78%)	134 (94%)	8 (6%)	30	10
1	6-A	142/181 (78%)	138 (97%)	4 (3%)	56	32
1	7-A	142/181 (78%)	139 (98%)	3 (2%)	66	45
1	8-A	142/181 (78%)	135 (95%)	7 (5%)	35	13
1	9-A	142/181 (78%)	132 (93%)	10 (7%)	21	5
1	10-A	142/181 (78%)	137 (96%)	5 (4%)	48	23
1	11-A	142/181 (78%)	137 (96%)	5 (4%)	48	23
1	12-A	142/181 (78%)	137 (96%)	5 (4%)	48	23
1	13-A	142/181 (78%)	135 (95%)	7 (5%)	35	13
1	14-A	142/181 (78%)	135 (95%)	7 (5%)	35	13
1	15-A	142/181 (78%)	129 (91%)	13 (9%)	13	2
1	16-A	142/181 (78%)	136 (96%)	6 (4%)	40	16
All	All	2272/2896 (78%)	2168 (95%)	104 (5%)	37	14

All (104) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1-A	56	ILE
1	1-A	66	LYS
1	1-A	111	ASP
1	1-A	142	LYS
1	1-A	163	GLU
1	1-A	174	LYS
1	1-A	185	ASP
1	2-A	39	ASP
1	2-A	55	VAL
1	2-A	68	LYS
1	2-A	142	LYS
1	2-A	143	ARG
1	2-A	144	CYS
1	2-A	174	LYS
1	2-A	196	ASP
1	3-A	39	ASP
1	3-A	51	ASP
1	3-A	142	LYS
1	3-A	174	LYS
1	3-A	209	ASP
1	4-A	33	CYS

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Mol	Chain	Res	Type
1	4-A	106	ARG
1	4-A	149	LYS
1	4-A	174	LYS
1	5-A	39	ASP
1	5-A	68	LYS
1	5-A	142	LYS
1	5-A	163	GLU
1	5-A	174	LYS
1	5-A	202	SER
1	5-A	208	ASP
1	5-A	209	ASP
1	6-A	26	VAL
1	6-A	142	LYS
1	6-A	163	GLU
1	6-A	174	LYS
1	7-A	51	ASP
1	7-A	146	PHE
1	7-A	151	SER
1	8-A	39	ASP
1	8-A	51	ASP
1	8-A	59	VAL
1	8-A	100	ASP
1	8-A	142	LYS
1	8-A	163	GLU
1	8-A	174	LYS
1	9-A	39	ASP
1	9-A	58	ASP
1	9-A	59	VAL
1	9-A	89	VAL
1	9-A	101	ARG
1	9-A	142	LYS
1	9-A	143	ARG
1	9-A	174	LYS
1	9-A	202	SER
1	9-A	210	VAL
1	10-A	51	ASP
1	10-A	82	ASP
1	10-A	132	ASP
1	10-A	163	GLU
1	10-A	174	LYS
1	11-A	121	ARG
1	11-A	129	THR

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Mol	Chain	Res	Type
1	11-A	142	LYS
1	11-A	174	LYS
1	11-A	194	ASN
1	12-A	39	ASP
1	12-A	142	LYS
1	12-A	143	ARG
1	12-A	163	GLU
1	12-A	174	LYS
1	13-A	26	VAL
1	13-A	80	LEU
1	13-A	106	ARG
1	13-A	117	TYR
1	13-A	144	CYS
1	13-A	165	ASP
1	13-A	174	LYS
1	14-A	59	VAL
1	14-A	63	LEU
1	14-A	64	LEU
1	14-A	101	ARG
1	14-A	117	TYR
1	14-A	142	LYS
1	14-A	157	CYS
1	15-A	38	ILE
1	15-A	58	ASP
1	15-A	64	LEU
1	15-A	68	LYS
1	15-A	82	ASP
1	15-A	118	THR
1	15-A	132	ASP
1	15-A	140	ASP
1	15-A	142	LYS
1	15-A	163	GLU
1	15-A	172	HIS
1	15-A	174	LYS
1	15-A	185	ASP
1	16-A	26	VAL
1	16-A	53	ASN
1	16-A	59	VAL
1	16-A	80	LEU
1	16-A	139	LYS
1	16-A	163	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (44) such

sidechains are listed below:

Mol	Chain	Res	Type
1	1-A	60	ASN
1	1-A	137	HIS
1	1-A	170	GLN
1	1-A	172	HIS
1	2-A	60	ASN
1	2-A	194	ASN
1	3-A	60	ASN
1	3-A	103	GLN
1	3-A	112	GLN
1	3-A	172	HIS
1	3-A	194	ASN
1	4-A	60	ASN
1	4-A	103	GLN
1	4-A	137	HIS
1	4-A	170	GLN
1	4-A	172	HIS
1	4-A	194	ASN
1	5-A	60	ASN
1	5-A	170	GLN
1	5-A	172	HIS
1	6-A	60	ASN
1	6-A	172	HIS
1	7-A	60	ASN
1	7-A	137	HIS
1	7-A	172	HIS
1	7-A	194	ASN
1	8-A	137	HIS
1	9-A	172	HIS
1	10-A	170	GLN
1	10-A	172	HIS
1	10-A	194	ASN
1	11-A	60	ASN
1	11-A	137	HIS
1	11-A	172	HIS
1	11-A	194	ASN
1	12-A	60	ASN
1	12-A	172	HIS
1	12-A	194	ASN
1	13-A	172	HIS
1	13-A	194	ASN
1	14-A	172	HIS
1	15-A	170	GLN

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Mol	Chain	Res	Type
1	15-A	172	HIS
1	16-A	62	ASN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

16 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	EDO	1-A	700	-	3,3,3	0.63	0	2,2,2	0.29	0
2	EDO	10-A	700	-	3,3,3	0.62	0	2,2,2	0.28	0
2	EDO	11-A	700	-	3,3,3	0.64	0	2,2,2	0.28	0
2	EDO	12-A	700	-	3,3,3	0.62	0	2,2,2	0.27	0
2	EDO	13-A	700	-	3,3,3	0.66	0	2,2,2	0.26	0
2	EDO	14-A	700	-	3,3,3	0.69	0	2,2,2	0.26	0
2	EDO	15-A	700	-	3,3,3	0.71	0	2,2,2	0.25	0
2	EDO	16-A	700	-	3,3,3	0.72	0	2,2,2	0.24	0
2	EDO	2-A	700	-	3,3,3	0.62	0	2,2,2	0.28	0
2	EDO	3-A	700	-	3,3,3	0.66	0	2,2,2	0.26	0
2	EDO	4-A	700	-	3,3,3	0.65	0	2,2,2	0.27	0
2	EDO	5-A	700	-	3,3,3	0.66	0	2,2,2	0.27	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	EDO	6-A	700	-	3,3,3	0.67	0	2,2,2	0.26	0
2	EDO	7-A	700	-	3,3,3	0.68	0	2,2,2	0.24	0
2	EDO	8-A	700	-	3,3,3	0.66	0	2,2,2	0.26	0
2	EDO	9-A	700	-	3,3,3	0.68	0	2,2,2	0.25	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	EDO	1-A	700	-	-	0/1/1/1	0/0/0/0
2	EDO	10-A	700	-	-	0/1/1/1	0/0/0/0
2	EDO	11-A	700	-	-	0/1/1/1	0/0/0/0
2	EDO	12-A	700	-	-	0/1/1/1	0/0/0/0
2	EDO	13-A	700	-	-	0/1/1/1	0/0/0/0
2	EDO	14-A	700	-	-	0/1/1/1	0/0/0/0
2	EDO	15-A	700	-	-	0/1/1/1	0/0/0/0
2	EDO	16-A	700	-	-	0/1/1/1	0/0/0/0
2	EDO	2-A	700	-	-	0/1/1/1	0/0/0/0
2	EDO	3-A	700	-	-	0/1/1/1	0/0/0/0
2	EDO	4-A	700	-	-	0/1/1/1	0/0/0/0
2	EDO	5-A	700	-	-	0/1/1/1	0/0/0/0
2	EDO	6-A	700	-	-	0/1/1/1	0/0/0/0
2	EDO	7-A	700	-	-	0/1/1/1	0/0/0/0
2	EDO	8-A	700	-	-	0/1/1/1	0/0/0/0
2	EDO	9-A	700	-	-	0/1/1/1	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.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS failed to run properly - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS failed to run properly - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS failed to run properly - this section will therefore be empty.

6.4 Ligands ⓘ

EDS failed to run properly - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS failed to run properly - this section will therefore be empty.