Full wwPDB X-ray Structure Validation Report (i)

Aug 6, 2023 – 09:26 AM EDT

PDB ID	:	1KAH
Title	:	L-HISTIDINOL DEHYDROGENASE (HISD) STRUCTURE COMPLEXED WITH L-HISTIDINE (PRODUCT), ZN AND NAD (COFACTOR)
Authors	:	Barbosa, J.A.R.G.; Sivaraman, J.; Li, Y.; Larocque, R.; Matte, A.; Schrag, J.D.; Cygler, M.
Deposited on	:	2001-11-02
Resolution	:	2.10 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 (i) 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 (i)) were used in the production of this report:

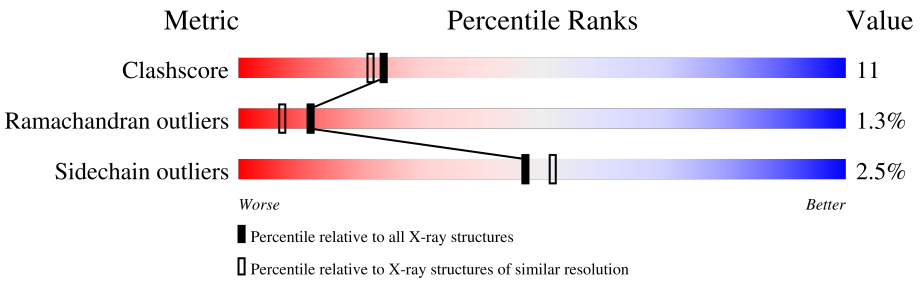
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 2.10 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	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)

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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	434	77% 20% • •
1	B	434	75% 23% •

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 6456 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 Histidinol dehydrogenase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	431	3210	2000	559	638	7	6	0	0	0
1	B	434	3222	2006	562	641	7	6	0	0	0

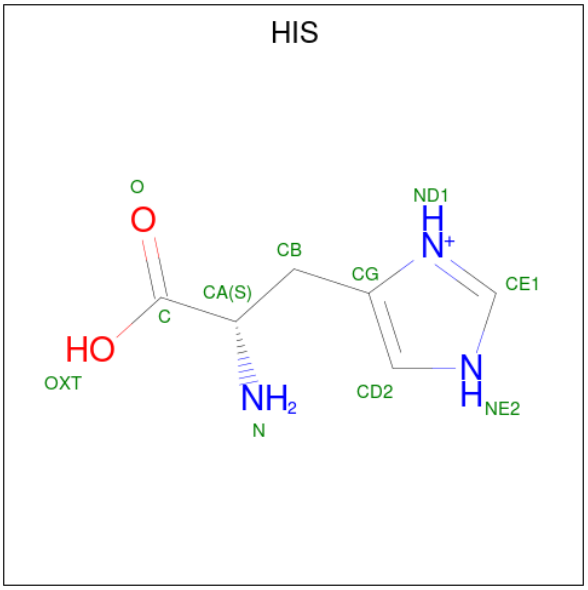
There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	modified residue	UNP P06988
A	15	GLU	VAL	SEE REMARK 999	UNP P06988
A	22	MSE	MET	modified residue	UNP P06988
A	88	MSE	MET	modified residue	UNP P06988
A	144	MSE	MET	modified residue	UNP P06988
A	150	SER	ARG	SEE REMARK 999	UNP P06988
A	232	MSE	MET	modified residue	UNP P06988
A	277	MSE	MET	modified residue	UNP P06988
A	313	LEU	SER	SEE REMARK 999	UNP P06988
A	390	MSE	MET	modified residue	UNP P06988
A	403	LEU	VAL	SEE REMARK 999	UNP P06988
B	1	MSE	MET	modified residue	UNP P06988
B	15	GLU	VAL	SEE REMARK 999	UNP P06988
B	22	MSE	MET	modified residue	UNP P06988
B	88	MSE	MET	modified residue	UNP P06988
B	144	MSE	MET	modified residue	UNP P06988
B	150	SER	ARG	SEE REMARK 999	UNP P06988
B	232	MSE	MET	modified residue	UNP P06988
B	277	MSE	MET	modified residue	UNP P06988
B	313	LEU	SER	SEE REMARK 999	UNP P06988
B	390	MSE	MET	modified residue	UNP P06988
B	403	LEU	VAL	SEE REMARK 999	UNP P06988

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Zn 1 1	0	0
2	B	1	Total Zn 1 1	0	0

- Molecule 3 is HISTIDINE (three-letter code: HIS) (formula: $C_6H_{10}N_3O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 11 6 3 2	0	0
3	A	1	Total C N O 11 6 3 2	5	0

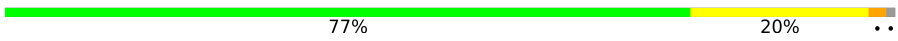
3 Residue-property plots (i)

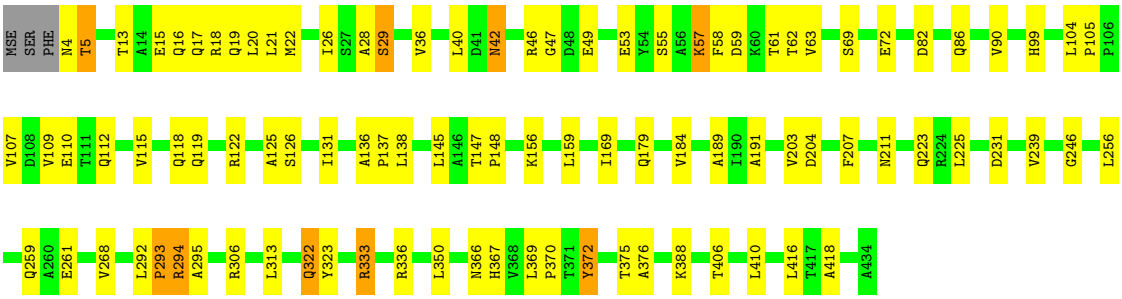
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

• Molecule 1: Histidinol dehydrogenase

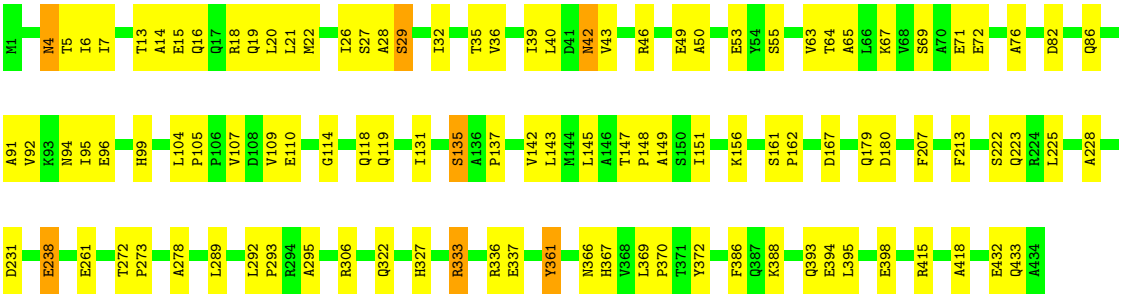
Chain A:





• Molecule 1: Histidinol dehydrogenase

Chain B:



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	55.26Å 109.09Å 157.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.12 – 2.10	Depositor
% Data completeness (in resolution range)	90.5 (38.12-2.10)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.252 , 0.286	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6456	wwPDB-VP
Average B, all atoms ($Å^2$)	36.0	wwPDB-VP

5 Model quality (i)

5.1 Standard geometry (i)

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

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	0.34	0/3252	0.60	0/4416
1	B	0.35	0/3264	0.60	1/4431 (0.0%)
All	All	0.34	0/6516	0.60	1/8847 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	361	TYR	N-CA-C	5.12	124.82	111.00

There are no chirality outliers.

There are no planarity outliers.

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	3210	0	3228	85	0
1	B	3222	0	3234	84	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	22	0	12	0	0
All	All	6456	0	6474	143	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 (143) 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:26:ILE:HD11	1:B:225:LEU:HD22	1.40	1.02
1:A:136:ALA:HB2	1:B:415:ARG:HE	1.32	0.94
1:A:112:GLN:HE21	1:B:94:ASN:HD21	1.16	0.92
1:A:336:ARG:HH12	1:B:118:GLN:NE2	1.68	0.89
1:A:336:ARG:HH12	1:B:118:GLN:HE22	1.21	0.87
1:A:118:GLN:HE22	1:B:336:ARG:HH22	1.23	0.87
1:A:225:LEU:HD11	1:B:26:ILE:HG12	1.56	0.87
1:A:112:GLN:NE2	1:B:94:ASN:HD21	1.75	0.84
1:B:42:ASN:HD21	1:B:46:ARG:HH11	1.28	0.79
1:B:5:THR:O	1:B:6:ILE:HD13	1.83	0.77
1:A:336:ARG:NH1	1:B:118:GLN:HE22	1.83	0.76
1:B:13:THR:OG1	1:B:16:GLN:HG3	1.91	0.71
1:B:69:SER:OG	1:B:72:GLU:HG3	1.92	0.70
1:A:40:LEU:CD2	1:A:191:ALA:HB2	2.22	0.69
1:A:26:ILE:HD12	1:A:26:ILE:N	2.08	0.68
1:A:376:ALA:O	1:B:388:LYS:HD3	1.93	0.68
1:B:21:LEU:HD13	1:B:322:GLN:HG2	1.75	0.68
1:A:18:ARG:O	1:A:22:MSE:HG2	1.95	0.67
1:B:333:ARG:HG2	1:B:333:ARG:HH11	1.59	0.67
1:B:6:ILE:HD12	1:B:278:ALA:HB1	1.78	0.66
1:A:105:PRO:HG3	1:B:105:PRO:HG2	1.78	0.66
1:B:29:SER:HB3	1:B:32:ILE:HG22	1.79	0.65
1:A:40:LEU:HD22	1:A:191:ALA:HB2	1.78	0.64
1:A:69:SER:OG	1:A:72:GLU:HG3	1.97	0.64
1:A:104:LEU:HD22	1:B:104:LEU:HD22	1.80	0.63
1:A:57:LYS:NZ	1:A:57:LYS:HB2	2.13	0.63
1:A:118:GLN:HE22	1:B:336:ARG:NH2	1.93	0.62
1:A:49:GLU:O	1:A:53:GLU:HG3	2.00	0.61
1:A:125:ALA:HB3	1:A:204:ASP:OD2	2.01	0.60
1:A:21:LEU:HD23	1:A:323:TYR:HB2	1.83	0.60
1:B:49:GLU:O	1:B:53:GLU:HG3	2.02	0.59
1:A:82:ASP:HB3	1:A:86:GLN:NE2	2.18	0.59
1:A:104:LEU:CD2	1:B:104:LEU:HD22	2.33	0.59
1:A:292:LEU:HB2	1:A:295:ALA:HB2	1.86	0.58
1:A:13:THR:O	1:A:17:GLN:HG3	2.03	0.57
1:A:42:ASN:HD21	1:A:46:ARG:NE	2.02	0.57
1:B:135:SER:O	1:B:137:PRO:HD3	2.05	0.57
1:B:36:VAL:O	1:B:40:LEU:HD13	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:13:THR:HG23	1:A:16:GLN:OE1	2.06	0.56
1:A:156:LYS:HA	1:A:179:GLN:OE1	2.07	0.55
1:B:29:SER:CB	1:B:32:ILE:HG22	2.37	0.54
1:B:107:VAL:HB	1:B:119:GLN:HB3	1.90	0.54
1:B:147:THR:HB	1:B:148:PRO:HD3	1.88	0.54
1:A:416:LEU:HD12	1:B:361:TYR:OH	2.07	0.54
1:B:333:ARG:HH11	1:B:333:ARG:CG	2.20	0.53
1:B:99:HIS:CE1	1:B:366:ASN:HD22	2.27	0.53
1:A:20:LEU:O	1:A:306:ARG:HD3	2.09	0.53
1:B:19:GLN:HA	1:B:22:MSE:CE	2.38	0.53
1:A:293:PRO:HG2	1:A:294:ARG:H	1.73	0.52
1:A:136:ALA:HB2	1:B:415:ARG:NE	2.14	0.52
1:A:370:PRO:HG2	1:A:375:THR:HG22	1.92	0.52
1:B:46:ARG:HH22	1:B:53:GLU:CD	2.12	0.52
1:A:58:PHE:O	1:A:59:ASP:HB3	2.10	0.52
1:B:82:ASP:HB3	1:B:86:GLN:NE2	2.26	0.51
1:B:292:LEU:HB2	1:B:295:ALA:HB2	1.92	0.51
1:A:59:ASP:OD2	1:A:61:THR:HB	2.11	0.51
1:A:207:PHE:CD2	1:A:231:ASP:HB3	2.46	0.51
1:A:292:LEU:CB	1:A:295:ALA:HB2	2.41	0.51
1:A:322:GLN:HE21	1:A:322:GLN:HA	1.76	0.51
1:A:99:HIS:CE1	1:A:366:ASN:HD22	2.29	0.50
1:A:42:ASN:HD21	1:A:46:ARG:CZ	2.24	0.50
1:A:40:LEU:HD23	1:A:191:ALA:HB2	1.93	0.50
1:A:55:SER:HB2	1:A:61:THR:HG23	1.93	0.50
1:A:4:ASN:OD1	1:A:5:THR:N	2.47	0.48
1:A:61:THR:O	1:A:62:THR:C	2.51	0.48
1:A:137:PRO:HB2	1:A:169:ILE:HD11	1.95	0.48
1:A:36:VAL:O	1:A:40:LEU:HG	2.14	0.48
1:B:39:ILE:O	1:B:43:VAL:HG23	2.13	0.48
1:B:32:ILE:HG13	1:B:213:PHE:CE2	2.49	0.48
1:A:26:ILE:HD11	1:B:225:LEU:CD2	2.28	0.47
1:A:261:GLU:CD	1:B:418:ALA:HB3	2.34	0.47
1:B:145:LEU:O	1:B:148:PRO:HD2	2.14	0.47
1:B:91:ALA:O	1:B:95:ILE:HG13	2.15	0.47
1:A:82:ASP:HB3	1:A:86:GLN:HE22	1.79	0.47
1:B:109:VAL:HG22	1:B:110:GLU:N	2.29	0.47
1:A:147:THR:HB	1:A:148:PRO:HD3	1.97	0.47
1:B:432:GLU:OE2	1:B:433:GLN:N	2.48	0.47
1:B:149:ALA:HB2	1:B:386:PHE:CE2	2.50	0.46
1:B:20:LEU:O	1:B:306:ARG:NH2	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:395:LEU:HD12	1:B:395:LEU:N	2.31	0.46
1:A:109:VAL:HG22	1:A:110:GLU:N	2.29	0.46
1:B:55:SER:OG	1:B:63:VAL:HG12	2.15	0.46
1:B:131:ILE:HG13	1:B:142:VAL:HG22	1.97	0.46
1:B:398:GLU:H	1:B:398:GLU:CD	2.19	0.46
1:A:57:LYS:HB2	1:A:57:LYS:HZ2	1.80	0.46
1:B:14:ALA:O	1:B:18:ARG:HG3	2.16	0.45
1:B:289:LEU:HD11	1:B:295:ALA:HB1	1.98	0.45
1:A:28:ALA:O	1:A:29:SER:C	2.55	0.45
1:B:19:GLN:HA	1:B:22:MSE:HE3	1.97	0.45
1:A:372:TYR:CZ	1:B:225:LEU:HD21	2.51	0.45
1:B:29:SER:HB3	1:B:32:ILE:CG2	2.46	0.45
1:A:369:LEU:HB3	1:A:370:PRO:HD2	1.99	0.44
1:B:76:ALA:HB1	1:B:167:ASP:HA	1.99	0.44
1:B:35:THR:O	1:B:39:ILE:HG13	2.18	0.44
1:A:112:GLN:HE21	1:B:94:ASN:ND2	1.99	0.44
1:B:6:ILE:HG22	1:B:7:ILE:N	2.32	0.44
1:A:256:LEU:HD22	1:A:268:VAL:CG1	2.47	0.44
1:B:156:LYS:HA	1:B:179:GLN:OE1	2.18	0.44
1:A:118:GLN:NE2	1:B:336:ARG:HH22	2.03	0.44
1:B:15:GLU:O	1:B:19:GLN:HG3	2.17	0.43
1:B:19:GLN:HA	1:B:22:MSE:HE2	2.00	0.43
1:B:92:VAL:CG2	1:B:143:LEU:HD22	2.48	0.43
1:B:5:THR:O	1:B:6:ILE:CD1	2.60	0.43
1:B:67:LYS:NZ	1:B:180:ASP:OD1	2.45	0.43
1:B:207:PHE:CD2	1:B:231:ASP:HB3	2.53	0.43
1:A:104:LEU:HD22	1:B:104:LEU:CD2	2.47	0.43
1:B:114:GLY:O	1:B:395:LEU:HA	2.18	0.43
1:A:122:ARG:HB2	1:A:388:LYS:HE3	1.99	0.43
1:A:350:LEU:HB2	1:B:394:GLU:HB2	2.00	0.43
1:A:16:GLN:O	1:A:20:LEU:HG	2.19	0.42
1:A:225:LEU:HD13	1:B:372:TYR:OH	2.19	0.42
1:A:246:GLY:HA3	1:A:333:ARG:HD3	2.00	0.42
1:A:107:VAL:HB	1:A:119:GLN:HB3	2.01	0.42
1:B:55:SER:CB	1:B:63:VAL:HG12	2.49	0.42
1:A:126:SER:CB	1:A:156:LYS:HB3	2.49	0.42
1:A:223:GLN:NE2	1:B:223:GLN:NE2	2.67	0.42
1:B:333:ARG:CG	1:B:333:ARG:NH1	2.80	0.42
1:A:110:GLU:HA	1:A:115:VAL:O	2.19	0.42
1:A:55:SER:HB3	1:A:63:VAL:HG12	2.02	0.42
1:B:238:GLU:O	1:B:327:HIS:HD2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:239:VAL:HB	1:A:259:GLN:HG2	2.02	0.42
1:B:161:SER:HA	1:B:162:PRO:HD3	1.92	0.42
1:B:272:THR:HA	1:B:273:PRO:HD3	1.91	0.41
1:A:406:THR:O	1:A:410:LEU:HG	2.20	0.41
1:A:86:GLN:O	1:A:90:VAL:HG23	2.20	0.41
1:A:184:VAL:HG22	1:A:189:ALA:HB2	2.02	0.41
1:B:4:ASN:HD22	1:B:4:ASN:HA	1.61	0.41
1:A:145:LEU:O	1:A:148:PRO:HD2	2.21	0.41
1:A:246:GLY:HA3	1:A:333:ARG:CD	2.51	0.41
1:B:46:ARG:HB2	1:B:50:ALA:HB2	2.03	0.41
1:A:138:LEU:HD12	1:A:138:LEU:N	2.36	0.41
1:A:418:ALA:HB3	1:B:261:GLU:CD	2.41	0.41
1:B:96:GLU:HG3	1:B:151:ILE:HD11	2.03	0.41
1:B:222:SER:HA	1:B:228:ALA:O	2.20	0.41
1:A:57:LYS:HB2	1:A:57:LYS:HZ3	1.87	0.40
1:A:57:LYS:HG2	1:A:58:PHE:N	2.35	0.40
1:A:49:GLU:HG2	1:A:53:GLU:OE2	2.22	0.40
1:A:55:SER:CB	1:A:63:VAL:HG12	2.52	0.40
1:A:126:SER:OG	1:A:203:VAL:HA	2.22	0.40
1:B:64:THR:OG1	1:B:65:ALA:N	2.52	0.40
1:B:369:LEU:HB3	1:B:370:PRO:HD2	2.03	0.40
1:A:109:VAL:CG2	1:A:110:GLU:N	2.85	0.40
1:A:131:ILE:HG13	1:A:159:LEU:HD11	2.03	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	429/434 (99%)	399 (93%)	24 (6%)	6 (1%)	11 6
1	B	432/434 (100%)	404 (94%)	23 (5%)	5 (1%)	13 8

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	861/868 (99%)	803 (93%)	47 (6%)	11 (1%)	12 7

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	5	THR
1	A	47	GLY
1	B	27	SER
1	B	29	SER
1	B	28	ALA
1	B	135	SER
1	A	29	SER
1	A	57	LYS
1	A	211	ASN
1	B	293	PRO
1	A	293	PRO

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	344/340 (101%)	335 (97%)	9 (3%)	46 50
1	B	344/340 (101%)	336 (98%)	8 (2%)	50 55
All	All	688/680 (101%)	671 (98%)	17 (2%)	47 52

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	GLU
1	A	19	GLN
1	A	42	ASN
1	A	294	ARG
1	A	313	LEU
1	A	322	GLN
1	A	333	ARG

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Mol	Chain	Res	Type
1	A	367	HIS
1	A	372	TYR
1	B	4	ASN
1	B	42	ASN
1	B	71	GLU
1	B	238	GLU
1	B	333	ARG
1	B	337	GLU
1	B	367	HIS
1	B	393	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	GLN
1	A	42	ASN
1	A	86	GLN
1	A	99	HIS
1	A	112	GLN
1	A	118	GLN
1	A	119	GLN
1	A	223	GLN
1	A	322	GLN
1	A	387	GLN
1	B	4	ASN
1	B	42	ASN
1	B	86	GLN
1	B	99	HIS
1	B	118	GLN
1	B	119	GLN
1	B	188	GLN
1	B	223	GLN
1	B	327	HIS
1	B	433	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)

Of 4 ligands modelled in this entry, 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	$\#\|Z\| > 2$
3	HIS	A	503	2	6,11,11	0.85	0	7,14,14	1.12	1 (14%)
3	HIS	A	502	2	6,11,11	0.84	0	7,14,14	1.12	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
3	HIS	A	503	2	-	2/8/8/8	0/1/1/1
3	HIS	A	502	2	-	2/8/8/8	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	503	HIS	CD2-NE2-CE1	2.06	108.99	105.78

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	502	HIS	OXT-C-CA-N
3	A	502	HIS	O-C-CA-N
3	A	503	HIS	O-C-CA-CB
3	A	503	HIS	OXT-C-CA-CB

There are no ring outliers.

No monomer is involved in short contacts.

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 (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.