Full wwPDB X-ray Structure Validation Report ⓘ

Nov 5, 2023 – 10:14 pm GMT

PDB ID	:	5LTM
Title	:	Crystal structure of phenylalanine ammonia-lyase from Anabaena variabilis (Y78F-C503S-C565S) bound to cinnamate
Authors	:	Dunstan, M.S.; Leys, D.
Deposited on	:	2016-09-07
Resolution	:	2.41 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

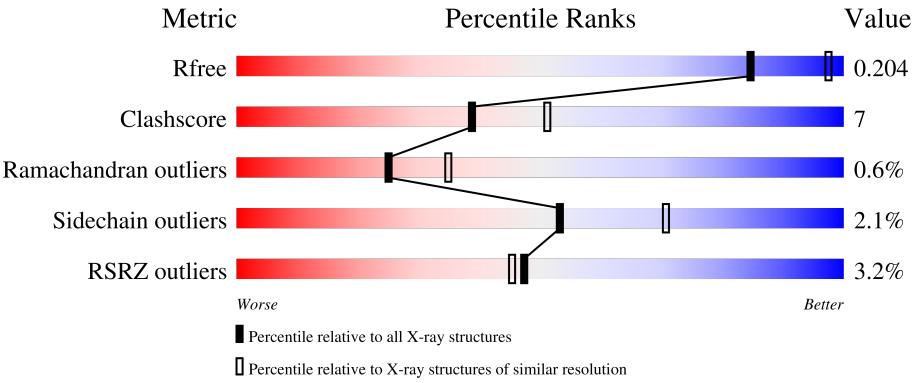
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.41 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	4647 (2.44-2.40)
Clashscore	141614	5161 (2.44-2.40)
Ramachandran outliers	138981	5073 (2.44-2.40)
Sidechain outliers	138945	5074 (2.44-2.40)
RSRZ outliers	127900	4543 (2.44-2.40)

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 of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	537	4% 84% 13%
1	B	537	2% 90% 9%

2 Entry composition

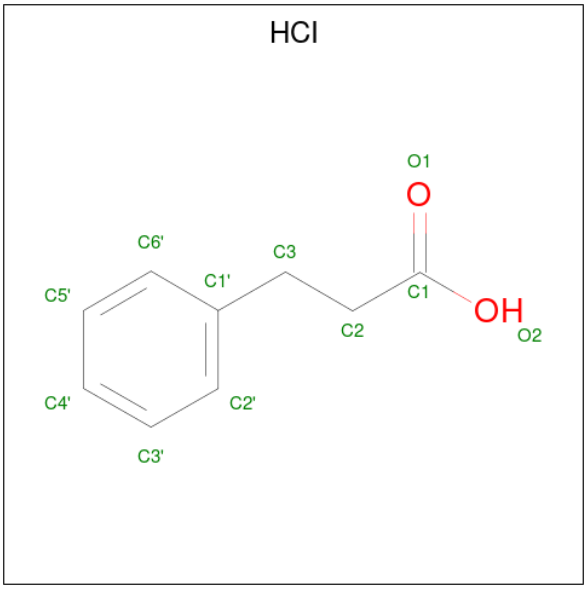
There are 3 unique types of molecules in this entry. The entry contains 8671 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 phenylalanine ammonia lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	537	Total	C	N	O	S	0	0	0
			4127	2600	726	782	19			
1	A	537	Total	C	N	O	S	0	0	0
			4127	2600	726	782	19			

- Molecule 2 is HYDROCINNAMIC ACID (three-letter code: HCI) (formula: $C_9H_{10}O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			11	9	2		
2	A	1	Total	C	O	0	0
			11	9	2		

- Molecule 3 is water.

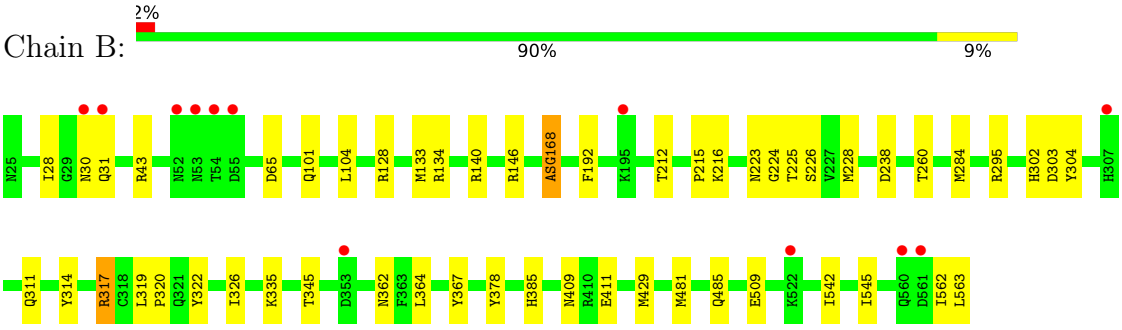
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	195	Total O 195 195	0	0
3	A	200	Total O 200 200	0	0

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.

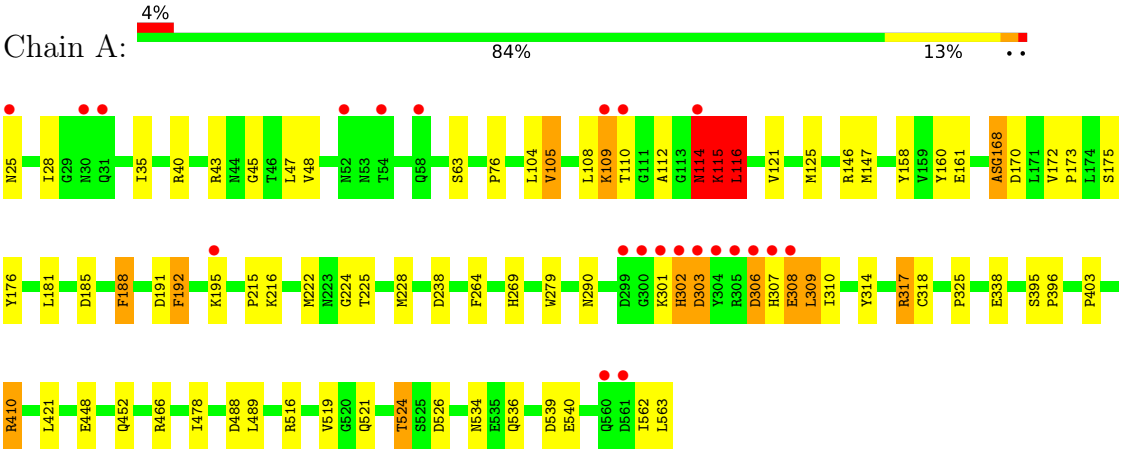
• Molecule 1: phenylalanine ammonia lyase

Chain B:



• Molecule 1: phenylalanine ammonia lyase

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 2 2	Depositor
Cell constants a, b, c, α, β, γ	78.08Å 78.08Å 354.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.83 – 2.41 29.83 – 2.41	Depositor EDS
% Data completeness (in resolution range)	99.7 (29.83-2.41) 96.1 (29.83-2.41)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.95 (at 2.42Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.156 , 0.206 0.157 , 0.204	Depositor DCC
R_{free} test set	2180 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	26.0	Xtriage
Anisotropy	0.139	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 40.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	8671	wwPDB-VP
Average B, all atoms (Å^2)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.51% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	0.48	3/4189 (0.1%)	0.62	3/5686 (0.1%)
1	B	0.41	0/4189	0.57	2/5686 (0.0%)
All	All	0.45	3/8378 (0.0%)	0.60	5/11372 (0.0%)

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	A	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	188	PHE	CD1-CE1	-5.10	1.29	1.39
1	A	114	ASN	N-CA	5.03	1.56	1.46
1	A	188	PHE	CB-CG	-5.03	1.42	1.51

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	303	ASP	CB-CG-OD1	6.80	124.42	118.30
1	A	114	ASN	N-CA-C	5.63	126.22	111.00
1	A	116	LEU	CA-CB-CG	5.51	127.97	115.30
1	B	317	ARG	NE-CZ-NH2	-5.14	117.73	120.30
1	A	115	LYS	N-CA-C	5.13	124.86	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	114	ASN	Peptide
1	A	302	HIS	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4127	0	4102	92	0
1	B	4127	0	4102	37	0
2	A	11	0	9	3	0
2	B	11	0	9	2	0
3	A	200	0	0	13	1
3	B	195	0	0	6	1
All	All	8671	0	8222	123	2

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 7.

All (123) 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:114:ASN:OD1	1:A:115:LYS:N	1.87	1.05
1:A:114:ASN:O	1:A:161:GLU:N	1.92	1.01
1:B:509:GLU:OE1	3:B:701:HOH:O	1.87	0.92
1:A:105:VAL:HG12	1:A:109:LYS:HZ3	1.34	0.91
1:B:128:ARG:NH2	1:B:223:ASN:O	2.04	0.91
1:A:109:LYS:HG2	1:A:110:THR:HG23	1.56	0.87
1:A:105:VAL:HG12	1:A:109:LYS:NZ	1.88	0.86
1:A:536:GLN:NE2	3:A:703:HOH:O	2.10	0.85
1:A:109:LYS:HZ2	1:A:188:PHE:HZ	1.24	0.82
1:A:116:LEU:HD21	1:A:121:VAL:CG2	2.11	0.80
1:A:410:ARG:NH1	3:A:707:HOH:O	2.16	0.77
1:B:317:ARG:NH2	2:B:601:HCI:O1	2.19	0.75
1:A:116:LEU:HD21	1:A:121:VAL:HG23	1.69	0.74
1:A:290:ASN:ND2	3:A:708:HOH:O	2.16	0.74
1:A:306:ASP:OD2	3:A:702:HOH:O	2.06	0.74
1:A:116:LEU:C	1:A:116:LEU:HD23	2.08	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:109:LYS:O	1:A:110:THR:OG1	2.11	0.69
1:B:65:ASP:OD2	3:B:702:HOH:O	2.13	0.67
1:A:317:ARG:HH22	2:A:601:HCI:C1	2.08	0.67
1:A:516:ARG:NH2	1:A:521:GLN:OE1	2.24	0.66
1:A:25:ASN:HD21	1:A:47:LEU:HB2	1.60	0.65
1:B:30:ASN:OD1	1:B:31:GLN:HG2	1.97	0.64
1:A:45:GLY:O	3:A:705:HOH:O	2.15	0.64
1:A:109:LYS:HD2	1:A:188:PHE:CE1	2.32	0.63
1:A:112:ALA:HB1	1:A:160:TYR:HB2	1.79	0.63
1:A:109:LYS:CD	1:A:188:PHE:HE1	2.13	0.62
1:A:125:MET:HE3	1:A:147:MET:HG2	1.80	0.62
1:A:114:ASN:O	1:A:160:TYR:CA	2.49	0.61
1:A:109:LYS:HB2	1:A:175:SER:OG	2.01	0.60
1:B:168:MDO:HB21	1:A:314:TYR:OH	2.02	0.60
1:A:191:ASP:OD1	3:A:706:HOH:O	2.16	0.60
1:A:114:ASN:O	1:A:160:TYR:HA	2.02	0.59
1:A:109:LYS:HB2	1:A:175:SER:CB	2.31	0.59
1:A:109:LYS:NZ	1:A:188:PHE:HZ	1.96	0.59
1:B:224:GLY:HA2	1:B:345:THR:HG22	1.85	0.59
1:A:25:ASN:ND2	1:A:47:LEU:HB2	2.19	0.57
1:A:109:LYS:CD	1:A:188:PHE:CE1	2.87	0.57
1:A:466:ARG:HD2	3:A:722:HOH:O	2.04	0.56
1:A:109:LYS:HG3	1:A:176:TYR:CE1	2.42	0.55
1:A:317:ARG:NH2	2:A:601:HCI:O2	2.40	0.55
1:A:116:LEU:CD2	1:A:121:VAL:HG23	2.37	0.55
1:A:104:LEU:O	1:A:108:LEU:HB2	2.07	0.54
1:B:317:ARG:HH22	2:B:601:HCI:C1	2.21	0.54
1:A:109:LYS:HG3	1:A:176:TYR:CD1	2.43	0.54
1:A:25:ASN:N	3:A:715:HOH:O	2.40	0.54
1:A:146:ARG:NH2	3:A:713:HOH:O	2.39	0.54
1:A:403:PRO:HG2	1:A:489:LEU:HD13	1.89	0.54
1:A:114:ASN:HB3	1:A:161:GLU:OE2	2.07	0.54
1:A:302:HIS:O	1:A:303:ASP:HB3	2.07	0.54
1:A:170:ASP:HB2	1:A:224:GLY:O	2.08	0.54
1:A:308:GLU:OE1	3:A:709:HOH:O	2.19	0.54
1:A:109:LYS:HB2	1:A:175:SER:HB2	1.91	0.53
1:B:314:TYR:OH	1:A:168:MDO:HB21	2.09	0.53
1:B:128:ARG:HD3	1:B:226:SER:OG	2.08	0.53
1:A:192:PHE:O	1:A:195:LYS:HD2	2.09	0.52
1:B:304:TYR:N	3:B:703:HOH:O	2.18	0.52
1:A:109:LYS:HG2	1:A:110:THR:N	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:43:ARG:NH1	1:B:238:ASP:OD1	2.33	0.51
1:A:308:GLU:HG2	1:A:309:LEU:H	1.76	0.51
1:A:40:ARG:NH1	3:A:710:HOH:O	2.39	0.51
1:B:326:ILE:HG23	1:B:378:TYR:HB3	1.92	0.51
1:A:308:GLU:HG2	1:A:309:LEU:HD12	1.93	0.50
1:A:105:VAL:O	1:A:109:LYS:HE3	2.11	0.50
1:B:481:MET:HE1	1:B:542:ILE:HA	1.94	0.50
1:A:35:ILE:HG13	1:A:338:GLU:HG2	1.94	0.49
1:B:104:LEU:HD11	2:A:601:HCI:H3'	1.93	0.49
1:A:185:ASP:O	1:A:188:PHE:HD2	1.94	0.49
1:B:146:ARG:NH2	3:B:712:HOH:O	2.45	0.49
1:A:116:LEU:HD21	1:A:121:VAL:HG22	1.90	0.49
1:A:264:PHE:HA	1:A:269:HIS:HE2	1.77	0.49
1:A:175:SER:HB3	1:A:222:MET:SD	2.53	0.49
1:A:168:MDO:N1	1:A:168:MDO:O3	2.46	0.48
1:B:409:ASN:OD1	1:B:411:GLU:HG2	2.13	0.48
1:A:105:VAL:CG1	1:A:109:LYS:HZ3	2.16	0.48
1:A:524:THR:HG23	1:A:526:ASP:H	1.78	0.48
1:A:109:LYS:HD3	1:A:188:PHE:HE1	1.79	0.47
1:A:279:TRP:HE1	1:A:563:LEU:HD13	1.79	0.47
1:A:116:LEU:HD23	1:A:116:LEU:O	2.14	0.47
1:B:225:THR:HA	1:B:228:MET:HE3	1.96	0.47
1:A:215:PRO:O	1:A:216:LYS:HB3	2.15	0.47
1:A:116:LEU:CD2	1:A:121:VAL:CG2	2.88	0.46
1:A:448:GLU:HB3	1:A:452:GLN:HG3	1.97	0.46
1:B:302:HIS:HD2	1:A:76:PRO:HG2	1.81	0.46
1:B:302:HIS:CD2	1:A:76:PRO:HG2	2.52	0.45
1:B:319:LEU:HB3	1:B:320:PRO:HD3	1.98	0.45
1:A:28:ILE:HD11	1:A:48:VAL:HG13	1.99	0.45
1:A:524:THR:HG22	3:A:733:HOH:O	2.15	0.45
1:A:108:LEU:HA	1:A:108:LEU:HD23	1.78	0.44
1:B:223:ASN:ND2	3:B:711:HOH:O	2.44	0.44
1:A:488:ASP:OD2	1:A:516:ARG:NH1	2.51	0.44
1:A:158:TYR:HE1	1:A:191:ASP:HB2	1.82	0.44
1:A:43:ARG:NH2	1:A:238:ASP:OD2	2.51	0.44
1:A:146:ARG:HD3	1:A:181:LEU:O	2.18	0.43
1:A:539:ASP:OD1	1:A:540:GLU:N	2.52	0.43
1:B:345:THR:HG23	1:B:362:ASN:O	2.18	0.43
1:B:367:TYR:CD2	1:A:325:PRO:HG3	2.53	0.43
1:A:168:MDO:O3	1:A:168:MDO:C1	2.58	0.43
1:A:516:ARG:HA	1:A:519:VAL:HG22	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:215:PRO:O	1:B:216:LYS:HB3	2.18	0.43
1:B:225:THR:H	1:B:345:THR:HG21	1.83	0.43
1:B:411:GLU:OE2	3:B:704:HOH:O	2.21	0.42
1:A:301:LYS:N	1:A:301:LYS:HD3	2.34	0.42
1:A:306:ASP:HB3	1:A:310:ILE:HD11	2.00	0.42
1:A:225:THR:HA	1:A:228:MET:HE3	2.01	0.42
1:B:128:ARG:HD2	1:B:128:ARG:HA	1.69	0.42
1:B:140:ARG:NH2	1:B:212:THR:O	2.53	0.41
1:A:108:LEU:C	1:A:109:LYS:O	2.58	0.41
1:A:109:LYS:HD3	1:A:176:TYR:HA	2.02	0.41
1:A:395:SER:HA	1:A:396:PRO:HD3	1.90	0.41
1:A:421:LEU:HG	1:A:478:ILE:HG23	2.02	0.41
1:B:28:ILE:HG22	1:B:133:MET:HG3	2.03	0.41
1:B:481:MET:HE2	1:B:545:ILE:HD12	2.01	0.41
1:B:225:THR:HG23	1:B:345:THR:HG21	2.03	0.41
1:A:28:ILE:HB	3:A:704:HOH:O	2.19	0.41
1:B:481:MET:HE3	1:B:542:ILE:HG12	2.02	0.41
1:B:322:TYR:CE2	1:B:385:HIS:HB2	2.56	0.40
1:B:260:THR:HB	1:B:295:ARG:NH1	2.37	0.40
1:A:109:LYS:NZ	1:A:188:PHE:CZ	2.64	0.40
1:A:306:ASP:OD1	1:A:307:HIS:N	2.53	0.40
1:B:101:GLN:O	1:B:104:LEU:HB3	2.20	0.40
1:B:364:LEU:HD22	1:A:318:CYS:HB3	2.04	0.40
1:A:25:ASN:HD22	1:A:25:ASN:HA	1.58	0.40
1:A:172:VAL:HB	1:A:173:PRO:HD3	2.03	0.40

All (2) 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:845:HOH:O	3:A:861:HOH:O[5_455]	1.90	0.30
3:B:810:HOH:O	3:B:853:HOH:O[7_465]	2.12	0.08

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	532/537 (99%)	510 (96%)	17 (3%)	5 (1%)	17 24
1	B	532/537 (99%)	519 (98%)	12 (2%)	1 (0%)	47 61
All	All	1064/1074 (99%)	1029 (97%)	29 (3%)	6 (1%)	25 35

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	114	ASN
1	A	109	LYS
1	A	308	GLU
1	A	306	ASP
1	A	562	ILE
1	B	562	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	443/443 (100%)	432 (98%)	11 (2%)	47 66
1	B	443/443 (100%)	435 (98%)	8 (2%)	59 75
All	All	886/886 (100%)	867 (98%)	19 (2%)	53 71

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	134	ARG
1	B	192	PHE
1	B	284	MET
1	B	311	GLN
1	B	335	LYS
1	B	429	MET
1	B	485	GLN

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Mol	Chain	Res	Type
1	B	563	LEU
1	A	63	SER
1	A	105	VAL
1	A	115	LYS
1	A	116	LEU
1	A	192	PHE
1	A	303	ASP
1	A	309	LEU
1	A	317	ARG
1	A	410	ARG
1	A	524	THR
1	A	534	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	132	HIS
1	A	25	ASN
1	A	96	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)

2 non-standard protein/DNA/RNA residues 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	$\#\|Z\| > 2$
1	MDO	A	168	1	12,13,14	2.82	4 (33%)	15,18,20	6.21	10 (66%)
1	MDO	B	168	1	12,13,14	2.66	4 (33%)	15,18,20	3.41	6 (40%)

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
1	MDO	A	168	1	-	2/4/23/24	0/1/1/1
1	MDO	B	168	1	-	0/4/23/24	0/1/1/1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	168	MDO	C1-N3	6.28	1.47	1.37
1	B	168	MDO	C1-N2	5.54	1.40	1.32
1	A	168	MDO	C1-N2	5.01	1.39	1.32
1	A	168	MDO	CA2-C2	4.48	1.52	1.43
1	B	168	MDO	CA2-C2	4.16	1.51	1.43
1	B	168	MDO	C1-N3	3.84	1.43	1.37
1	B	168	MDO	CA3-N3	-3.12	1.41	1.47
1	A	168	MDO	CA1-N1	-2.07	1.41	1.48

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	168	MDO	O3-C3-CA3	-13.87	84.51	126.39
1	A	168	MDO	CA2-C2-N3	11.73	108.92	103.37
1	A	168	MDO	CA3-N3-C1	8.66	137.56	127.16
1	B	168	MDO	CA2-C2-N3	8.18	107.24	103.37
1	A	168	MDO	C2-N3-C1	-8.11	103.86	107.97
1	A	168	MDO	O2-C2-CA2	-6.35	127.39	130.96
1	B	168	MDO	O2-C2-CA2	-6.01	127.59	130.96
1	B	168	MDO	CA2-N2-C1	5.23	110.13	105.40
1	A	168	MDO	CA2-N2-C1	4.44	109.42	105.40
1	B	168	MDO	C2-CA2-N2	-4.09	106.07	108.93
1	A	168	MDO	C2-CA2-N2	-3.80	106.27	108.93
1	A	168	MDO	CA1-C1-N2	-3.41	119.70	124.05
1	A	168	MDO	CA1-C1-N3	3.36	128.78	124.75
1	B	168	MDO	C2-N3-C1	-3.02	106.44	107.97
1	B	168	MDO	O3-C3-CA3	2.50	133.95	126.39
1	A	168	MDO	CA3-N3-C2	-2.29	118.55	123.80

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	168	MDO	N2-C1-CA1-CB
1	A	168	MDO	N3-C1-CA1-CB

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	168	MDO	3	0
1	B	168	MDO	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

2 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	HCI	A	601	-	11,11,11	0.59	0	13,13,13	1.09	1 (7%)
2	HCI	B	601	-	11,11,11	0.59	0	13,13,13	1.25	1 (7%)

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	HCI	A	601	-	-	3/5/5/5	0/1/1/1
2	HCI	B	601	-	-	4/5/5/5	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	601	HCI	O2-C1-C2	2.60	122.38	114.03
2	A	601	HCI	O2-C1-C2	2.40	121.73	114.03

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	601	HCI	C6'-C1'-C3-C2
2	B	601	HCI	C2'-C1'-C3-C2
2	A	601	HCI	C6'-C1'-C3-C2
2	A	601	HCI	C2'-C1'-C3-C2
2	B	601	HCI	O1-C1-C2-C3
2	B	601	HCI	O2-C1-C2-C3
2	A	601	HCI	O2-C1-C2-C3

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	HCI	3	0
2	B	601	HCI	2	0

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, 95^{th} 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	536/537 (99%)	-0.33	22 (4%)	37	35	15, 24, 45, 114	0
1	B	536/537 (99%)	-0.47	12 (2%)	62	59	14, 24, 42, 69	0
All	All	1072/1074 (99%)	-0.40	34 (3%)	47	45	14, 24, 43, 114	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	306	ASP	10.5
1	A	302	HIS	10.2
1	A	303	ASP	8.2
1	A	305	ARG	8.2
1	A	307	HIS	8.1
1	B	307	HIS	5.3
1	A	308	GLU	5.1
1	A	110	THR	5.0
1	A	301	LYS	4.8
1	A	299	ASP	4.4
1	A	109	LYS	4.3
1	A	300	GLY	4.2
1	A	114	ASN	4.1
1	A	304	TYR	3.8
1	A	561	ASP	2.9
1	A	54	THR	2.9
1	B	561	ASP	2.8
1	A	195	LYS	2.8
1	B	54	THR	2.6
1	A	25	ASN	2.5
1	A	52	ASN	2.5
1	B	55	ASP	2.5
1	B	195	LYS	2.4
1	B	353	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	53	ASN	2.3
1	A	560	GLN	2.3
1	B	52	ASN	2.3
1	A	58	GLN	2.2
1	B	31	GLN	2.2
1	B	560	GLN	2.1
1	A	31	GLN	2.1
1	B	30	ASN	2.1
1	B	522	LYS	2.1
1	A	30	ASN	2.1

6.2 Non-standard residues in protein, DNA, RNA chains (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, 95^{th} 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(Å^2)	Q<0.9
1	MDO	A	168	13/14	0.94	0.15	17,21,26,30	0
1	MDO	B	168	13/14	0.96	0.13	17,22,28,29	0

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, 95^{th} 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(Å^2)	Q<0.9
2	HCI	B	601	11/11	0.93	0.14	20,23,27,30	0
2	HCI	A	601	11/11	0.98	0.11	18,20,28,32	0

6.5 Other polymers (i)

There are no such residues in this entry.