



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 1YJ4
Title : Y305F Trichodiene Synthase
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Deposited on : 2005-01-13
Resolution : 2.30 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.23.2
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) : 2.23.2

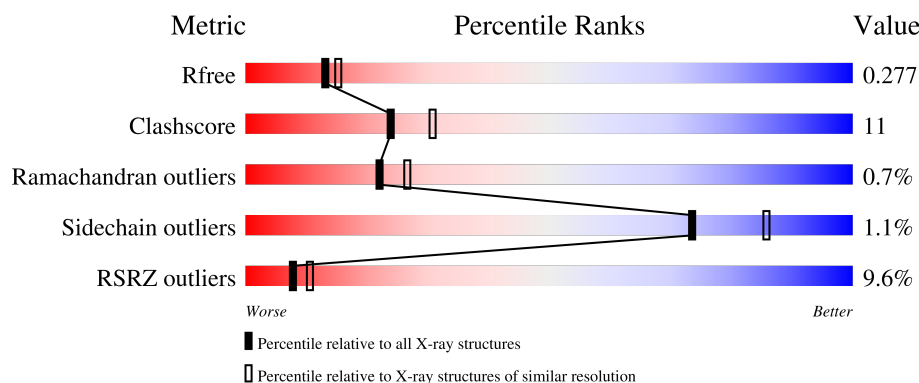
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	374	<div> <div>5%</div> <div> <div></div> <div>75%</div> <div>20%</div> <div>5%</div> </div> </div>
1	B	374	<div> <div>12%</div> <div> <div></div> <div>67%</div> <div>26%</div> <div>7%</div> </div> </div>

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	B	703	-	-	-	X

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6013 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 Trichodiene synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	354	Total	C	N	O	S	54	0	0
			2939	1882	493	546	18			
1	B	349	Total	C	N	O	S	167	0	0
			2899	1859	486	537	17			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	305	PHE	TYR	engineered mutation	UNP P13513
B	305	PHE	TYR	engineered mutation	UNP P13513

- 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		

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

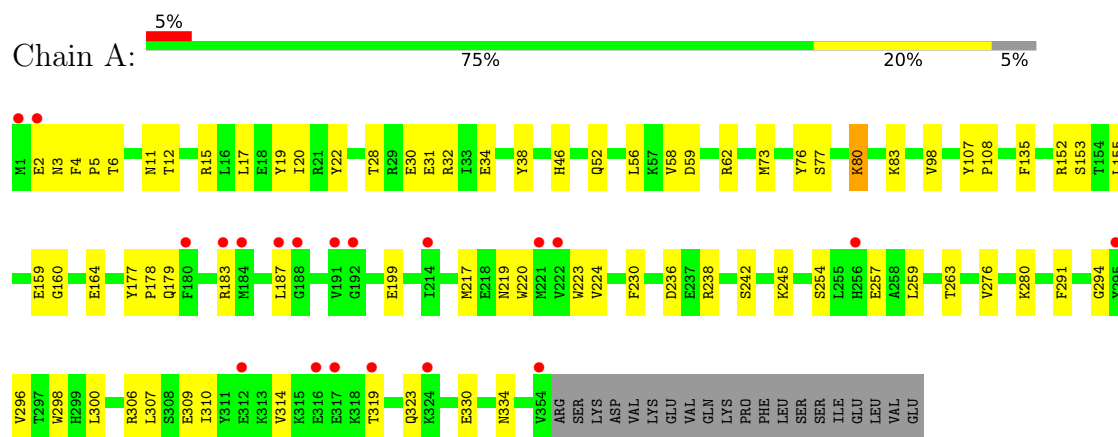
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	82	Total O 82 82	0	0
3	B	77	Total O 77 77	0	0

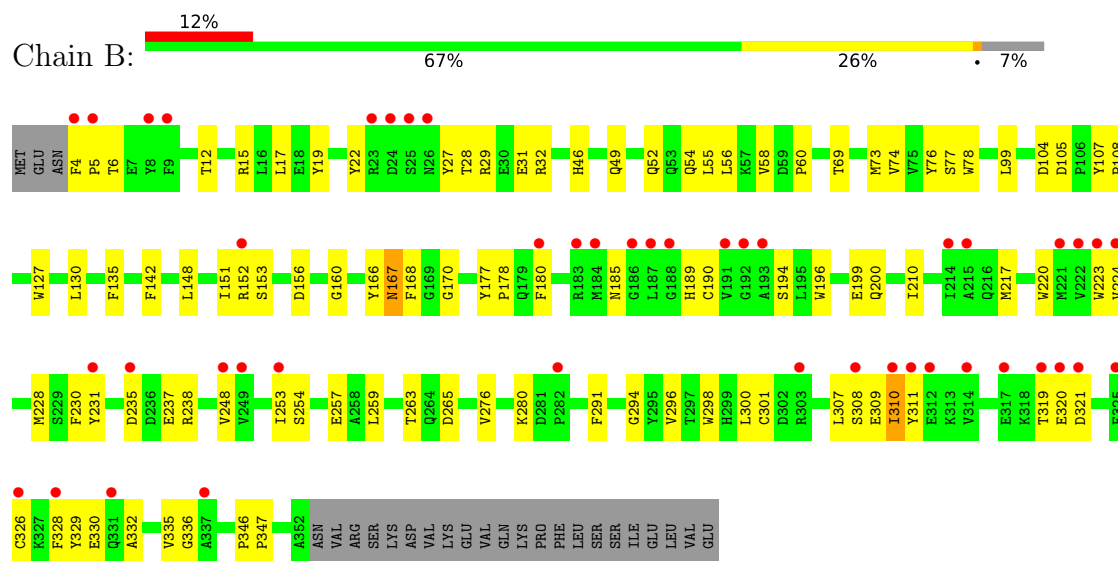
3 Residue-property plots [i](#)

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: Trichodiene synthase



• Molecule 1: Trichodiene synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	122.24Å 122.24Å 151.72Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.00 – 2.30 38.69 – 2.30	Depositor EDS
% Data completeness (in resolution range)	93.9 (40.00-2.30) 93.6 (38.69-2.30)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.68 (at 2.29Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.244 , 0.275 0.244 , 0.277	Depositor DCC
R_{free} test set	2770 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	45.7	Xtriage
Anisotropy	0.059	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 42.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.016 for -h,-k,l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6013	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.72% 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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.38	0/3024	0.56	0/4104
1	B	0.36	0/2984	0.53	0/4050
All	All	0.37	0/6008	0.55	0/8154

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2939	0	2793	52	0
1	B	2899	0	2754	73	0
2	A	8	0	12	0	0
2	B	8	0	12	1	0
3	A	82	0	0	1	0
3	B	77	0	0	0	0
All	All	6013	0	5571	122	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 11.

All (122) 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:17:LEU:HD21	1:A:296:VAL:HG11	1.33	1.04
1:A:217:MET:HE1	1:A:220:TRP:HB3	1.59	0.85
1:A:319:THR:O	1:A:323:GLN:HG2	1.76	0.85
1:B:12:THR:HG23	1:B:263:THR:HG23	1.65	0.79
1:A:59:ASP:HB3	1:A:62:ARG:HG3	1.64	0.78
1:B:217:MET:HE1	1:B:220:TRP:HB3	1.66	0.77
1:A:30:GLU:O	1:A:34:GLU:HG3	1.89	0.72
1:B:300:LEU:HA	1:B:307:LEU:HD12	1.73	0.71
1:B:32:ARG:HG3	1:B:32:ARG:HH11	1.56	0.69
1:A:306:ARG:HD2	1:A:309:GLU:OE2	1.93	0.68
1:A:107:TYR:HB3	1:A:108:PRO:HD3	1.78	0.65
1:B:199:GLU:HG3	1:B:200:GLN:NE2	2.13	0.63
1:B:15:ARG:O	1:B:19:TYR:HD1	1.82	0.63
1:B:224:VAL:O	1:B:228:MET:HG2	1.99	0.62
1:A:217:MET:CE	1:A:220:TRP:HB3	2.29	0.62
1:B:308:SER:HA	1:B:329:TYR:OH	2.00	0.61
1:A:160:GLY:O	1:A:164:GLU:HG3	2.01	0.60
1:A:276:VAL:O	1:A:280:LYS:HD3	2.02	0.60
1:A:254:SER:OG	1:A:257:GLU:HG3	2.02	0.59
1:B:276:VAL:O	1:B:280:LYS:HD3	2.02	0.59
1:B:310:ILE:HG22	1:B:310:ILE:O	2.03	0.58
1:B:74:VAL:HA	1:B:78:TRP:CE3	2.39	0.58
1:A:59:ASP:HB3	1:A:62:ARG:CG	2.33	0.58
1:B:332:ALA:O	1:B:336:GLY:N	2.38	0.57
1:B:217:MET:CE	1:B:220:TRP:HE3	2.18	0.56
1:B:107:TYR:HB3	1:B:108:PRO:HD3	1.85	0.56
1:B:329:TYR:O	1:B:332:ALA:HB3	2.05	0.56
1:B:46:HIS:O	1:B:52:GLN:HG3	2.06	0.56
1:A:58:VAL:HG21	1:A:98:VAL:HG11	1.87	0.56
1:A:17:LEU:HD22	1:A:22:TYR:CG	2.41	0.55
1:A:17:LEU:HD23	1:A:20:ILE:HD11	1.90	0.54
1:B:32:ARG:HG3	1:B:32:ARG:NH1	2.23	0.54
1:B:69:THR:HG22	1:B:298:TRP:HZ2	1.72	0.54
1:A:217:MET:O	1:A:217:MET:HE3	2.08	0.54
1:A:38:TYR:CD2	1:A:83:LYS:HB3	2.44	0.53
1:A:80:LYS:HE3	1:A:80:LYS:HA	1.90	0.53
1:A:217:MET:HE2	1:A:220:TRP:HE3	1.74	0.52
1:B:29:ARG:HG3	1:B:29:ARG:HH11	1.74	0.52
1:B:28:THR:OG1	1:B:31:GLU:HG3	2.10	0.52
1:B:217:MET:HE1	1:B:220:TRP:CE3	2.46	0.51
1:A:58:VAL:HG21	1:A:98:VAL:CG1	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:179:GLN:O	1:A:183:ARG:HB2	2.09	0.51
1:B:231:TYR:CE1	1:B:310:ILE:HD11	2.46	0.51
1:B:217:MET:CE	1:B:220:TRP:HB3	2.38	0.50
1:A:32:ARG:HH11	1:A:32:ARG:HG3	1.76	0.50
1:B:76:TYR:O	1:B:294:GLY:HA3	2.11	0.50
1:B:301:CYS:SG	1:B:336:GLY:HA3	2.52	0.50
1:A:15:ARG:O	1:A:19:TYR:CD1	2.64	0.50
1:B:217:MET:HE2	1:B:220:TRP:HE3	1.76	0.50
1:A:155:LEU:HG	1:B:152:ARG:HG2	1.93	0.50
1:B:29:ARG:HG3	1:B:29:ARG:NH1	2.27	0.50
1:B:27:TYR:O	1:B:32:ARG:NH1	2.46	0.49
1:A:217:MET:CE	1:A:220:TRP:HE3	2.25	0.49
1:A:12:THR:HG23	1:A:263:THR:HG23	1.94	0.49
1:B:248:VAL:HG13	1:B:253:ILE:O	2.13	0.49
1:B:300:LEU:HD23	1:B:307:LEU:HD13	1.95	0.49
1:A:76:TYR:O	1:A:294:GLY:HA3	2.13	0.48
1:B:168:PHE:CE2	1:B:170:GLY:HA2	2.48	0.48
1:B:319:THR:HG22	1:B:320:GLU:N	2.28	0.48
1:B:326:CYS:O	1:B:330:GLU:HG3	2.13	0.48
1:B:223:TRP:CZ3	1:B:265:ASP:HB3	2.48	0.48
1:B:4:PHE:O	1:B:6:THR:N	2.46	0.47
1:B:17:LEU:CD2	1:B:296:VAL:HG11	2.44	0.47
1:A:73:MET:HB2	1:A:298:TRP:CE2	2.49	0.47
1:B:153:SER:HB3	1:B:190:CYS:HB2	1.96	0.47
1:B:217:MET:CE	1:B:220:TRP:CE3	2.96	0.47
1:A:56:LEU:HG	1:A:58:VAL:HG23	1.96	0.47
1:A:219:ASN:HB3	1:A:223:TRP:CZ3	2.49	0.47
1:A:199:GLU:HG3	3:A:783:HOH:O	2.15	0.47
1:A:152:ARG:HD2	1:B:156:ASP:OD1	2.15	0.46
1:B:54:GLN:HG2	1:B:55:LEU:HD23	1.97	0.46
1:B:152:ARG:NH2	1:B:189:HIS:ND1	2.59	0.46
1:A:242:SER:OG	1:A:245:LYS:HG3	2.16	0.46
1:B:217:MET:O	1:B:217:MET:HE3	2.17	0.45
1:B:309:GLU:C	1:B:311:TYR:H	2.19	0.45
1:B:230:PHE:CE2	1:B:259:LEU:HD22	2.52	0.45
1:A:17:LEU:HD22	1:A:22:TYR:HB2	1.98	0.45
1:B:17:LEU:HB3	1:B:22:TYR:HB2	1.98	0.45
1:B:166:TYR:O	1:B:167:ASN:C	2.54	0.44
1:B:160:GLY:HA3	1:B:185:ASN:HB3	1.99	0.44
1:B:17:LEU:HD21	1:B:296:VAL:HG11	1.99	0.44
1:B:32:ARG:HD2	1:B:335:VAL:HG22	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:99:LEU:HB2	1:B:127:TRP:NE1	2.33	0.44
1:A:217:MET:CE	1:A:220:TRP:CE3	3.01	0.44
1:B:17:LEU:HB3	1:B:22:TYR:CB	2.48	0.44
1:B:77:SER:HB3	1:B:291:PHE:CD1	2.53	0.44
1:A:177:TYR:HB3	1:A:178:PRO:HD3	2.00	0.44
1:A:153:SER:OG	1:A:187:LEU:HA	2.18	0.43
1:B:107:TYR:CD1	1:B:107:TYR:C	2.91	0.43
1:A:28:THR:OG1	1:A:31:GLU:HG3	2.18	0.43
1:B:307:LEU:O	1:B:329:TYR:HE2	2.01	0.43
1:A:2:GLU:HG2	1:A:3:ASN:N	2.33	0.43
1:B:177:TYR:HB3	1:B:178:PRO:HD3	1.99	0.43
1:A:236:ASP:OD1	1:A:238:ARG:HB3	2.19	0.43
1:A:310:ILE:O	1:A:314:VAL:HG22	2.19	0.43
1:B:105:ASP:OD2	1:B:108:PRO:HD3	2.19	0.43
1:B:73:MET:HB2	1:B:298:TRP:CE2	2.53	0.43
1:B:254:SER:OG	1:B:257:GLU:HG3	2.18	0.43
1:A:4:PHE:O	1:A:6:THR:N	2.50	0.43
1:B:55:LEU:HB2	1:B:130:LEU:HD11	2.00	0.43
1:A:300:LEU:HA	1:A:307:LEU:HD12	2.01	0.43
1:B:319:THR:HG22	1:B:321:ASP:H	1.84	0.43
1:A:230:PHE:CE2	1:A:259:LEU:HD22	2.54	0.43
1:B:168:PHE:CZ	1:B:170:GLY:HA2	2.54	0.43
1:B:142:PHE:CE2	1:B:194:SER:HA	2.54	0.42
1:B:27:TYR:HA	1:B:31:GLU:OE1	2.19	0.42
1:A:11:ASN:O	1:A:15:ARG:HG3	2.20	0.42
1:A:220:TRP:O	1:A:224:VAL:HG23	2.20	0.42
1:B:56:LEU:HG	1:B:58:VAL:HG23	2.00	0.42
1:B:49:GLN:HB2	1:B:52:GLN:HG2	2.02	0.41
1:A:77:SER:HB3	1:A:291:PHE:CD1	2.55	0.41
1:B:346:PRO:HB2	1:B:347:PRO:HD2	2.02	0.41
1:B:151:ILE:HG23	2:B:701:EDO:H22	2.03	0.41
1:B:196:TRP:CD1	1:B:210:ILE:HG23	2.56	0.41
1:A:46:HIS:O	1:A:52:GLN:HG3	2.21	0.41
1:B:32:ARG:NH1	1:B:32:ARG:CG	2.84	0.41
1:B:320:GLU:HG2	1:B:320:GLU:O	2.20	0.41
1:A:4:PHE:HA	1:A:5:PRO:HD3	1.91	0.40
1:A:17:LEU:HD23	1:A:17:LEU:HA	1.87	0.40
1:A:159:GLU:HB2	1:B:148:LEU:HD21	2.03	0.40
1:A:330:GLU:O	1:A:334:ASN:ND2	2.55	0.40
1:B:17:LEU:HD12	1:B:328:PHE:CG	2.57	0.40

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	A	352/374 (94%)	339 (96%)	13 (4%)	0	100	100
1	B	347/374 (93%)	320 (92%)	22 (6%)	5 (1%)	11	11
All	All	699/748 (93%)	659 (94%)	35 (5%)	5 (1%)	22	26

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	238	ARG
1	B	237	GLU
1	B	5	PRO
1	B	235	ASP
1	B	310	ILE

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	A	320/340 (94%)	318 (99%)	2 (1%)	86	94
1	B	315/340 (93%)	310 (98%)	5 (2%)	62	78
All	All	635/680 (93%)	628 (99%)	7 (1%)	73	86

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	80	LYS

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Mol	Chain	Res	Type
1	A	135	PHE
1	B	60	PRO
1	B	104	ASP
1	B	135	PHE
1	B	167	ASN
1	B	180	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	GLN
1	A	331	GLN
1	A	334	ASN
1	A	350	GLN
1	B	54	GLN
1	B	331	GLN
1	B	350	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](#)

4 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	700	-	3,3,3	0.60	0	2,2,2	0.53	0
2	EDO	B	703	-	3,3,3	0.54	0	2,2,2	0.60	0
2	EDO	B	701	-	3,3,3	0.55	0	2,2,2	0.47	0
2	EDO	A	702	-	3,3,3	0.64	0	2,2,2	0.66	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	700	-	-	1/1/1/1	-
2	EDO	B	703	-	-	1/1/1/1	-
2	EDO	B	701	-	-	1/1/1/1	-
2	EDO	A	702	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	700	EDO	O1-C1-C2-O2
2	A	702	EDO	O1-C1-C2-O2
2	B	701	EDO	O1-C1-C2-O2
2	B	703	EDO	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	701	EDO	1	0

5.7 Other polymers [i](#)

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	348/374 (93%)	0.31	20 (5%) 23 30	31, 47, 73, 103	0
1	B	331/374 (88%)	0.59	45 (13%) 3 4	20, 50, 102, 116	1 (0%)
All	All	679/748 (90%)	0.44	65 (9%) 8 10	20, 48, 92, 116	1 (0%)

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	26	ASN	11.5
1	A	1	MET	7.5
1	B	235	ASP	6.0
1	B	312	GLU	5.5
1	A	319	THR	5.2
1	B	5	PRO	5.2
1	B	187	LEU	4.6
1	A	187	LEU	4.5
1	A	354	VAL	4.4
1	B	337	ALA	4.3
1	B	325	PHE	4.0
1	B	308	SER	4.0
1	B	310	ILE	3.9
1	B	222	VAL	3.9
1	B	311	TYR	3.8
1	B	314	VAL	3.8
1	B	317	GLU	3.7
1	B	221	MET	3.7
1	A	183	ARG	3.5
1	B	23	ARG	3.5
1	B	328	PHE	3.5
1	B	320	GLU	3.5
1	A	191	VAL	3.3
1	B	319	THR	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	4	PHE	3.3
1	B	183	ARG	3.1
1	B	188	GLY	3.1
1	B	8	TYR	3.1
1	A	180	PHE	3.0
1	B	184	MET	3.0
1	A	188	GLY	2.9
1	B	331	GLN	2.8
1	B	9	PHE	2.7
1	B	214	ILE	2.7
1	A	316	GLU	2.7
1	A	221	MET	2.6
1	B	191	VAL	2.6
1	A	2	GLU	2.6
1	A	214	ILE	2.5
1	B	231	TYR	2.5
1	B	321	ASP	2.5
1	B	253	ILE	2.5
1	B	248	VAL	2.5
1	A	222	VAL	2.5
1	B	215	ALA	2.5
1	B	180	PHE	2.4
1	A	312	GLU	2.4
1	B	192	GLY	2.4
1	A	184	MET	2.4
1	A	192	GLY	2.3
1	A	256	HIS	2.3
1	A	317	GLU	2.3
1	B	193	ALA	2.3
1	B	152	ARG	2.2
1	B	24	ASP	2.2
1	B	186	GLY	2.2
1	B	303	ARG	2.2
1	B	25	SER	2.2
1	B	223	TRP	2.2
1	B	282	PRO	2.2
1	B	224	VAL	2.2
1	A	295	TYR	2.1
1	B	249	VAL	2.1
1	B	326	CYS	2.1
1	A	324	LYS	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	EDO	B	703	4/4	0.80	0.89	74,75,76,77	0
2	EDO	A	702	4/4	0.90	0.47	45,46,48,52	0
2	EDO	B	701	4/4	0.96	0.13	36,39,39,39	0
2	EDO	A	700	4/4	0.96	0.11	34,36,36,39	0

6.5 Other polymers [i](#)

There are no such residues in this entry.