



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 16, 2017 – 05:28 PM EST

PDB ID : 5G1W
Title : Apo Structure of Linalool Dehydratase-Isomerase
Authors : Chambers, S.; Hau, A.; Man, H.; Omar, M.; Turkenburg, J.P.; Grogan, G.
Deposited on : 2016-03-30
Resolution : 1.76 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20028442
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20028442

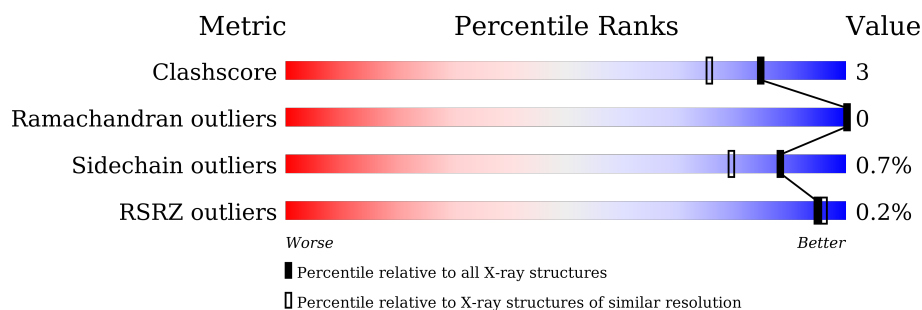
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.76 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))
Clashscore	102246	1730 (1.76-1.76)
Ramachandran outliers	100387	1711 (1.76-1.76)
Sidechain outliers	100360	1711 (1.76-1.76)
RSRZ outliers	91569	1610 (1.76-1.76)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	372	
1	B	372	
1	C	372	
1	D	372	
1	E	372	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	EDO	E	1366	-	-	-	X
3	DXX	A	1370	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 16596 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 LINALOOL DEHYDRATASE/ISOMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	364	Total	C	N	O	S	0	1	0
			2887	1868	478	528	13			
1	B	364	Total	C	N	O	S	0	1	0
			2885	1866	478	528	13			
1	C	365	Total	C	N	O	S	0	0	0
			2888	1868	479	528	13			
1	D	364	Total	C	N	O	S	0	2	0
			2899	1873	482	531	13			
1	E	365	Total	C	N	O	S	0	1	0
			2885	1867	478	527	13			

There are 5 discrepancies between the modelled and reference sequences:

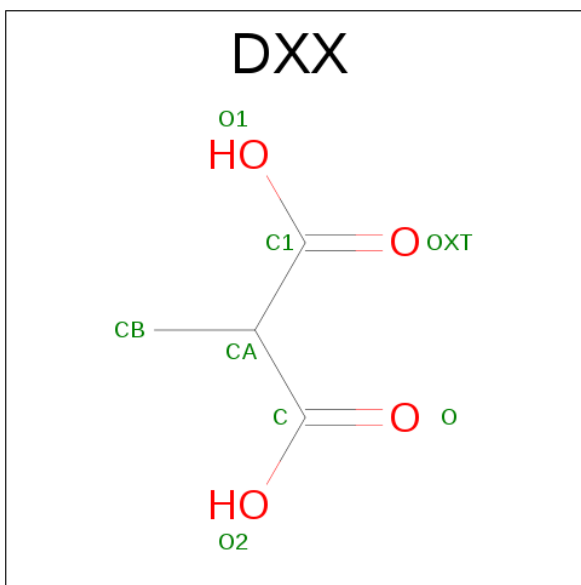
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	EXPRESSION TAG	UNP E1XUJ2
B	1	MET	-	EXPRESSION TAG	UNP E1XUJ2
C	1	MET	-	EXPRESSION TAG	UNP E1XUJ2
D	1	MET	-	EXPRESSION TAG	UNP E1XUJ2
E	1	MET	-	EXPRESSION TAG	UNP E1XUJ2

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	C	1	Total	C	O	0	0
			4	2	2		
2	D	1	Total	C	O	0	0
			4	2	2		
2	D	1	Total	C	O	0	0
			4	2	2		
2	E	1	Total	C	O	0	0
			4	2	2		

- Molecule 3 is METHYLMALONIC ACID (three-letter code: DXX) (formula: C₄H₆O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			7	3	4		
3	B	1	Total	C	O	0	0
			7	3	4		

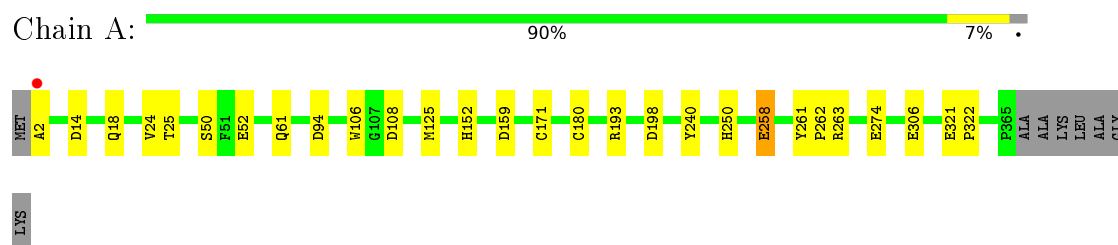
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	466	Total	O	0	0
			466	466		
4	B	407	Total	O	0	0
			407	407		
4	C	416	Total	O	0	0
			416	416		
4	D	425	Total	O	0	0
			425	425		
4	E	380	Total	O	0	0
			380	380		

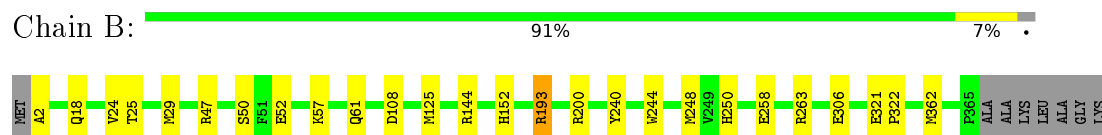
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

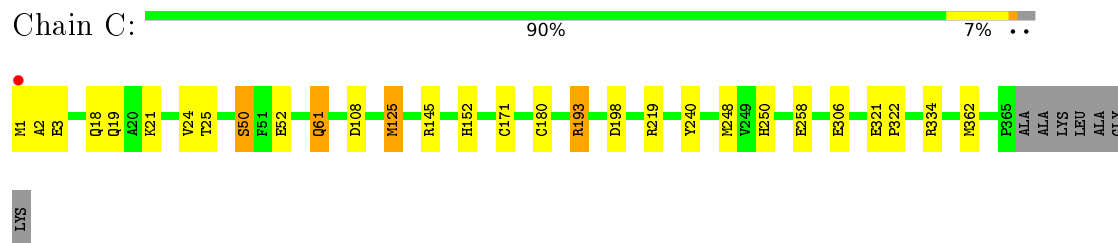
- Molecule 1: LINALOOL DEHYDRATASE/ISOMERASE



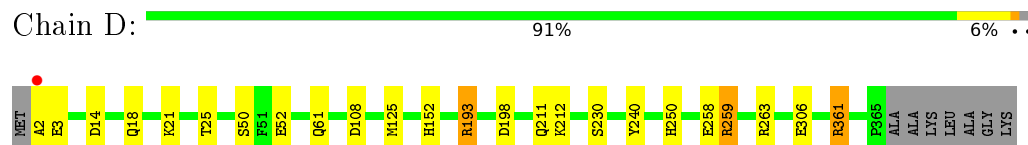
- Molecule 1: LINALOOL DEHYDRATASE/ISOMERASE



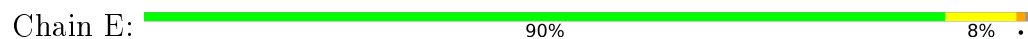
- Molecule 1: LINALOOL DEHYDRATASE/ISOMERASE

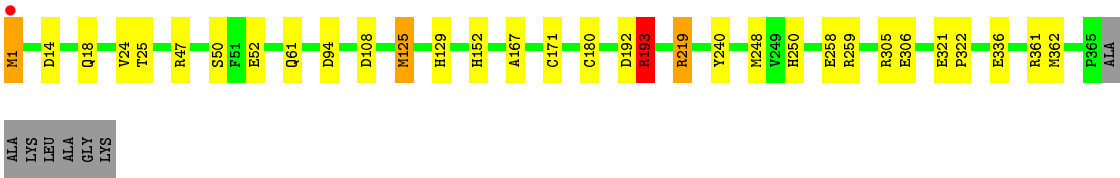


- Molecule 1: LINALOOL DEHYDRATASE/ISOMERASE



- Molecule 1: LINALOOL DEHYDRATASE/ISOMERASE





4 Data and refinement statistics

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	108.06Å 110.15Å 195.34Å 90.00° 91.32° 90.00°	Depositor
Resolution (Å)	47.97 – 1.76 47.97 – 1.76	Depositor EDS
% Data completeness (in resolution range)	96.9 (47.97-1.76) 96.9 (47.97-1.76)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.84 (at 1.76Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.150 , 0.176 (Not available) , (Not available)	Depositor DCC
R_{free} test set	NotAvailable	DCC
Wilson B-factor (Å ²)	17.7	Xtriage
Anisotropy	0.728	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 49.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.013 for k,h,-l 0.012 for -k,-h,-l 0.023 for h,-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	16596	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 7.17% 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

5.1 Standard geometry

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

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	1.03	3/2976 (0.1%)	0.97	8/4051 (0.2%)
1	B	1.00	2/2974 (0.1%)	0.92	5/4049 (0.1%)
1	C	1.04	2/2974 (0.1%)	0.95	8/4049 (0.2%)
1	D	1.04	2/2991 (0.1%)	1.01	10/4070 (0.2%)
1	E	1.04	2/2974 (0.1%)	0.98	14/4050 (0.3%)
All	All	1.03	11/14889 (0.1%)	0.97	45/20269 (0.2%)

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	D	0	1

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	258	GLU	CD-OE2	7.04	1.33	1.25
1	B	258	GLU	CD-OE2	6.71	1.33	1.25
1	B	244	TRP	CE3-CZ3	6.48	1.49	1.38
1	D	3	GLU	CD-OE2	6.40	1.32	1.25
1	A	274	GLU	CD-OE2	-6.11	1.19	1.25
1	A	106	TRP	CE3-CZ3	6.05	1.48	1.38
1	E	248	MET	CG-SD	-5.97	1.65	1.81
1	A	258	GLU	CD-OE2	5.70	1.31	1.25
1	C	3	GLU	CD-OE2	5.64	1.31	1.25
1	D	258	GLU	CD-OE2	-5.44	1.19	1.25
1	C	258	GLU	CD-OE2	5.25	1.31	1.25

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	193	ARG	NE-CZ-NH1	17.67	129.14	120.30
1	D	193	ARG	NE-CZ-NH2	-17.32	111.64	120.30
1	D	193	ARG	NE-CZ-NH1	13.73	127.17	120.30
1	E	193	ARG	NE-CZ-NH2	-11.64	114.48	120.30
1	A	193	ARG	NE-CZ-NH2	-10.31	115.14	120.30
1	E	259	ARG	NE-CZ-NH1	9.59	125.09	120.30
1	E	193	ARG	NE-CZ-NH1	9.27	124.94	120.30
1	D	193	ARG	CG-CD-NE	-8.26	94.45	111.80
1	E	219	ARG	NE-CZ-NH1	8.23	124.41	120.30
1	C	219	ARG	NE-CZ-NH1	7.74	124.17	120.30
1	C	125	MET	CG-SD-CE	7.06	111.49	100.20
1	D	125	MET	CG-SD-CE	6.89	111.22	100.20
1	E	125	MET	CG-SD-CE	6.50	110.61	100.20
1	A	193	ARG	CD-NE-CZ	6.49	132.69	123.60
1	B	125	MET	CG-SD-CE	6.44	110.51	100.20
1	E	219	ARG	NE-CZ-NH2	-6.32	117.14	120.30
1	C	50	SER	N-CA-CB	-6.22	101.17	110.50
1	D	361	ARG	NE-CZ-NH1	6.18	123.39	120.30
1	C	21	LYS	CD-CE-NZ	6.17	125.90	111.70
1	D	193	ARG	CD-NE-CZ	6.09	132.12	123.60
1	C	198	ASP	CB-CG-OD1	6.07	123.77	118.30
1	C	193	ARG	CG-CD-NE	-6.06	99.08	111.80
1	A	94	ASP	CB-CG-OD2	-6.03	112.87	118.30
1	A	125	MET	CG-SD-CE	6.02	109.83	100.20
1	D	263	ARG	NE-CZ-NH1	6.01	123.30	120.30
1	D	198	ASP	CB-CG-OD1	5.86	123.58	118.30
1	A	263	ARG	NE-CZ-NH1	5.84	123.22	120.30
1	B	193	ARG	CG-CD-NE	-5.84	99.54	111.80
1	C	1	MET	C-N-CA	5.78	136.16	121.70
1	E	1	MET	C-N-CA	5.71	135.97	121.70
1	B	263	ARG	NE-CZ-NH1	5.66	123.13	120.30
1	A	198	ASP	CB-CG-OD1	5.66	123.39	118.30
1	D	14	ASP	CB-CG-OD2	-5.63	113.23	118.30
1	E	193	ARG	CG-CD-NE	-5.55	100.13	111.80
1	E	305	ARG	NE-CZ-NH1	5.53	123.06	120.30
1	E	47	ARG	CB-CA-C	-5.48	99.44	110.40
1	D	259	ARG	NE-CZ-NH1	5.43	123.02	120.30
1	E	361	ARG	NE-CZ-NH1	5.34	122.97	120.30
1	B	47	ARG	CB-CA-C	-5.33	99.73	110.40
1	A	14	ASP	CB-CG-OD2	-5.31	113.52	118.30
1	E	192	ASP	CB-CG-OD1	5.26	123.03	118.30
1	E	305	ARG	NE-CZ-NH2	-5.16	117.72	120.30
1	C	2	ALA	N-CA-C	5.08	124.71	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	200	ARG	NE-CZ-NH1	5.07	122.84	120.30
1	E	94	ASP	CB-CG-OD1	5.00	122.80	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	193	ARG	Sidechain

5.2 Too-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 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	2887	0	2771	16	0
1	B	2885	0	2767	15	0
1	C	2888	0	2769	17	0
1	D	2899	0	2792	15	0
1	E	2885	0	2763	19	0
2	A	16	0	24	0	0
2	B	12	0	18	0	0
2	C	4	0	6	0	0
2	D	8	0	12	0	0
2	E	4	0	6	0	0
3	A	7	0	0	0	11
3	B	7	0	0	0	0
4	A	466	0	0	8	0
4	B	407	0	0	7	0
4	C	416	0	0	9	0
4	D	425	0	0	9	0
4	E	380	0	0	10	0
All	All	16596	0	13928	82	11

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 3.

All (82) 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:A:171:CYS:SG	4:A:2285:HOH:O	2.27	0.91
1:C:125:MET:HE3	4:C:2200:HOH:O	1.72	0.89
1:C:180:CYS:SG	4:C:2243:HOH:O	2.33	0.86
1:A:180:CYS:SG	4:A:2285:HOH:O	2.41	0.79
1:E:171:CYS:SG	4:E:2213:HOH:O	2.43	0.76
1:E:14:ASP:OD2	4:E:2030:HOH:O	2.04	0.74
1:C:171:CYS:SG	4:C:2243:HOH:O	2.45	0.73
1:B:29:MET:CE	4:B:2026:HOH:O	2.35	0.73
1:E:250:HIS:HD2	1:E:306:GLU:OE2	1.72	0.73
1:C:250:HIS:HD2	1:C:306:GLU:OE2	1.72	0.73
1:B:250:HIS:HD2	1:B:306:GLU:OE2	1.72	0.72
1:A:50:SER:OG	1:A:52:GLU:OE1	2.10	0.70
1:D:250:HIS:HD2	1:D:306:GLU:OE2	1.75	0.69
1:E:50:SER:OG	1:E:52:GLU:OE1	2.11	0.69
1:E:180:CYS:SG	4:E:2213:HOH:O	2.52	0.68
1:B:50:SER:OG	1:B:52:GLU:OE1	2.11	0.68
1:A:250:HIS:HD2	1:A:306:GLU:OE2	1.76	0.68
1:D:50[B]:SER:OG	1:D:52:GLU:OE1	2.11	0.67
1:C:50:SER:OG	1:C:52:GLU:OE1	2.12	0.67
4:A:2168:HOH:O	1:D:230:SER:HB2	1.93	0.67
1:B:144:ARG:CG	4:B:2212:HOH:O	2.47	0.62
1:A:152:HIS:HE1	4:A:2264:HOH:O	1.84	0.60
1:A:152:HIS:HD2	4:A:2261:HOH:O	1.84	0.59
1:D:250:HIS:HE1	4:D:2302:HOH:O	1.85	0.59
1:D:212:LYS:HE2	4:D:2280:HOH:O	2.03	0.58
1:C:125:MET:CE	4:C:2200:HOH:O	2.41	0.58
1:E:1:MET:CB	4:E:2002:HOH:O	2.51	0.58
1:E:152:HIS:HE1	4:E:2197:HOH:O	1.86	0.57
1:E:1:MET:HA	4:E:2002:HOH:O	2.04	0.57
1:B:29:MET:HE2	4:B:2026:HOH:O	2.00	0.57
1:B:152:HIS:HE1	4:B:2217:HOH:O	1.87	0.56
1:D:361:ARG:NH2	4:D:2421:HOH:O	2.36	0.56
1:A:159:ASP:OD2	4:A:2275:HOH:O	2.17	0.56
1:A:18:GLN:HE21	1:A:25:THR:H	1.55	0.55
1:D:152:HIS:HE1	4:D:2222:HOH:O	1.89	0.54
1:E:219:ARG:NH1	4:E:2246:HOH:O	2.40	0.54
1:C:152:HIS:HE1	4:C:2224:HOH:O	1.91	0.54
1:C:334:ARG:CB	4:C:2401:HOH:O	2.55	0.54
1:C:193:ARG:NH2	1:C:362:MET:O	2.37	0.54
1:D:2:ALA:HB1	4:D:2003:HOH:O	2.07	0.52
1:B:18:GLN:HE21	1:B:25:THR:H	1.58	0.51
1:E:18:GLN:HE21	1:E:25:THR:H	1.59	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:61:GLN:HE22	1:D:108:ASP:HB3	1.76	0.51
1:C:152:HIS:HD2	4:C:2222:HOH:O	1.93	0.51
1:D:21:LYS:HE3	4:D:2038:HOH:O	2.10	0.50
1:C:61:GLN:HE22	1:C:108:ASP:HB3	1.76	0.50
1:C:19:GLN:OE1	4:C:2047:HOH:O	2.20	0.49
1:E:336:GLU:CB	4:E:2359:HOH:O	2.60	0.49
1:E:193:ARG:NH2	1:E:362:MET:O	2.29	0.48
1:C:18:GLN:HE21	1:C:25:THR:H	1.60	0.48
1:C:145:ARG:NH2	4:C:2144:HOH:O	2.47	0.47
1:D:18:GLN:HE21	1:D:25:THR:H	1.61	0.47
1:B:193:ARG:NE	4:B:2253:HOH:O	2.48	0.46
1:C:250:HIS:CD2	1:C:306:GLU:OE2	2.62	0.46
1:E:61:GLN:HE22	1:E:108:ASP:HB3	1.81	0.46
1:A:2:ALA:HB3	4:A:2035:HOH:O	2.16	0.46
1:B:152:HIS:HD2	4:B:2213:HOH:O	1.99	0.45
1:A:61:GLN:HE22	1:A:108:ASP:HB3	1.82	0.45
1:C:321:GLU:HB3	1:C:322:PRO:HD3	1.99	0.44
1:C:18:GLN:HE21	1:C:24:VAL:HA	1.82	0.44
1:A:250:HIS:CD2	1:A:306:GLU:OE2	2.65	0.44
1:B:2:ALA:HB1	4:B:2002:HOH:O	2.18	0.44
1:E:152:HIS:HD2	4:E:2193:HOH:O	2.00	0.44
1:A:321:GLU:HB3	1:A:322:PRO:HD3	2.00	0.43
1:D:21:LYS:CE	4:D:2038:HOH:O	2.66	0.43
1:A:250:HIS:HE1	1:A:258:GLU:OE2	2.02	0.43
1:E:250:HIS:CD2	1:E:306:GLU:OE2	2.61	0.43
1:E:321:GLU:HB3	1:E:322:PRO:HD3	2.00	0.43
1:D:211:GLN:HE22	1:D:259:ARG:HH21	1.67	0.43
1:D:250:HIS:CE1	4:D:2302:HOH:O	2.67	0.42
1:B:61:GLN:HE22	1:B:108:ASP:HB3	1.84	0.42
1:E:167:ALA:HA	4:E:2209:HOH:O	2.18	0.41
1:B:321:GLU:HB3	1:B:322:PRO:HD3	2.02	0.41
1:A:2:ALA:CB	4:A:2035:HOH:O	2.68	0.41
1:B:18:GLN:HE21	1:B:24:VAL:HA	1.86	0.41
1:A:18:GLN:HE21	1:A:24:VAL:HA	1.86	0.41
1:E:125:MET:HE2	1:E:129:HIS:CD2	2.56	0.41
1:B:193:ARG:NH2	1:B:362:MET:O	2.48	0.41
1:B:250:HIS:CD2	1:B:306:GLU:OE2	2.62	0.40
1:A:261:TYR:HB3	1:A:262:PRO:HD3	2.03	0.40
1:D:152:HIS:HD2	4:D:2221:HOH:O	2.03	0.40
1:E:18:GLN:HE21	1:E:24:VAL:HA	1.86	0.40

All (11) 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	Interatomic distance (Å)	Clash overlap (Å)
3:A:1370:DXX:C1	3:A:1370:DXX:C[2_555]	0.00	2.20
3:A:1370:DXX:O1	3:A:1370:DXX:O[2_555]	0.00	2.20
3:A:1370:DXX:OXT	3:A:1370:DXX:O2[2_555]	0.00	2.20
3:A:1370:DXX:C1	3:A:1370:DXX:O2[2_555]	1.20	1.00
3:A:1370:DXX:OXT	3:A:1370:DXX:C[2_555]	1.20	1.00
3:A:1370:DXX:C1	3:A:1370:DXX:O[2_555]	1.20	1.00
3:A:1370:DXX:O1	3:A:1370:DXX:C[2_555]	1.20	1.00
3:A:1370:DXX:C1	3:A:1370:DXX:CA[2_555]	1.50	0.70
3:A:1370:DXX:CA	3:A:1370:DXX:C[2_555]	1.50	0.70
3:A:1370:DXX:O1	3:A:1370:DXX:O2[2_555]	2.11	0.09
3:A:1370:DXX:OXT	3:A:1370:DXX:O[2_555]	2.11	0.09

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	363/372 (98%)	356 (98%)	7 (2%)	0	100	100
1	B	363/372 (98%)	357 (98%)	6 (2%)	0	100	100
1	C	363/372 (98%)	354 (98%)	9 (2%)	0	100	100
1	D	364/372 (98%)	357 (98%)	7 (2%)	0	100	100
1	E	364/372 (98%)	358 (98%)	6 (2%)	0	100	100
All	All	1817/1860 (98%)	1782 (98%)	35 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	293/303 (97%)	292 (100%)	1 (0%)	94	92
1	B	293/303 (97%)	290 (99%)	3 (1%)	82	69
1	C	292/303 (96%)	289 (99%)	3 (1%)	82	69
1	D	297/303 (98%)	296 (100%)	1 (0%)	94	92
1	E	291/303 (96%)	289 (99%)	2 (1%)	88	79
All	All	1466/1515 (97%)	1456 (99%)	10 (1%)	88	79

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	240	TYR
1	B	57	LYS
1	B	240	TYR
1	B	248	MET
1	C	61	GLN
1	C	240	TYR
1	C	248	MET
1	D	240	TYR
1	E	193	ARG
1	E	240	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	GLN
1	A	61	GLN
1	A	152	HIS
1	A	211	GLN
1	A	227	HIS
1	A	250	HIS
1	B	18	GLN
1	B	61	GLN
1	B	152	HIS
1	B	227	HIS
1	B	250	HIS
1	C	18	GLN
1	C	61	GLN

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Mol	Chain	Res	Type
1	C	152	HIS
1	C	211	GLN
1	C	227	HIS
1	C	250	HIS
1	D	18	GLN
1	D	61	GLN
1	D	152	HIS
1	D	211	GLN
1	D	227	HIS
1	D	250	HIS
1	E	18	GLN
1	E	61	GLN
1	E	152	HIS
1	E	211	GLN
1	E	227	HIS
1	E	250	HIS
1	E	310	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

13 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	A	1366	-	3,3,3	0.40	0	2,2,2	0.21	0
2	EDO	A	1367	-	3,3,3	0.55	0	2,2,2	0.65	0
2	EDO	A	1368	-	3,3,3	0.55	0	2,2,2	0.21	0
2	EDO	A	1369	-	3,3,3	0.30	0	2,2,2	0.74	0
3	DXX	A	1370	-	0,6,7	0.00	-	0,7,9	0.00	-
2	EDO	B	1366	-	3,3,3	0.53	0	2,2,2	0.59	0
2	EDO	B	1367	-	3,3,3	0.67	0	2,2,2	0.59	0
2	EDO	B	1368	-	3,3,3	0.50	0	2,2,2	0.43	0
3	DXX	B	1369	-	0,6,7	0.00	-	0,7,9	0.00	-
2	EDO	C	1366	-	3,3,3	0.49	0	2,2,2	0.42	0
2	EDO	D	1366	-	3,3,3	0.71	0	2,2,2	0.03	0
2	EDO	D	1367	-	3,3,3	0.64	0	2,2,2	0.58	0
2	EDO	E	1366	-	3,3,3	0.64	0	2,2,2	0.16	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	A	1366	-	-	0/1/1/1	0/0/0/0
2	EDO	A	1367	-	-	0/1/1/1	0/0/0/0
2	EDO	A	1368	-	-	0/1/1/1	0/0/0/0
2	EDO	A	1369	-	-	0/1/1/1	0/0/0/0
3	DXX	A	1370	-	-	0/0/4/8	0/0/0/0
2	EDO	B	1366	-	-	0/1/1/1	0/0/0/0
2	EDO	B	1367	-	-	0/1/1/1	0/0/0/0
2	EDO	B	1368	-	-	0/1/1/1	0/0/0/0
3	DXX	B	1369	-	-	0/0/4/8	0/0/0/0
2	EDO	C	1366	-	-	0/1/1/1	0/0/0/0
2	EDO	D	1366	-	-	0/1/1/1	0/0/0/0
2	EDO	D	1367	-	-	0/1/1/1	0/0/0/0
2	EDO	E	1366	-	-	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.

1 monomer is involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1370	DXX	0	11

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	364/372 (97%)	-0.46	1 (0%) 94 95	12, 17, 30, 45	0
1	B	364/372 (97%)	-0.33	0 100 100	12, 18, 30, 41	0
1	C	365/372 (98%)	-0.33	1 (0%) 94 95	13, 18, 30, 52	0
1	D	364/372 (97%)	-0.36	1 (0%) 94 95	13, 18, 30, 47	0
1	E	365/372 (98%)	-0.38	1 (0%) 94 95	13, 18, 31, 44	0
All	All	1822/1860 (97%)	-0.37	4 (0%) 95 96	12, 18, 31, 52	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	1	MET	4.9
1	E	1	MET	3.1
1	A	2	ALA	2.4
1	D	2	ALA	2.1

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	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	EDO	E	1366	4/4	0.96	0.22	7.20	20,20,20,20	0
3	DXX	B	1369	7/8	0.98	0.09	1.43	16,18,20,20	0
2	EDO	D	1366	4/4	0.96	0.12	0.95	18,21,23,23	0
2	EDO	D	1367	4/4	0.95	0.09	0.94	24,25,25,25	0
2	EDO	C	1366	4/4	0.97	0.08	-0.02	22,23,24,24	0
2	EDO	A	1368	4/4	0.98	0.07	-0.03	22,23,25,27	0
2	EDO	B	1367	4/4	0.98	0.06	-0.47	21,22,25,27	0
2	EDO	A	1367	4/4	0.98	0.06	-0.84	23,24,24,27	0
2	EDO	B	1366	4/4	0.96	0.15	-	24,31,31,36	0
2	EDO	A	1366	4/4	0.96	0.15	-	25,27,28,30	0
2	EDO	B	1368	4/4	0.95	0.09	-	23,28,29,31	0
2	EDO	A	1369	4/4	0.96	0.09	-	25,31,37,43	0
3	DXX	A	1370	7/8	0.95	0.20	-	16,17,160,161	0

6.5 Other polymers

There are no such residues in this entry.