



Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 01:11 am BST

PDB ID : 3CRK
Title : Crystal structure of the PDHK2-L2 complex.
Authors : Green, T.J.; Popov, K.M.; Luo, M.; Grigorian, A.; Klyuyeva, A.; Tuganova, A.
Deposited on : 2008-04-07
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 : 2.11
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) : 2.11

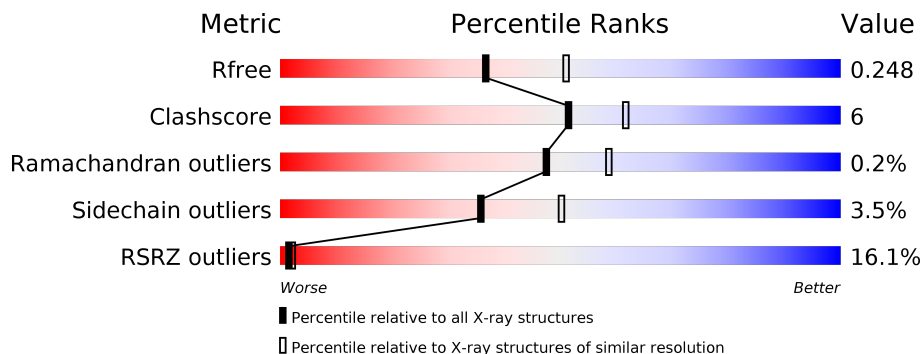
1 Overall quality at a glance

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 on 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	407	 7% (poor fit), 76% (0-1 outliers), 14% (2 outliers), 9% (3+ outliers)
1	B	407	 7% (poor fit), 79% (0-1 outliers), 11% (2 outliers), 9% (3+ outliers)
2	C	87	 62% (poor fit), 77% (0-1 outliers), 22% (2 outliers)
2	D	87	 40% (poor fit), 82% (0-1 outliers), 8% (2 outliers), 10% (3+ outliers)

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7490 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 Pyruvate dehydrogenase [lipoamide] kinase isozyme 2, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	370	2964	1896	489	561	18	0	0	0
1	B	370	2968	1898	489	563	18	0	0	0

- Molecule 2 is a protein called Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	87	680	436	105	133	6	0	0	0
2	D	78	609	390	95	118	6	0	0	0

- Molecule 3 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total K 1 1	0	0
3	A	1	Total K 1 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	130	Total O 130 130	0	0
4	B	124	Total O 124 124	0	0
4	C	8	Total O 8 8	0	0

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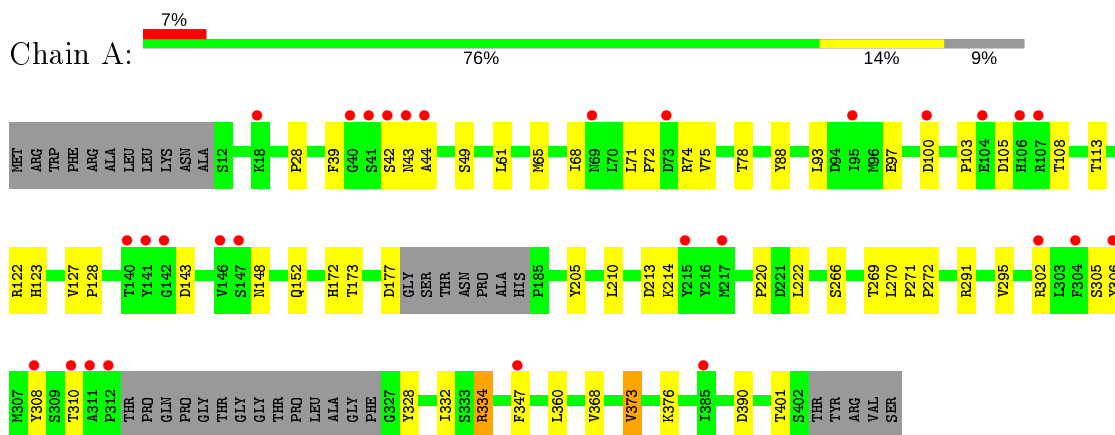
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	5	Total	O	0	0
			5	5		

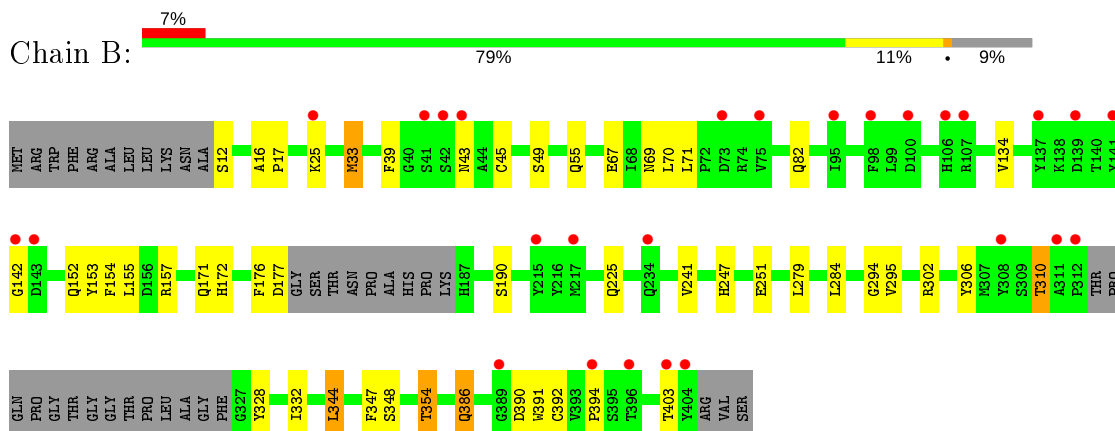
3 Residue-property plots i

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

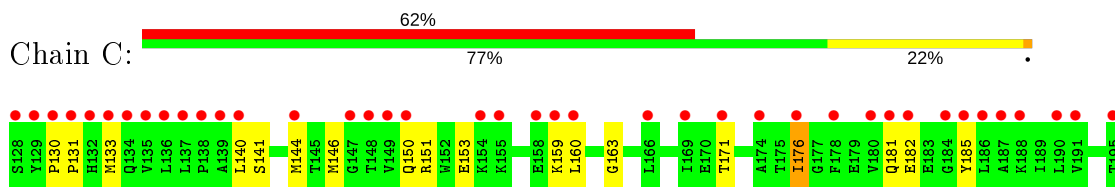
- Molecule 1: Pyruvate dehydrogenase [lipoamide] kinase isozyme 2, mitochondrial

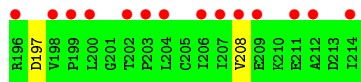


- Molecule 1: Pyruvate dehydrogenase [lipoamide] kinase isozyme 2, mitochondrial

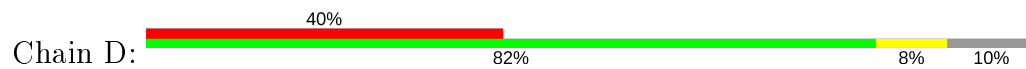


- Molecule 2: Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial





- Molecule 2: Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial



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4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	71.38Å 120.68Å 71.47Å 90.00° 96.03° 90.00°	Depositor
Resolution (Å)	50.00 – 2.30 32.01 – 2.30	Depositor EDS
% Data completeness (in resolution range)	94.9 (50.00-2.30) 94.8 (32.01-2.30)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.24 (at 2.31Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.208 , 0.251 0.206 , 0.248	Depositor DCC
R_{free} test set	2551 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	44.0	Xtrriage
Anisotropy	0.202	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 53.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	0.237 for l,-k,h	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7490	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.17% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: K, LA2

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	0/3035	0.52	0/4114
1	B	0.39	0/3039	0.54	1/4122 (0.0%)
2	C	0.30	0/671	0.48	0/911
2	D	0.33	0/597	0.52	0/809
All	All	0.38	0/7342	0.52	1/9956 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	344	LEU	CA-CB-CG	5.50	127.94	115.30

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	2964	0	2922	42	0
1	B	2968	0	2918	31	0
2	C	680	0	695	11	0
2	D	609	0	628	6	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	130	0	0	3	0
4	B	124	0	0	2	0
4	C	8	0	0	2	0
4	D	5	0	0	0	0
All	All	7490	0	7163	81	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 6.

All (81) 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:348:SER:HB3	1:B:354:THR:HB	1.53	0.91
1:B:171:GLN:HE22	1:B:190:SER:H	1.24	0.84
1:A:122:ARG:HG3	1:A:123:HIS:HD2	1.47	0.80
2:C:171:THR:HG21	4:C:220:HOH:O	1.84	0.76
1:B:348:SER:CB	1:B:354:THR:HB	2.17	0.74
1:A:143:ASP:HB2	1:A:148:ASN:HD21	1.51	0.74
1:A:61:LEU:HB3	1:A:65:MET:HE1	1.68	0.74
2:D:171:THR:HG22	2:D:172:ASP:H	1.53	0.72
1:A:61:LEU:HB3	1:A:65:MET:CE	2.19	0.71
1:A:220:PRO:HA	1:A:270:LEU:CD1	2.22	0.69
1:A:373:VAL:HG13	1:B:392:CYS:SG	2.34	0.68
1:A:390:ASP:O	1:B:157:ARG:NH2	2.28	0.67
1:A:360:LEU:HG	4:A:3127:HOH:O	1.95	0.66
1:A:152:GLN:HE22	1:A:306:TYR:H	1.42	0.65
1:A:68:ILE:O	1:A:71:LEU:HG	1.97	0.65
1:A:28:PRO:HD2	1:A:373:VAL:HG12	1.80	0.62
1:A:220:PRO:HA	1:A:270:LEU:HD11	1.82	0.62
1:B:33:MET:CE	1:B:241:VAL:HG23	2.29	0.61
1:B:152:GLN:HE22	1:B:306:TYR:H	1.47	0.61
2:D:171:THR:HG22	2:D:172:ASP:N	2.17	0.60
1:A:376:LYS:HD3	2:C:163:GLY:HA2	1.85	0.59
2:C:146:MET:HB2	2:C:197:ASP:HA	1.84	0.58
1:B:153:TYR:O	1:B:157:ARG:HG3	2.04	0.57
1:A:65:MET:HE2	1:A:88:TYR:HB3	1.86	0.57
1:A:143:ASP:HB2	1:A:148:ASN:ND2	2.19	0.56
1:A:368:VAL:HG11	1:B:394:PRO:HB3	1.87	0.55
1:B:354:THR:CG2	4:B:3034:HOH:O	2.54	0.55
1:B:43:ASN:C	1:B:45:CYS:H	2.09	0.54
1:A:28:PRO:HD2	1:A:373:VAL:CG1	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:159:LYS:HB3	2:C:185:TYR:CE1	2.42	0.54
1:A:71:LEU:HD13	1:A:75:VAL:HB	1.90	0.54
1:B:354:THR:HG23	4:B:3034:HOH:O	2.08	0.54
1:B:171:GLN:NE2	1:B:190:SER:H	2.01	0.52
1:B:247:HIS:O	1:B:251:GLU:HG2	2.10	0.51
1:A:44:ALA:HA	4:A:3120:HOH:O	2.11	0.51
2:C:141:SER:HB2	4:C:220:HOH:O	2.09	0.51
1:A:390:ASP:HB2	1:B:157:ARG:NH2	2.27	0.50
1:A:347:PHE:HB3	1:B:347:PHE:CZ	2.47	0.50
1:A:266:SER:HB3	1:A:269:THR:HG22	1.94	0.50
2:D:137:LEU:HD22	2:D:198:VAL:HG23	1.93	0.49
1:A:43:ASN:HB3	1:B:403:THR:HG21	1.94	0.49
1:B:67:GLU:OE1	1:B:157:ARG:NH1	2.45	0.49
1:A:334:ARG:HD2	4:A:3097:HOH:O	2.13	0.49
1:B:49:SER:OG	1:B:172:HIS:HD2	1.96	0.49
2:C:150:GLN:HE21	2:C:151:ARG:HD3	1.76	0.49
1:B:306:TYR:O	1:B:310:THR:OG1	2.31	0.48
1:A:71:LEU:HB2	1:A:72:PRO:HD2	1.95	0.48
1:A:173:THR:O	1:A:177:ASP:HB3	2.13	0.48
1:B:390:ASP:HB3	1:B:391:TRP:CD1	2.49	0.47
1:A:61:LEU:HB3	1:A:65:MET:HE3	1.96	0.47
1:B:16:ALA:N	1:B:17:PRO:HD2	2.30	0.47
1:A:103:PRO:C	1:A:105:ASP:H	2.19	0.46
1:B:328:TYR:HB3	1:B:332:ILE:HD12	1.96	0.46
2:D:147:GLY:O	2:D:198:VAL:HG22	2.16	0.46
1:A:302:ARG:HG3	1:A:308:TYR:CG	2.51	0.45
1:A:93:LEU:O	1:A:97:GLU:HG3	2.16	0.45
2:C:141:SER:HB3	2:C:144:MET:HB2	1.99	0.45
1:A:270:LEU:HA	1:A:271:PRO:HD3	1.81	0.45
1:B:176:PHE:O	1:B:177:ASP:HB2	2.16	0.45
1:A:113:THR:HG21	1:A:177:ASP:HB2	1.98	0.44
1:A:328:TYR:HB3	1:A:332:ILE:HD12	1.99	0.44
1:B:71:LEU:HD11	1:B:154:PHE:CG	2.52	0.44
2:C:140:LEU:HD13	2:C:176:ILE:HG12	1.99	0.44
1:B:294:GLY:HA2	1:B:354:THR:HG22	2.00	0.44
2:C:133:MET:HG2	2:C:182:GLU:HG3	2.01	0.43
1:A:376:LYS:NZ	2:C:181:GLN:HA	2.32	0.43
1:B:279:LEU:HD13	1:B:284:LEU:HD12	2.00	0.43
1:A:270:LEU:O	1:A:270:LEU:HD12	2.19	0.43
1:A:272:PRO:O	1:A:291:ARG:NH2	2.53	0.42
1:A:205:TYR:CE1	1:A:222:LEU:HB2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:190:LEU:HD22	2:D:203:PRO:HB2	2.01	0.41
1:A:210:LEU:O	1:A:214:LYS:HG2	2.19	0.41
2:D:171:THR:CG2	2:D:172:ASP:H	2.28	0.41
1:B:134:VAL:HG21	1:B:155:LEU:HD11	2.03	0.41
2:C:130:PRO:HA	2:C:131:PRO:HD2	1.95	0.41
1:A:127:VAL:HB	1:A:128:PRO:HD3	2.03	0.40
1:B:43:ASN:C	1:B:45:CYS:N	2.75	0.40
1:B:386:GLN:HB2	1:B:386:GLN:HE21	1.71	0.40
1:A:39:PHE:CZ	1:A:49:SER:HB2	2.56	0.40
1:A:49:SER:OG	1:A:172:HIS:HD2	2.03	0.40
1:A:401:THR:HB	1:B:39:PHE:HB2	2.02	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	364/407 (89%)	353 (97%)	10 (3%)	1 (0%)	41	50
1	B	364/407 (89%)	353 (97%)	10 (3%)	1 (0%)	41	50
2	C	84/87 (97%)	79 (94%)	5 (6%)	0	100	100
2	D	75/87 (86%)	73 (97%)	2 (3%)	0	100	100
All	All	887/988 (90%)	858 (97%)	27 (3%)	2 (0%)	47	58

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	42	SER
1	B	142	GLY

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	334/363 (92%)	324 (97%)	10 (3%)	41	57
1	B	335/363 (92%)	321 (96%)	14 (4%)	30	42
2	C	74/74 (100%)	70 (95%)	4 (5%)	22	30
2	D	66/74 (89%)	66 (100%)	0	100	100
All	All	809/874 (93%)	781 (96%)	28 (4%)	36	50

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	74	ARG
1	A	78	THR
1	A	100	ASP
1	A	108	THR
1	A	213	ASP
1	A	295	VAL
1	A	305	SER
1	A	310	THR
1	A	334	ARG
1	A	373	VAL
1	B	12	SER
1	B	25	LYS
1	B	33	MET
1	B	55	GLN
1	B	69	ASN
1	B	70	LEU
1	B	82	GLN
1	B	225	GLN
1	B	295	VAL
1	B	302	ARG
1	B	310	THR
1	B	344	LEU
1	B	354	THR
1	B	386	GLN

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Mol	Chain	Res	Type
2	C	153	GLU
2	C	160	LEU
2	C	176	ILE
2	C	208	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	148	ASN
1	A	152	GLN
1	A	172	HIS
1	A	237	HIS
1	A	247	HIS
1	A	341	GLN
1	B	55	GLN
1	B	148	ASN
1	B	152	GLN
1	B	171	GLN
1	B	172	HIS
1	B	386	GLN
2	C	150	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	$\# Z > 2$
2	LA2	D	173	2	17,19,20	0.37	0	12,21,23	1.35	2 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	LA2	C	173	2	17,19,20	0.34	0	12,21,23	1.47	3 (25%)

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	LA2	D	173	2	-	2/18/20/22	-
2	LA2	C	173	2	-	4/18/20/22	-

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	173	LA2	C7-C8-S8	-3.02	110.60	113.74
2	D	173	LA2	C7-C8-S8	-2.69	110.94	113.74
2	C	173	LA2	CE-NZ-C1	2.66	127.77	122.84
2	D	173	LA2	CD-CE-NZ	-2.18	105.97	112.21
2	C	173	LA2	CD-CE-NZ	-2.08	106.27	112.21

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	173	LA2	C6-C7-C8-S8
2	C	173	LA2	C5-C6-C7-C8
2	C	173	LA2	C6-C7-C8-S8
2	D	173	LA2	C1-C2-C3-C4
2	C	173	LA2	C1-C2-C3-C4
2	C	173	LA2	C3-C4-C5-C6

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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.

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, 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	370/407 (90%)	0.91	29 (7%) 13 17	35, 44, 58, 66	0
1	B	370/407 (90%)	0.78	27 (7%) 15 20	36, 42, 62, 71	0
2	C	86/87 (98%)	2.57	54 (62%) 0 0	91, 101, 106, 107	0
2	D	77/87 (88%)	2.23	35 (45%) 0 0	82, 90, 96, 96	0
All	All	903/988 (91%)	1.13	145 (16%) 1 2	35, 44, 101, 107	0

All (145) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	312	PRO	11.7
1	A	311	ALA	9.8
1	A	42	SER	9.7
1	A	41	SER	9.0
2	D	132	HIS	8.3
1	B	404	TYR	8.0
2	D	208	VAL	7.8
2	D	157	GLY	7.7
1	B	312	PRO	7.6
2	D	186	LEU	7.2
1	B	311	ALA	6.8
2	D	156	VAL	6.4
2	D	187	ALA	6.4
2	C	206	ILE	6.0
2	C	128	SER	5.7
2	C	214	ILE	5.5
2	D	133	MET	5.2
2	D	206	ILE	5.1
2	C	185	TYR	5.0
2	C	135	VAL	5.0
2	D	188	LYS	4.9

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Mol	Chain	Res	Type	RSRZ
2	C	199	PRO	4.9
2	D	185	TYR	4.9
1	A	43	ASN	4.7
2	C	208	VAL	4.6
2	C	169	ILE	4.5
2	C	137	LEU	4.5
1	A	385	ILE	4.4
2	C	200	LEU	4.3
1	B	141	TYR	4.1
2	C	191	VAL	4.1
2	C	155	LYS	4.1
2	C	129	TYR	4.1
2	C	159	LYS	4.0
1	A	100	ASP	4.0
2	C	184	GLY	4.0
1	A	310	THR	3.9
2	C	182	GLU	3.8
2	C	147	GLY	3.8
2	C	149	VAL	3.8
1	A	141	TYR	3.8
2	C	136	LEU	3.8
1	B	42	SER	3.7
2	C	203	PRO	3.7
1	A	106	HIS	3.6
2	C	134	GLN	3.6
1	A	146	VAL	3.6
2	C	148	THR	3.6
1	A	104	GLU	3.5
2	C	187	ALA	3.5
2	D	160	LEU	3.3
1	B	106	HIS	3.2
2	D	198	VAL	3.2
2	C	133	MET	3.2
2	C	158	GLU	3.2
2	C	178	PHE	3.1
1	A	147	SER	3.1
2	D	200	LEU	3.1
2	C	188	LYS	3.1
2	D	155	LYS	3.0
2	D	159	LYS	3.0
1	B	394	PRO	3.0
2	C	176	ILE	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	396	THR	3.0
2	C	190	LEU	3.0
2	C	207	ILE	3.0
2	D	158	GLU	3.0
2	C	131	PRO	3.0
2	D	183	GLU	2.9
1	B	139	ASP	2.9
2	D	207	ILE	2.9
2	C	166	LEU	2.9
1	A	215	TYR	2.9
2	C	196	ARG	2.9
1	A	40	GLY	2.8
2	C	180	VAL	2.8
2	D	204	LEU	2.8
1	B	143	ASP	2.7
2	C	204	LEU	2.7
2	C	202	THR	2.7
2	C	195	THR	2.7
1	B	43	ASN	2.7
2	C	186	LEU	2.7
1	B	308	TYR	2.6
2	D	201	GLY	2.6
2	C	211	GLU	2.6
2	D	203	PRO	2.6
2	D	189	ILE	2.6
1	A	73	ASP	2.6
1	B	389	GLY	2.6
1	B	73	ASP	2.6
1	B	142	GLY	2.6
1	B	403	THR	2.5
1	B	100	ASP	2.5
1	A	142	GLY	2.5
1	A	18	LYS	2.5
2	C	212	ALA	2.5
2	C	138	PRO	2.5
1	A	95	ILE	2.5
1	A	140	THR	2.5
1	B	217	MET	2.5
1	A	302	ARG	2.5
2	C	209	GLU	2.4
2	D	134	GLN	2.4
2	C	132	HIS	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	215	TYR	2.4
2	D	152	TRP	2.4
1	A	304	PHE	2.4
1	B	41	SER	2.4
1	A	107	ARG	2.3
2	C	160	LEU	2.3
2	C	181	GLN	2.3
2	C	130	PRO	2.3
2	D	172	ASP	2.3
1	A	69	ASN	2.3
2	C	140	LEU	2.3
2	C	154	LYS	2.3
1	A	44	ALA	2.3
2	C	174	ALA	2.3
1	B	234	GLN	2.3
1	B	75	VAL	2.3
2	C	198	VAL	2.3
1	B	95	ILE	2.3
2	D	190	LEU	2.2
1	B	107	ARG	2.2
2	D	199	PRO	2.2
1	A	347	PHE	2.2
2	C	139	ALA	2.2
2	D	195	THR	2.2
2	D	191	VAL	2.2
1	B	98	PHE	2.2
2	C	171	THR	2.2
1	B	25	LYS	2.2
2	D	171	THR	2.2
2	D	180	VAL	2.1
1	A	217	MET	2.1
1	B	137	TYR	2.1
2	C	150	GLN	2.1
2	D	141	SER	2.1
2	D	151	ARG	2.0
1	A	306	TYR	2.0
1	A	308	TYR	2.0
2	D	169	ILE	2.0
2	C	144	MET	2.0
2	D	197	ASP	2.0

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, 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(Å ²)	Q<0.9
2	LA2	C	173	20/21	0.90	0.20	80,83,90,91	0
2	LA2	D	173	20/21	0.93	0.17	76,80,83,83	0

6.3 Carbohydrates [i](#)

There are no carbohydrates 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(Å ²)	Q<0.9
3	K	A	3001	1/1	0.65	0.17	75,75,75,75	0
3	K	B	3002	1/1	0.92	0.28	67,67,67,67	0

6.5 Other polymers [i](#)

There are no such residues in this entry.