



Full wwPDB X-ray Structure Validation Report

Mar 1, 2014 – 12:43 AM GMT

PDB ID : 3N1X
Title : X-ray Crystal Structure of Toluene/o-Xylene Monooxygenase Hydroxylase
T201C Mutant
Authors : Sazinsky, M.H.; McCormick, M.S.; Lippard, S.J.
Deposited on : 2010-05-17
Resolution : 2.40 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>

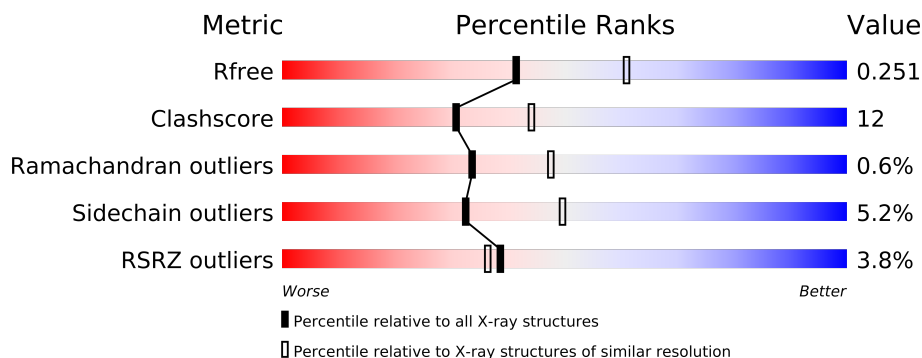
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
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 2.40 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}	66092	2207 (2.40-2.40)
Clashscore	79885	2789 (2.40-2.40)
Ramachandran outliers	78287	2736 (2.40-2.40)
Sidechain outliers	78261	2737 (2.40-2.40)
RSRZ outliers	66119	2210 (2.40-2.40)

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.

Mol	Chain	Length	Quality of chain
1	A	498	
2	B	330	
3	C	86	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
6	EDO	A	502	-	X

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 7520 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 Toluene o-xylene monooxygenase component.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	491	Total	C	N	O	S	0	1	0
			4021	2567	673	754	27			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	201	CYS	THR	ENGINEERED MUTATION	UNP Q6IV66

- Molecule 2 is a protein called Toluene o-xylene monooxygenase component.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	324	Total	C	N	O	S	0	0	0
			2658	1685	469	494	10			

- Molecule 3 is a protein called Toluene o-xylene monooxygenase component.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	85	Total	C	N	O	S	0	0	0
			689	432	123	129	5			

- Molecule 4 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Fe	0	0
			2	2		

- Molecule 5 is HYDROXIDE ION (three-letter code: OH) (formula: HO).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O		0	0
			1	1			

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 8 is water.

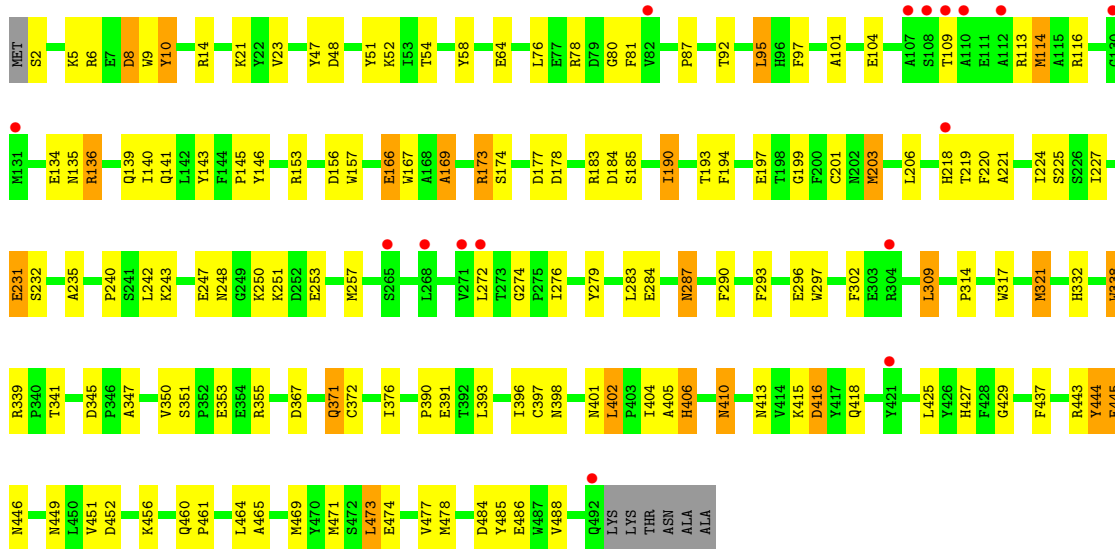
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	73	Total	O	0	0
			73	73		
8	B	62	Total	O	0	0
			62	62		
8	C	5	Total	O	0	0
			5	5		

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.

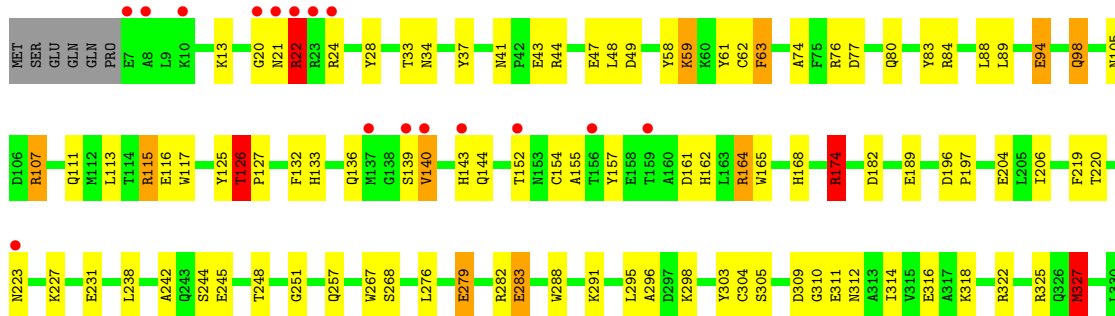
- Molecule 1: Toluene o-xylene monooxygenase component

Chain A: 



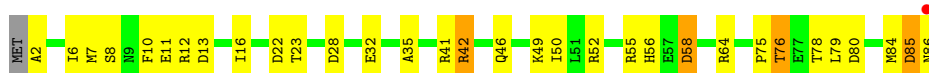
- Molecule 2: Toluene o-xylene monooxygenase component

Chain B: 



- Molecule 3: Toluene o-xylene monooxygenase component

Chain C: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	183.29Å 183.29Å 68.13Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	38.02 – 2.40 38.02 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.2 (38.02-2.40) 99.2 (38.02-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.90 (at 2.39Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.184 , 0.242 0.194 , 0.251	Depositor DCC
R_{free} test set	2592 reflections (5.34%)	DCC
Wilson B-factor (Å ²)	50.8	Xtriage
Anisotropy	0.134	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 41.3	EDS
Estimated twinning fraction	0.021 for -h,-k,l	Xtriage
L-test for twinning	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	1 of 51115 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7520	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.17% 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: OH, FE, SO4, 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	A	1.46	28/4148 (0.7%)	1.26	33/5637 (0.6%)
2	B	1.54	32/2730 (1.2%)	1.20	14/3711 (0.4%)
3	C	1.29	1/703 (0.1%)	1.28	6/952 (0.6%)
All	All	1.48	61/7581 (0.8%)	1.24	53/10300 (0.5%)

All (61) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	437	PHE	CE2-CZ	8.88	1.54	1.37
2	B	283	GLU	CB-CG	8.02	1.67	1.52
2	B	182	ASP	CB-CG	7.98	1.68	1.51
2	B	311	GLU	CG-CD	7.68	1.63	1.51
1	A	101	ALA	CA-CB	7.18	1.67	1.52
2	B	116	GLU	CG-CD	7.15	1.62	1.51
2	B	155	ALA	CA-CB	7.07	1.67	1.52
2	B	74	ALA	CA-CB	6.68	1.66	1.52
1	A	231	GLU	CB-CG	6.54	1.64	1.52
2	B	165	TRP	CZ3-CH2	6.54	1.50	1.40
2	B	311	GLU	CD-OE2	6.40	1.32	1.25
1	A	253	GLU	CG-CD	6.39	1.61	1.51
3	C	32	GLU	CG-CD	6.38	1.61	1.51
1	A	201	CYS	CB-SG	-6.36	1.71	1.82
2	B	140	VAL	CB-CG1	6.30	1.66	1.52
1	A	64	GLU	CG-CD	6.26	1.61	1.51
1	A	402	LEU	CG-CD2	6.19	1.74	1.51
2	B	157	TYR	CE2-CZ	6.12	1.46	1.38
2	B	44	ARG	CB-CG	6.12	1.69	1.52
1	A	64	GLU	CB-CG	6.09	1.63	1.52
2	B	283	GLU	CG-CD	6.03	1.60	1.51
2	B	37	TYR	CD1-CE1	5.98	1.48	1.39
2	B	251	GLY	N-CA	5.89	1.54	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	28	TYR	CG-CD1	5.70	1.46	1.39
1	A	353	GLU	CG-CD	5.67	1.60	1.51
2	B	98	GLN	CG-CD	5.66	1.64	1.51
1	A	444	TYR	CE2-CZ	5.61	1.45	1.38
2	B	63	PHE	CE1-CZ	5.60	1.48	1.37
1	A	157	TRP	CB-CG	5.51	1.60	1.50
2	B	61	TYR	CE1-CZ	5.50	1.45	1.38
1	A	143	TYR	CD2-CE2	5.49	1.47	1.39
1	A	465	ALA	CA-CB	5.49	1.64	1.52
1	A	284	GLU	CG-CD	5.49	1.60	1.51
2	B	47	GLU	CG-CD	5.44	1.60	1.51
1	A	51	TYR	CD2-CE2	5.44	1.47	1.39
1	A	58	TYR	CD1-CE1	-5.42	1.31	1.39
2	B	94	GLU	CG-CD	5.39	1.60	1.51
2	B	174	ARG	CB-CG	-5.39	1.38	1.52
2	B	43	GLU	CG-CD	5.38	1.60	1.51
2	B	62	CYS	CB-SG	5.37	1.91	1.82
1	A	437	PHE	CG-CD1	5.36	1.46	1.38
1	A	146	TYR	CD2-CE2	5.35	1.47	1.39
1	A	437	PHE	CD1-CE1	5.33	1.50	1.39
2	B	303	TYR	CD2-CE2	5.31	1.47	1.39
2	B	296	ALA	CA-CB	5.30	1.63	1.52
1	A	231	GLU	CG-CD	5.29	1.59	1.51
2	B	132	PHE	CE2-CZ	5.29	1.47	1.37
1	A	169	ALA	CA-CB	5.28	1.63	1.52
1	A	23	VAL	CB-CG1	5.26	1.63	1.52
1	A	167	TRP	CB-CG	5.25	1.59	1.50
2	B	28	TYR	CE1-CZ	5.25	1.45	1.38
1	A	350	VAL	CB-CG2	5.12	1.63	1.52
2	B	231	GLU	CB-CG	5.12	1.61	1.52
2	B	279	GLU	CG-CD	5.12	1.59	1.51
1	A	166	GLU	CG-CD	5.11	1.59	1.51
1	A	279	TYR	CD1-CE1	5.11	1.47	1.39
1	A	10	TYR	CE2-CZ	5.05	1.45	1.38
2	B	116	GLU	CD-OE1	5.05	1.31	1.25
1	A	338	TRP	CE3-CZ3	5.05	1.47	1.38
2	B	58	TYR	CG-CD1	5.03	1.45	1.39
2	B	291	LYS	CD-CE	5.00	1.63	1.51

All (53) bond angle outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	153	ARG	NE-CZ-NH2	-12.76	113.92	120.30
1	A	173	ARG	NE-CZ-NH2	-11.70	114.45	120.30
1	A	443	ARG	NE-CZ-NH1	11.50	126.05	120.30
3	C	42	ARG	NE-CZ-NH2	-11.07	114.76	120.30
1	A	136	ARG	NE-CZ-NH1	10.27	125.43	120.30
1	A	443	ARG	NE-CZ-NH2	-9.88	115.36	120.30
1	A	136	ARG	NE-CZ-NH2	-9.85	115.37	120.30
1	A	173	ARG	NE-CZ-NH1	9.52	125.06	120.30
2	B	115	ARG	NE-CZ-NH1	8.42	124.51	120.30
2	B	164	ARG	NE-CZ-NH1	-8.02	116.29	120.30
1	A	156	ASP	CB-CG-OD2	7.82	125.34	118.30
1	A	339	ARG	NE-CZ-NH1	-7.67	116.47	120.30
2	B	44	ARG	NE-CZ-NH1	7.48	124.04	120.30
1	A	416	ASP	CB-CG-OD1	7.39	124.95	118.30
1	A	257	MET	CG-SD-CE	-7.17	88.72	100.20
3	C	58	ASP	CB-CG-OD2	-7.10	111.91	118.30
1	A	116	ARG	NE-CZ-NH1	-7.10	116.75	120.30
2	B	325	ARG	NE-CZ-NH2	-7.08	116.76	120.30
3	C	58	ASP	CB-CG-OD1	6.98	124.58	118.30
1	A	339	ARG	NE-CZ-NH2	6.88	123.74	120.30
2	B	174	ARG	NE-CZ-NH2	6.63	123.61	120.30
3	C	42	ARG	CG-CD-NE	-6.49	98.17	111.80
1	A	48	ASP	CB-CG-OD1	6.49	124.14	118.30
3	C	41	ARG	NE-CZ-NH1	6.45	123.53	120.30
1	A	177	ASP	CB-CG-OD1	6.44	124.09	118.30
2	B	115	ARG	NE-CZ-NH2	-6.33	117.14	120.30
1	A	201	CYS	CA-CB-SG	-6.31	102.64	114.00
1	A	153	ARG	NE-CZ-NH1	6.28	123.44	120.30
1	A	14	ARG	NE-CZ-NH1	6.25	123.42	120.30
1	A	248	ASN	C-N-CA	-6.19	109.30	122.30
1	A	141	GLN	CA-CB-CG	-6.16	99.85	113.40
1	A	287	ASN	CB-CA-C	6.13	122.65	110.40
1	A	478	MET	CG-SD-CE	-6.09	90.45	100.20
1	A	345	ASP	CB-CG-OD1	6.07	123.77	118.30
1	A	184	ASP	CB-CG-OD2	-5.95	112.94	118.30
1	A	114	MET	CG-SD-CE	-5.92	90.73	100.20
2	B	182	ASP	CB-CG-OD2	5.88	123.59	118.30
1	A	473	LEU	CB-CG-CD2	-5.88	101.00	111.00
2	B	84	ARG	NE-CZ-NH1	5.80	123.20	120.30
1	A	48	ASP	CB-CG-OD2	-5.67	113.19	118.30
2	B	44	ARG	NE-CZ-NH2	-5.62	117.49	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	76	ARG	NE-CZ-NH2	5.47	123.03	120.30
1	A	8	ASP	CB-CG-OD2	-5.38	113.46	118.30
2	B	59	LYS	CD-CE-NZ	5.34	123.98	111.70
1	A	183	ARG	NE-CZ-NH2	-5.29	117.66	120.30
1	A	321	MET	CG-SD-CE	-5.28	91.76	100.20
2	B	174	ARG	NE-CZ-NH1	-5.24	117.68	120.30
1	A	190	ILE	CB-CA-C	-5.19	101.21	111.60
1	A	184	ASP	CB-CG-OD1	5.15	122.94	118.30
3	C	41	ARG	NE-CZ-NH2	-5.12	117.74	120.30
1	A	153	ARG	CG-CD-NE	-5.12	101.05	111.80
2	B	283	GLU	CA-CB-CG	5.10	124.63	113.40
2	B	327	MET	CG-SD-CE	5.07	108.30	100.20

There are no chirality outliers.

There are no planarity outliers.

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	A	4021	0	3770	92	0
2	B	2658	0	2554	67	0
3	C	689	0	678	29	0
4	A	2	0	0	0	0
5	A	1	0	0	1	0
6	A	4	0	6	0	0
7	B	5	0	0	0	0
8	A	73	0	0	0	0
8	B	62	0	0	0	0
8	C	5	0	0	0	0
All	All	7520	0	7008	169	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 12.

All (169) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:402:LEU:CD2	1:A:402:LEU:CG	1.74	1.59
2:B:219:PHE:O	2:B:223:ASN:HB2	1.53	1.06
1:A:445:GLU:HG2	1:A:446:ASN:H	1.16	1.06
1:A:445:GLU:HG2	1:A:446:ASN:N	1.70	1.05
1:A:427:HIS:HE1	3:C:76:THR:HG23	1.22	1.04
1:A:445:GLU:CG	1:A:446:ASN:N	2.27	0.96
2:B:305:SER:HB3	2:B:314:ILE:HD11	1.52	0.90
2:B:126:THR:HB	2:B:189:GLU:CG	2.01	0.90
2:B:168:HIS:HD2	2:B:257:GLN:HE21	1.20	0.89
2:B:126:THR:OG1	2:B:127:PRO:HD3	1.72	0.88
1:A:139:GLN:HE22	2:B:83:TYR:H	1.19	0.88
1:A:372:CYS:O	1:A:376:ILE:HD13	1.75	0.85
1:A:474:GLU:O	1:A:477:VAL:HG22	1.76	0.84
1:A:427:HIS:CE1	3:C:76:THR:HG23	2.12	0.83
2:B:126:THR:HB	2:B:189:GLU:HG3	1.62	0.80
2:B:327:MET:HA	2:B:327:MET:CE	2.11	0.80
1:A:416:ASP:OD2	1:A:427:HIS:HD2	1.67	0.77
1:A:8:ASP:O	2:B:174:ARG:HD2	1.85	0.77
1:A:76:LEU:CD1	1:A:218:HIS:HB2	2.14	0.76
2:B:168:HIS:CD2	2:B:257:GLN:HE21	2.05	0.75
1:A:445:GLU:HG2	2:B:49:ASP:OD1	1.85	0.75
3:C:2:ALA:HA	3:C:23:THR:OG1	1.86	0.73
1:A:2:SER:N	2:B:105:ASN:HD22	1.85	0.73
1:A:9:TRP:HB3	2:B:174:ARG:HG3	1.71	0.72
2:B:219:PHE:O	2:B:223:ASN:CB	2.37	0.70
2:B:162:HIS:HE1	2:B:227:LYS:NZ	1.91	0.69
2:B:126:THR:HG21	2:B:189:GLU:OE1	1.93	0.68
3:C:52:ARG:HH11	3:C:52:ARG:HG3	1.59	0.67
3:C:55:ARG:HD2	3:C:58:ASP:OD1	1.94	0.67
1:A:9:TRP:CB	2:B:174:ARG:HG3	2.24	0.67
2:B:162:HIS:HE1	2:B:227:LYS:HZ3	1.42	0.67
1:A:203:MET:HG3	1:A:297:TRP:HB3	1.78	0.66
3:C:56:HIS:HD2	3:C:80:ASP:OD1	1.79	0.65
1:A:367:ASP:HB3	1:A:410:ASN:ND2	2.12	0.65
3:C:75:PRO:O	3:C:76:THR:CB	2.45	0.65
3:C:75:PRO:O	3:C:76:THR:HB	1.97	0.64
1:A:402:LEU:CD1	1:A:402:LEU:CD2	2.70	0.64
1:A:398:ASN:HD22	1:A:427:HIS:H	1.45	0.64
2:B:21:ASN:O	2:B:22:ARG:HB2	1.98	0.63
2:B:59:LYS:HA	2:B:63:PHE:HD2	1.64	0.62
1:A:314:PRO:HD2	1:A:317:TRP:CE3	2.34	0.62
1:A:474:GLU:H	1:A:477:VAL:CG2	2.13	0.62
2:B:327:MET:HE2	2:B:327:MET:HA	1.81	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:92:THR:HG23	1:A:276:ILE:HD13	1.80	0.62
1:A:402:LEU:CD2	1:A:402:LEU:CB	2.75	0.61
2:B:204:GLU:OE1	2:B:298:LYS:NZ	2.33	0.61
2:B:126:THR:HB	2:B:189:GLU:HG2	1.79	0.61
2:B:21:ASN:O	2:B:22:ARG:CB	2.50	0.59
2:B:126:THR:CB	2:B:127:PRO:HD3	2.33	0.59
2:B:143:HIS:CG	2:B:152:THR:HG23	2.37	0.59
3:C:75:PRO:O	3:C:76:THR:HG22	2.02	0.58
1:A:405:ALA:O	1:A:406:HIS:HB2	2.01	0.58
1:A:317:TRP:O	1:A:321:MET:HG2	2.05	0.57
1:A:243:LYS:O	1:A:247:GLU:HG3	2.05	0.57
2:B:219:PHE:HE1	2:B:223:ASN:HD22	1.50	0.56
1:A:425:LEU:HD23	3:C:76:THR:HG22	1.87	0.56
3:C:11:GLU:HG2	3:C:12:ARG:HG3	1.88	0.56
1:A:139:GLN:NE2	2:B:83:TYR:H	1.97	0.56
2:B:33:THR:HB	2:B:34:ASN:HD22	1.71	0.56
1:A:97:PHE:CD2	1:A:145:PRO:HB3	2.40	0.55
1:A:95:LEU:C	1:A:95:LEU:HD12	2.27	0.55
1:A:231:GLU:OE1	5:A:501:OH:O	2.25	0.55
2:B:94:GLU:O	2:B:98:GLN:HG2	2.07	0.55
1:A:427:HIS:HE1	3:C:76:THR:CG2	2.08	0.55
1:A:95:LEU:HD11	1:A:272:LEU:HD22	1.87	0.55
1:A:413:ASN:OD1	1:A:415:LYS:HE2	2.08	0.54
2:B:126:THR:CG2	2:B:189:GLU:OE1	2.55	0.54
2:B:219:PHE:CE1	2:B:223:ASN:ND2	2.76	0.54
2:B:327:MET:HA	2:B:327:MET:HE3	1.88	0.54
1:A:218:HIS:O	1:A:219:THR:C	2.46	0.53
1:A:190:ILE:HD12	1:A:242:LEU:CD2	2.38	0.53
3:C:52:ARG:NH1	3:C:52:ARG:HG3	2.23	0.52
1:A:485:TYR:O	1:A:488:VAL:HB	2.09	0.52
1:A:416:ASP:H	3:C:56:HIS:CE1	2.28	0.52
2:B:161:ASP:O	2:B:164:ARG:HB3	2.11	0.51
2:B:305:SER:CB	2:B:314:ILE:HD11	2.32	0.51
1:A:113:ARG:HH11	2:B:144:GLN:HE21	1.58	0.51
1:A:220:PHE:CE2	1:A:224:ILE:HG13	2.46	0.51
3:C:85:ASP:O	3:C:86:ASN:CB	2.59	0.50
1:A:193:THR:HA	1:A:197:GLU:OE1	2.11	0.50
1:A:449:ASN:O	1:A:452:ASP:HB2	2.11	0.50
2:B:127:PRO:HA	2:B:189:GLU:HB3	1.93	0.50
2:B:107:ARG:HG3	2:B:107:ARG:O	2.12	0.50
3:C:2:ALA:O	3:C:23:THR:N	2.42	0.50
3:C:2:ALA:O	3:C:22:ASP:HA	2.12	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:445:GLU:CG	2:B:49:ASP:OD1	2.60	0.49
3:C:75:PRO:O	3:C:76:THR:CG2	2.60	0.49
2:B:125:TYR:O	2:B:126:THR:C	2.50	0.49
2:B:77:ASP:HB2	2:B:154:CYS:SG	2.53	0.49
1:A:460:GLN:HA	1:A:461:PRO:C	2.33	0.49
3:C:50:ILE:N	3:C:84:MET:O	2.26	0.48
3:C:28:ASP:OD1	3:C:64:ARG:HB3	2.13	0.48
3:C:13:ASP:OD1	3:C:42:ARG:HD2	2.13	0.48
1:A:218:HIS:O	1:A:221:ALA:N	2.47	0.48
1:A:391:GLU:HA	1:A:464:LEU:HD11	1.94	0.48
2:B:223:ASN:ND2	2:B:268:SER:OG	2.47	0.48
1:A:444:TYR:O	1:A:445:GLU:C	2.53	0.47
1:A:135:ASN:O	1:A:139:GLN:HG3	2.13	0.47
1:A:351:SER:O	1:A:355:ARG:HG3	2.14	0.47
1:A:341:THR:HA	1:A:473:LEU:HD13	1.95	0.47
2:B:304:CYS:HB2	2:B:314:ILE:HG12	1.97	0.47
1:A:76:LEU:CD1	1:A:218:HIS:CB	2.90	0.47
3:C:6:ILE:HD13	3:C:79:LEU:HD12	1.96	0.47
1:A:396:ILE:CG2	1:A:401:ASN:HA	2.45	0.46
1:A:166:GLU:HA	1:A:471:MET:HB3	1.98	0.46
1:A:332:HIS:HE1	1:A:347:ALA:O	1.99	0.46
1:A:169:ALA:O	1:A:173:ARG:HG3	2.15	0.46
2:B:312:ASN:O	2:B:316:GLU:HG3	2.16	0.46
2:B:133:HIS:O	2:B:136:GLN:HB3	2.15	0.46
1:A:76:LEU:HD11	1:A:218:HIS:HB2	1.95	0.46
1:A:76:LEU:HD11	1:A:218:HIS:CB	2.46	0.45
2:B:117:TRP:CZ2	2:B:242:ALA:HA	2.52	0.45
2:B:305:SER:HB3	2:B:314:ILE:CD1	2.35	0.45
2:B:117:TRP:CE3	2:B:245:GLU:HG3	2.52	0.45
2:B:126:THR:HG1	2:B:127:PRO:HD3	1.79	0.45
1:A:6:ARG:HD2	1:A:54:THR:HG23	1.99	0.44
1:A:445:GLU:HG3	1:A:446:ASN:N	2.24	0.44
3:C:7:MET:HG2	3:C:76:THR:O	2.16	0.44
1:A:104:GLU:O	1:A:134:GLU:HB3	2.18	0.44
3:C:10:PHE:CE1	3:C:35:ALA:HA	2.52	0.44
2:B:154:CYS:HB3	2:B:267:TRP:CE2	2.52	0.44
1:A:47:TYR:CE1	1:A:240:PRO:HB2	2.52	0.44
1:A:371:GLN:H	1:A:371:GLN:HG2	1.64	0.44
1:A:10:TYR:CZ	1:A:52:LYS:HB3	2.53	0.44
1:A:80:GLY:O	1:A:81:PHE:C	2.56	0.44
1:A:190:ILE:O	1:A:194:PHE:HB3	2.17	0.43
2:B:318:LYS:O	2:B:322:ARG:HG3	2.18	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:126:THR:CB	2:B:127:PRO:CD	2.97	0.43
2:B:276:LEU:HD22	2:B:282:ARG:HB2	2.01	0.43
1:A:367:ASP:HB3	1:A:410:ASN:HD21	1.82	0.43
1:A:178:ASP:HA	2:B:48:LEU:HD11	2.01	0.43
2:B:295:LEU:HA	2:B:295:LEU:HD23	1.80	0.43
1:A:416:ASP:H	3:C:56:HIS:HE1	1.67	0.42
1:A:404:ILE:HG12	1:A:429:GLY:HA2	2.01	0.42
1:A:474:GLU:H	1:A:477:VAL:HG22	1.83	0.42
1:A:398:ASN:ND2	1:A:427:HIS:H	2.15	0.42
2:B:304:CYS:O	2:B:310:GLY:HA2	2.19	0.42
1:A:293:PHE:C	1:A:293:PHE:CD2	2.93	0.42
1:A:109:THR:HG23	2:B:144:GLN:HB2	2.01	0.42
1:A:232:SER:HA	1:A:235:ALA:HB3	2.02	0.42
2:B:196:ASP:O	2:B:197:PRO:C	2.58	0.42
1:A:199:GLY:HA3	1:A:302:PHE:CZ	2.55	0.42
1:A:78:ARG:HA	1:A:78:ARG:HD3	1.94	0.42
1:A:396:ILE:HG12	1:A:451:VAL:HG23	2.02	0.42
1:A:418:GLN:HE22	3:C:78:THR:H	1.68	0.42
1:A:309:LEU:HD13	1:A:309:LEU:HA	1.85	0.42
2:B:312:ASN:ND2	2:B:316:GLU:OE1	2.52	0.41
1:A:393:LEU:HD23	1:A:393:LEU:N	2.34	0.41
3:C:13:ASP:OD2	3:C:42:ARG:NH1	2.52	0.41
2:B:117:TRP:CH2	2:B:242:ALA:HA	2.55	0.41
1:A:338:TRP:CD1	1:A:390:PRO:HG3	2.55	0.41
2:B:111:GLN:OE1	2:B:111:GLN:N	2.46	0.41
1:A:274:GLY:HA2	1:A:290:PHE:CG	2.56	0.41
3:C:46:GLN:O	3:C:49:LYS:HB2	2.21	0.41
1:A:224:ILE:HD13	1:A:224:ILE:HA	1.86	0.41
1:A:114:MET:HA	1:A:185:SER:OG	2.20	0.41
1:A:140:ILE:CG2	1:A:227:ILE:HD11	2.51	0.41
2:B:220:THR:HG21	2:B:288:TRP:HB3	2.02	0.41
3:C:8:SER:O	3:C:16:ILE:HA	2.21	0.41
2:B:125:TYR:HB2	2:B:238:LEU:HD21	2.03	0.41
2:B:88:LEU:HD23	2:B:88:LEU:HA	1.98	0.41
2:B:298:LYS:HB3	2:B:298:LYS:HE2	1.90	0.40
1:A:396:ILE:HG22	1:A:401:ASN:HA	2.03	0.40
1:A:474:GLU:H	1:A:477:VAL:HG21	1.86	0.40
1:A:484:ASP:O	1:A:485:TYR:HB2	2.22	0.40
1:A:486:GLU:C	1:A:488:VAL:H	2.24	0.40
1:A:136:ARG:HB2	2:B:83:TYR:CD1	2.56	0.40
2:B:139:SER:OG	2:B:162:HIS:HD2	2.05	0.40
1:A:76:LEU:HD13	1:A:218:HIS:HB2	2.01	0.40

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	490/498 (98%)	451 (92%)	37 (8%)	2 (0%)	43	61
2	B	322/330 (98%)	310 (96%)	9 (3%)	3 (1%)	25	35
3	C	83/86 (96%)	74 (89%)	9 (11%)	0	100	100
All	All	895/914 (98%)	835 (93%)	55 (6%)	5 (1%)	33	47

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	445	GLU
1	A	406	HIS
2	B	22	ARG
2	B	126	THR
2	B	20	GLY

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	417/422 (99%)	398 (95%)	19 (5%)	37	55
2	B	276/282 (98%)	257 (93%)	19 (7%)	22	33
3	C	78/79 (99%)	76 (97%)	2 (3%)	59	79
All	All	771/783 (98%)	731 (95%)	40 (5%)	32	49

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	LYS
1	A	21	LYS
1	A	87	PRO
1	A	95	LEU
1	A	174	SER
1	A	203	MET
1	A	206	LEU
1	A	225	SER
1	A	250	LYS
1	A	251	LYS
1	A	283	LEU
1	A	287	ASN
1	A	296	GLU
1	A	309	LEU
1	A	371	GLN
1	A	397	CYS
1	A	410	ASN
1	A	456	LYS
1	A	469	MET
2	B	13	LYS
2	B	22	ARG
2	B	24	ARG
2	B	41	ASN
2	B	80	GLN
2	B	89	LEU
2	B	107	ARG
2	B	113	LEU
2	B	115	ARG
2	B	126	THR
2	B	140	VAL
2	B	174	ARG
2	B	206	ILE
2	B	244	SER
2	B	248	THR
2	B	279	GLU
2	B	283	GLU
2	B	309	ASP
2	B	327	MET
3	C	76	THR
3	C	85	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	139	GLN
1	A	237	GLN
1	A	248	ASN
1	A	322	GLN
1	A	379	ASN
1	A	398	ASN
1	A	418	GLN
1	A	427	HIS
2	B	34	ASN
2	B	98	GLN
2	B	144	GLN
2	B	153	ASN
2	B	162	HIS
2	B	168	HIS
2	B	223	ASN
3	C	56	HIS

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 ⓘ

Of 5 ligands modelled in this entry, 1 is modelled with single atom and 2 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
6	EDO	A	502	4	3,3,3	1.03	0	2,2,2	0.54	0
7	SO4	B	331	-	4,4,4	0.21	0	6,6,6	0.87	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
6	EDO	A	502	4	-	0/1/1/1	0/0/0/0
7	SO4	B	331	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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 ⓘ

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	491/498 (98%)	0.02	16 (3%) 44 42	42, 54, 69, 85	0
2	B	324/330 (98%)	-0.08	16 (4%) 28 26	40, 51, 71, 95	1 (0%)
3	C	85/86 (98%)	-0.29	1 (1%) 75 75	52, 61, 72, 84	0
All	All	900/914 (98%)	-0.04	33 (3%) 38 38	40, 54, 71, 95	1 (0%)

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	218	HIS	5.9
2	B	22	ARG	3.6
3	C	86	ASN	3.4
2	B	223	ASN	3.4
2	B	7	GLU	3.3
2	B	140	VAL	3.2
2	B	23	ARG	3.2
2	B	21	ASN	3.2
1	A	112	ALA	3.1
1	A	272	LEU	3.0
2	B	159	THR	3.0
1	A	421	TYR	2.8
2	B	8	ALA	2.7
1	A	304	ARG	2.7
1	A	107	ALA	2.7
1	A	130	GLY	2.6
1	A	268	LEU	2.6
1	A	108	SER	2.6
2	B	10	LYS	2.6
1	A	109	THR	2.6
1	A	110	ALA	2.5
2	B	24	ARG	2.5
2	B	156	THR	2.5

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Mol	Chain	Res	Type	RSRZ
2	B	139	SER	2.5
2	B	20	GLY	2.4
1	A	492	GLN	2.4
1	A	131	MET	2.3
2	B	137	MET	2.3
2	B	152	THR	2.2
1	A	271	VAL	2.1
1	A	82	VAL	2.1
1	A	265	SER	2.1
2	B	143	HIS	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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, 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
6	EDO	A	502	4/4	0.60	8.34	57,60,64,66	0
7	SO4	B	331	5/5	0.17	1.51	93,96,97,98	0
5	OH	A	501	1/1	0.26	0.31	43,43,43,43	0
4	FE	A	500	1/1	0.20	-1.29	52,52,52,52	0
4	FE	A	499	1/1	0.18	-1.33	48,48,48,48	0

6.5 Other polymers ⓘ

There are no such residues in this entry.