Full wwPDB X-ray Structure Validation Report ⓘ

Oct 11, 2021 – 03:42 PM EDT

PDB ID	:	2HDK
Title	:	Crystal Structure of Cys315Ala-Cys318Ala Mutant of Human Mitochondrial Branched Chain Aminotransferase
Authors	:	Yennawar, N.H.; Hutson, S.M.
Deposited on	:	2006-06-20
Resolution	:	2.40 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:

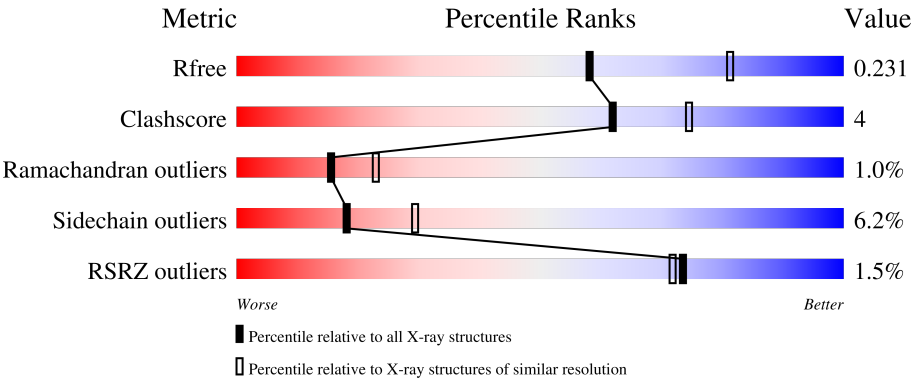
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

1 Overall quality at a glance (i)

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

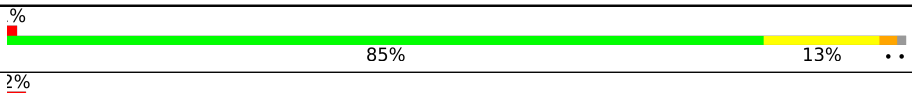
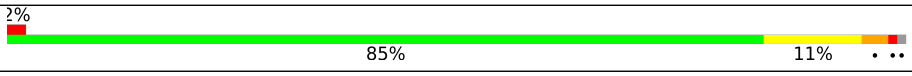
The reported resolution of this entry is 2.40 Å.

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}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (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 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	365	
1	B	365	

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
3	ACY	A	1001	-	-	-	X

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 5979 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.

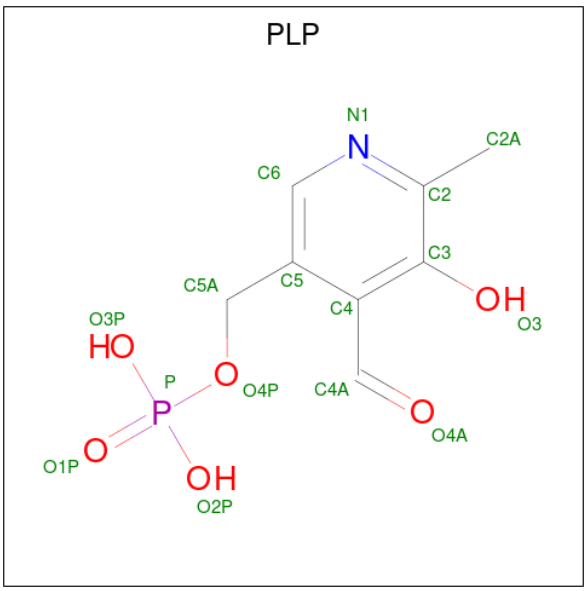
- Molecule 1 is a protein called Branched-chain-amino-acid aminotransferase, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	363	Total	C	N	O	S	0	0	0
			2897	1869	505	507	16			
1	B	363	Total	C	N	O	S	0	0	0
			2897	1869	505	507	16			

There are 6 discrepancies between the modelled and reference sequences:

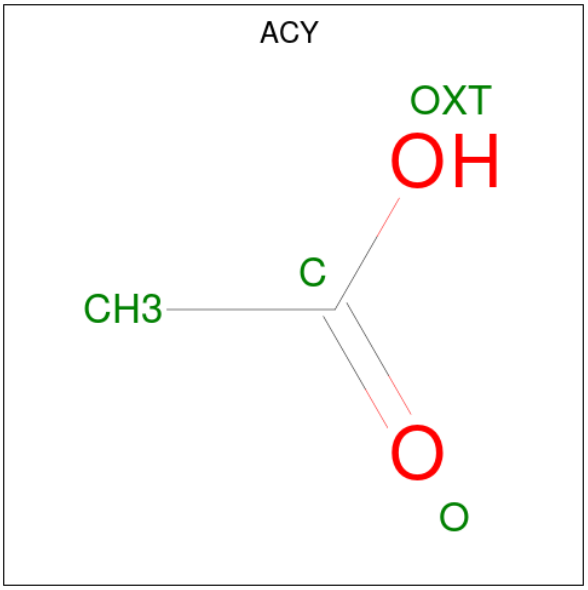
Chain	Residue	Modelled	Actual	Comment	Reference
A	159	ARG	THR	conflict	UNP O15382
A	315	ALA	CYS	engineered mutation	UNP O15382
A	318	ALA	CYS	engineered mutation	UNP O15382
B	659	ARG	THR	conflict	UNP O15382
B	815	ALA	CYS	engineered mutation	UNP O15382
B	818	ALA	CYS	engineered mutation	UNP O15382

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: $C_8H_{10}NO_6P$).



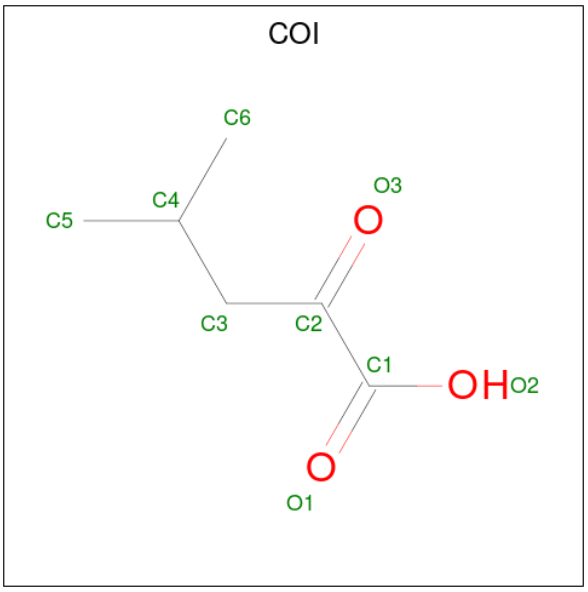
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	B	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

- Molecule 3 is ACETIC ACID (three-letter code: ACY) (formula: $C_2H_4O_2$).



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

- Molecule 4 is 2-OXO-4-METHYLPENTANOIC ACID (three-letter code: COI) (formula: $C_6H_{10}O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C O 9 6 3	0	0

- Molecule 5 is water.

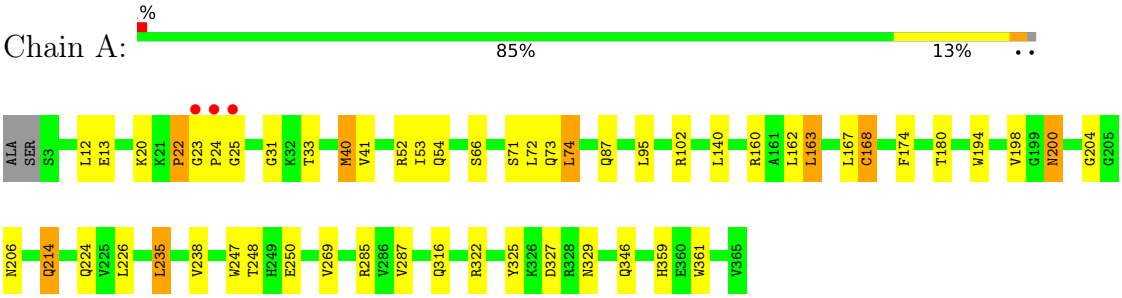
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	74	Total O 74 74	0	0
5	B	68	Total O 68 68	0	0

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.

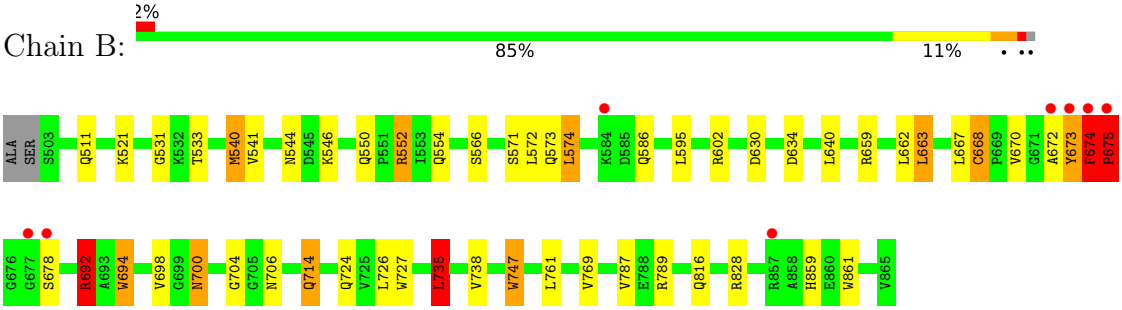
• Molecule 1: Branched-chain-amino-acid aminotransferase, mitochondrial

Chain A:



• Molecule 1: Branched-chain-amino-acid aminotransferase, mitochondrial

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	59.48Å 112.19Å 60.27Å 90.00° 96.16° 90.00°	Depositor
Resolution (Å)	25.00 – 2.40 32.57 – 2.40	Depositor EDS
% Data completeness (in resolution range)	87.2 (25.00-2.40) 87.7 (32.57-2.40)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.88 (at 2.42Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.182 , 0.237 0.177 , 0.231	Depositor DCC
R_{free} test set	1850 reflections (6.90%)	wwPDB-VP
Wilson B-factor (Å^2)	30.0	Xtriage
Anisotropy	0.426	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 36.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.027 for l,-k,h	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	5979	wwPDB-VP
Average B, all atoms (Å^2)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.35% 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: PLP, COI, ACY

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	0.97	1/2974 (0.0%)	0.93	6/4036 (0.1%)
1	B	0.98	4/2974 (0.1%)	1.04	10/4036 (0.2%)
All	All	0.97	5/5948 (0.1%)	0.98	16/8072 (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	A	0	1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	168	CYS	CB-SG	-7.73	1.69	1.82
1	B	694	TRP	CB-CG	6.62	1.62	1.50
1	B	668	CYS	CB-SG	-6.37	1.71	1.82
1	B	673	TYR	CD1-CE1	5.06	1.47	1.39
1	B	747	TRP	CB-CG	5.00	1.59	1.50

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	692	ARG	NE-CZ-NH2	-11.03	114.78	120.30
1	B	692	ARG	NE-CZ-NH1	9.54	125.07	120.30
1	B	674	PHE	N-CA-C	-8.56	87.89	111.00
1	B	574	LEU	CA-CB-CG	7.22	131.92	115.30
1	A	74	LEU	CA-CB-CG	7.21	131.88	115.30
1	B	789	ARG	NE-CZ-NH2	-6.36	117.12	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	163	LEU	CA-CB-CG	6.20	129.56	115.30
1	B	789	ARG	NE-CZ-NH1	6.15	123.37	120.30
1	B	663	LEU	CA-CB-CG	5.83	128.71	115.30
1	A	160	ARG	NE-CZ-NH1	5.78	123.19	120.30
1	A	53	ILE	N-CA-C	-5.71	95.58	111.00
1	B	673	TYR	N-CA-C	5.15	124.91	111.00
1	B	675	PRO	N-CA-C	5.15	125.49	112.10
1	B	735	LEU	CA-CB-CG	5.13	127.11	115.30
1	A	248	THR	N-CA-C	-5.12	97.17	111.00
1	A	285	ARG	NE-CZ-NH1	5.08	122.84	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	325	TYR	Sidechain

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	2897	0	2925	27	0
1	B	2897	0	2925	30	0
2	A	15	0	6	0	0
2	B	15	0	6	0	0
3	A	4	0	3	0	0
4	B	9	0	9	0	0
5	A	74	0	0	1	0
5	B	68	0	0	2	0
All	All	5979	0	5874	52	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 4.

All (52) 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:B:700:ASN:HD22	1:B:700:ASN:H	1.10	0.99
1:A:200:ASN:H	1:A:200:ASN:HD22	1.08	0.94
1:A:52:ARG:HH11	1:A:54:GLN:NE2	1.80	0.79
1:A:224:GLN:NE2	5:A:1041:HOH:O	2.22	0.71
1:B:552:ARG:HH11	1:B:554:GLN:NE2	1.89	0.71
1:A:71:SER:H	1:B:573:GLN:HE22	1.40	0.70
1:A:200:ASN:HD22	1:A:200:ASN:N	1.86	0.69
1:B:692:ARG:NH2	5:B:77:HOH:O	2.27	0.67
1:B:724:GLN:NE2	5:B:48:HOH:O	2.25	0.67
1:A:33:THR:O	1:A:168:CYS:HB2	1.94	0.67
1:B:700:ASN:H	1:B:700:ASN:ND2	1.90	0.66
1:A:52:ARG:HH11	1:A:54:GLN:HE22	1.42	0.65
1:B:533:THR:O	1:B:668:CYS:HB2	1.98	0.64
1:A:73:GLN:HE22	1:B:571:SER:H	1.47	0.62
1:A:359:HIS:HD2	1:A:361:TRP:H	1.47	0.62
1:A:200:ASN:H	1:A:200:ASN:ND2	1.89	0.60
1:A:73:GLN:HE21	1:A:204:GLY:HA3	1.67	0.58
1:A:40:MET:SD	1:A:162:LEU:HD11	2.46	0.55
1:B:573:GLN:HE21	1:B:704:GLY:HA3	1.71	0.55
1:B:700:ASN:HD22	1:B:700:ASN:N	1.90	0.53
1:A:23:GLY:HA2	1:A:25:GLY:H	1.74	0.53
1:A:226:LEU:HD21	1:A:235:LEU:HD13	1.90	0.53
1:A:95:LEU:HD12	1:A:269:VAL:HG13	1.90	0.52
1:B:698:VAL:HG23	1:B:706:ASN:HD21	1.74	0.51
1:B:521:LYS:NZ	1:B:630:ASP:HB2	2.26	0.51
1:A:52:ARG:HD2	1:A:54:GLN:HE21	1.76	0.51
1:B:552:ARG:HH11	1:B:554:GLN:HE22	1.59	0.51
1:A:198:VAL:HG23	1:A:206:ASN:HD21	1.76	0.50
1:B:595:LEU:HD12	1:B:769:VAL:HG13	1.93	0.49
1:B:511:GLN:HE21	1:B:550:GLN:NE2	2.10	0.49
1:B:566:SER:HB2	1:B:572:LEU:HD12	1.95	0.49
1:B:726:LEU:HD21	1:B:735:LEU:HD13	1.94	0.48
1:B:521:LYS:HZ1	1:B:630:ASP:HB2	1.77	0.48
1:B:859:HIS:HD2	1:B:861:TRP:H	1.62	0.48
1:A:31:GLY:HA2	1:A:168:CYS:SG	2.53	0.47
1:A:140:LEU:HD21	1:A:167:LEU:HD13	1.95	0.47
1:B:670:VAL:HG13	1:B:672:ALA:H	1.78	0.47
1:B:531:GLY:HA2	1:B:668:CYS:SG	2.55	0.47
1:A:66:SER:HB2	1:A:72:LEU:HD12	1.96	0.46
1:A:71:SER:H	1:B:573:GLN:NE2	2.12	0.46
1:B:544:ASN:HA	1:B:659:ARG:O	2.16	0.46
1:A:194:TRP:HB2	1:B:694:TRP:CE3	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:322:ARG:HD2	1:A:329:ASN:OD1	2.18	0.44
1:B:540:MET:SD	1:B:662:LEU:HD11	2.58	0.43
1:B:640:LEU:HD21	1:B:667:LEU:HD13	2.01	0.42
1:A:214:GLN:HE21	1:A:214:GLN:HB3	1.70	0.42
1:B:692:ARG:HB2	1:B:727:TRP:CE3	2.55	0.42
1:A:71:SER:N	1:B:573:GLN:HE22	2.13	0.41
1:B:674:PHE:HD2	1:B:674:PHE:HA	1.78	0.41
1:A:174:PHE:HD2	1:A:180:THR:HG22	1.86	0.41
1:A:23:GLY:CA	1:A:25:GLY:H	2.33	0.41
1:B:714:GLN:HE21	1:B:714:GLN:HB3	1.69	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	361/365 (99%)	344 (95%)	14 (4%)	3 (1%)	19	29
1	B	361/365 (99%)	343 (95%)	14 (4%)	4 (1%)	14	20
All	All	722/730 (99%)	687 (95%)	28 (4%)	7 (1%)	15	23

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	22	PRO
1	B	675	PRO
1	B	678	SER
1	B	673	TYR
1	A	316	GLN
1	B	816	GLN
1	A	24	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	313/314 (100%)	294 (94%)	19 (6%)	18	30
1	B	313/314 (100%)	293 (94%)	20 (6%)	17	28
All	All	626/628 (100%)	587 (94%)	39 (6%)	18	29

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	LEU
1	A	13	GLU
1	A	20	LYS
1	A	22	PRO
1	A	40	MET
1	A	41	VAL
1	A	74	LEU
1	A	87	GLN
1	A	102	ARG
1	A	163	LEU
1	A	200	ASN
1	A	214	GLN
1	A	235	LEU
1	A	238	VAL
1	A	247	TRP
1	A	250	GLU
1	A	287	VAL
1	A	327	ASP
1	A	346	GLN
1	B	540	MET
1	B	541	VAL
1	B	546	LYS
1	B	552	ARG
1	B	574	LEU
1	B	586	GLN
1	B	602	ARG
1	B	634	ASP

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Mol	Chain	Res	Type
1	B	663	LEU
1	B	674	PHE
1	B	675	PRO
1	B	692	ARG
1	B	700	ASN
1	B	714	GLN
1	B	735	LEU
1	B	738	VAL
1	B	747	TRP
1	B	761	LEU
1	B	787	VAL
1	B	828	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	GLN
1	A	73	GLN
1	A	96	ASN
1	A	200	ASN
1	A	206	ASN
1	A	214	GLN
1	A	234	GLN
1	A	242	ASN
1	A	272	GLN
1	A	295	GLN
1	A	359	HIS
1	B	550	GLN
1	B	554	GLN
1	B	573	GLN
1	B	586	GLN
1	B	596	ASN
1	B	700	ASN
1	B	706	ASN
1	B	714	GLN
1	B	724	GLN
1	B	734	GLN
1	B	742	ASN
1	B	795	GLN
1	B	859	HIS

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	PLP	B	401	1	15,15,16	1.45	3 (20%)	20,22,23	1.63	3 (15%)
4	COI	B	900	-	5,8,8	2.17	1 (20%)	6,10,10	0.31	0
2	PLP	A	400	1	15,15,16	1.42	2 (13%)	20,22,23	1.73	5 (25%)
3	ACY	A	1001	-	1,3,3	4.00	1 (100%)	0,3,3	-	-

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	PLP	B	401	1	-	0/6/6/8	0/1/1/1
4	COI	B	900	-	-	2/4/8/8	-
2	PLP	A	400	1	-	0/6/6/8	0/1/1/1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	900	COI	O3-C2	4.57	1.29	1.22
3	A	1001	ACY	CH3-C	4.00	1.53	1.48
2	B	401	PLP	C4A-C4	2.49	1.56	1.51
2	A	400	PLP	C2A-C2	2.36	1.54	1.50
2	B	401	PLP	O3-C3	-2.14	1.32	1.37
2	A	400	PLP	C4A-C4	2.09	1.56	1.51
2	B	401	PLP	P-O3P	-2.04	1.47	1.54

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	400	PLP	O4P-C5A-C5	3.80	116.60	109.35
2	B	401	PLP	O4P-C5A-C5	3.69	116.39	109.35
2	A	400	PLP	O3P-P-O1P	2.86	121.87	110.68
2	A	400	PLP	C6-C5-C4	2.78	120.35	118.16
2	B	401	PLP	O3P-P-O1P	2.71	121.30	110.68
2	B	401	PLP	C6-C5-C4	2.39	120.04	118.16
2	A	400	PLP	C5A-C5-C6	-2.39	115.44	119.37
2	A	400	PLP	O4P-P-O1P	2.15	112.50	106.47

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	900	COI	C2-C3-C4-C5
4	B	900	COI	C2-C3-C4-C6

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

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	363/365 (99%)	-0.56	3 (0%)	86	84	17, 28, 46, 63	0
1	B	363/365 (99%)	-0.55	8 (2%)	62	60	16, 29, 45, 62	0
All	All	726/730 (99%)	-0.56	11 (1%)	73	72	16, 28, 46, 63	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	677	GLY	7.6
1	B	678	SER	5.3
1	A	25	GLY	4.9
1	A	24	PRO	4.8
1	A	23	GLY	4.1
1	B	675	PRO	3.9
1	B	673	TYR	3.8
1	B	672	ALA	2.4
1	B	857	ARG	2.3
1	B	674	PHE	2.1
1	B	584	LYS	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 monosaccharides 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. 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
3	ACY	A	1001	4/4	0.80	0.41	46,47,47,48	0
4	COI	B	900	9/9	0.91	0.26	34,37,38,39	0
2	PLP	A	400	15/16	0.99	0.15	15,18,19,20	0
2	PLP	B	401	15/16	0.99	0.13	17,19,21,23	0

6.5 Other polymers

There are no such residues in this entry.