



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:57 AM GMT

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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

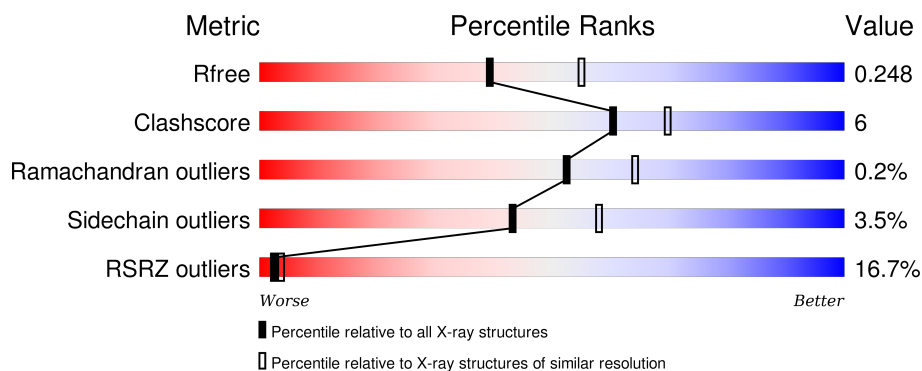
1 Overall quality at a glance

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}	91344	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (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. 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	<div> <div>7%</div> <div>76% 14% 9%</div> </div>
1	B	407	<div> <div>7%</div> <div>79% 11% 9%</div> </div>
2	C	87	<div> <div>64%</div> <div>77% 22%</div> </div>
2	D	87	<div> <div>41%</div> <div>82% 8% 10%</div> </div>

2 Entry composition

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
1	A	370	Total	C	N	O	S	0	0	0
			2964	1896	489	561	18			
1	B	370	Total	C	N	O	S	0	0	0
			2968	1898	489	563	18			

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

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

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

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

- Molecule 4 is water.

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

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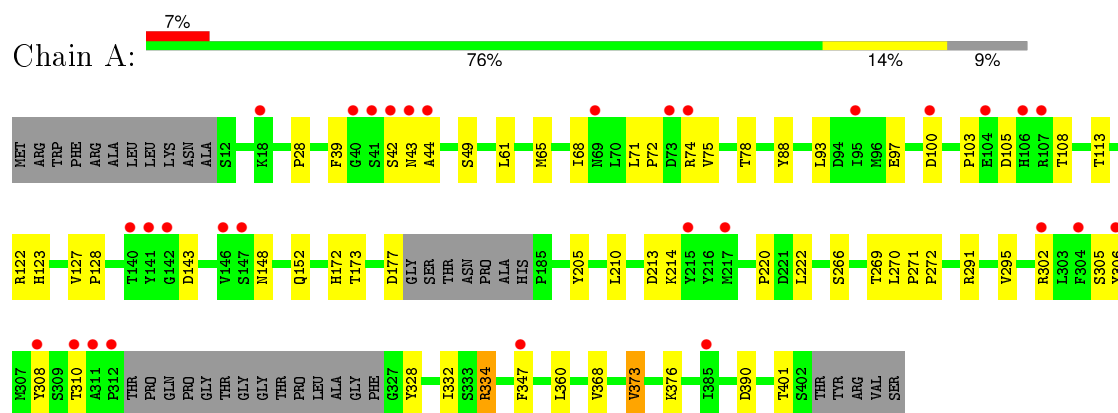
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	5	Total	O	0	0
			5	5		

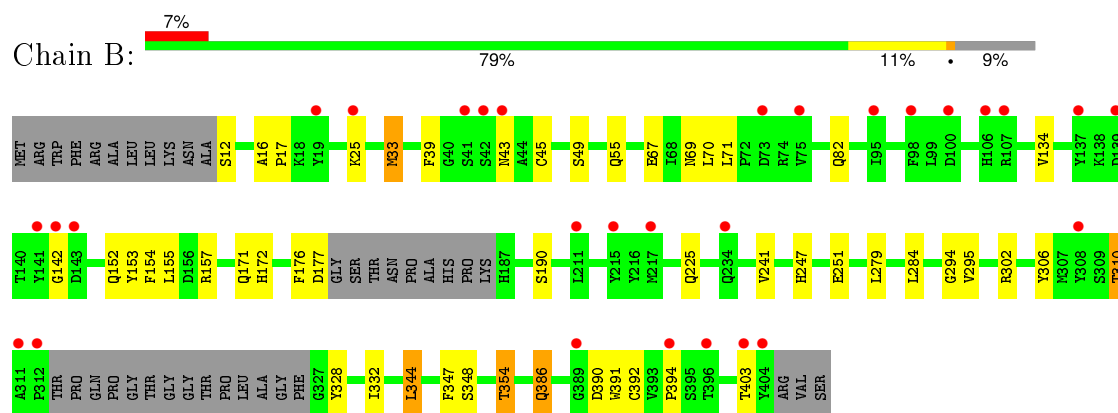
3 Residue-property plots [i](#)

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

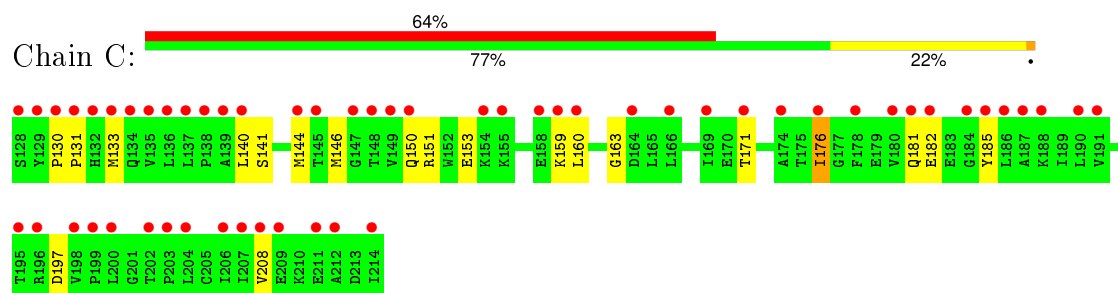
- Molecule 1: Pyruvate dehydrogenase [lipoamide] kinase isozyme 2, mitochondrial



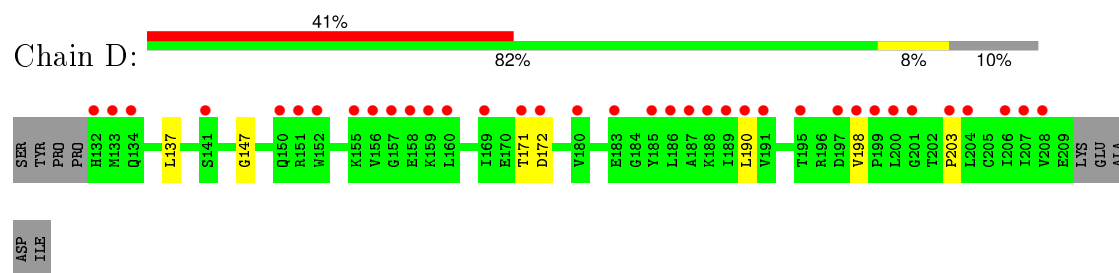
- Molecule 1: Pyruvate dehydrogenase [lipoamide] kinase isozyme 2, mitochondrial



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



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



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)	Xtriage
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 (5.33%)	DCC
Wilson B-factor (Å ²)	44.0	Xtriage
Anisotropy	0.202	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 53.5	EDS
Estimated twinning fraction	0.237 for l,-k,h	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	0 of 50377 reflections	Xtriage
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

Xtriage'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, 0.375 respectively for untwinned datasets, and 0.333, 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
2:C:141:SER:HB2	4:C:220:HOH:O	2.09	0.51
1:A:44:ALA:HA	4:A:3120:HOH:O	2.11	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:B:67:GLU:OE1	1:B:157:ARG:NH1	2.45	0.49
1:A:43:ASN:HB3	1:B:403:THR:HG21	1.94	0.49
1:A:334:ARG:HD2	4:A:3097:HOH:O	2.13	0.49
2:C:150:GLN:HE21	2:C:151:ARG:HD3	1.76	0.49
1:B:49:SER:OG	1:B:172:HIS:HD2	1.96	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:B:328:TYR:HB3	1:B:332:ILE:HD12	1.96	0.46
1:A:103:PRO:C	1:A:105:ASP:H	2.19	0.46
2:D:147:GLY:O	2:D:198:VAL:HG22	2.16	0.46
1:A:93:LEU:O	1:A:97:GLU:HG3	2.16	0.45
1:A:302:ARG:HG3	1:A:308:TYR:CG	2.51	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:B:71:LEU:HD11	1:B:154:PHE:CG	2.52	0.44
1:A:328:TYR:HB3	1:A:332:ILE:HD12	1.99	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
2:D:171:THR:CG2	2:D:172:ASP:H	2.28	0.41
1:A:210:LEU:O	1:A:214:LYS:HG2	2.19	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:B:43:ASN:C	1:B:45:CYS:N	2.75	0.40
1:A:127:VAL:HB	1:A:128:PRO:HD3	2.03	0.40
1:B:386:GLN:HB2	1:B:386:GLN:HE21	1.71	0.40
1:A:49:SER:OG	1:A:172:HIS:HD2	2.03	0.40
1:A:39:PHE:CZ	1:A:49:SER:HB2	2.56	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%)	46	57
1	B	364/407 (89%)	353 (97%)	10 (3%)	1 (0%)	46	57
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%)	52	64

All (2) Ramachandran outliers are listed below:

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

5.3.2 Protein sidechains ⓘ

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%)	48	65
1	B	335/363 (92%)	321 (96%)	14 (4%)	36	49
2	C	74/74 (100%)	70 (95%)	4 (5%)	27	36
2	D	66/74 (89%)	66 (100%)	0	100	100
All	All	809/874 (93%)	781 (96%)	28 (4%)	43	58

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 ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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	C	173	2	16,19,20	0.35	0	14,21,23	1.24	2 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	LA2	D	173	2	16,19,20	0.35	0	14,21,23	1.10	2 (14%)

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	C	173	2	-	0/16/20/22	0/0/0/0
2	LA2	D	173	2	-	0/16/20/22	0/0/0/0

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	173	LA2	CD-CE-NZ	-2.13	105.97	112.19
2	D	173	LA2	O-C-CA	-2.03	120.21	125.49
2	C	173	LA2	CD-CE-NZ	-2.02	106.27	112.19
2	C	173	LA2	CE-NZ-C1	2.53	127.77	122.79

There are no chirality outliers.

There are no torsion outliers.

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

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	370/407 (90%)	0.99	30 (8%) 15 21	35, 44, 58, 66	0
1	B	370/407 (90%)	0.85	29 (7%) 16 22	36, 42, 62, 71	0
2	C	86/87 (98%)	2.69	56 (65%) 0 0	91, 101, 106, 107	0
2	D	77/87 (88%)	2.34	36 (46%) 0 0	82, 90, 96, 96	0
All	All	903/988 (91%)	1.21	151 (16%) 2 4	35, 44, 101, 107	0

All (151) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	312	PRO	12.1
1	A	311	ALA	10.1
1	A	42	SER	10.0
1	A	41	SER	9.2
2	D	132	HIS	8.6
1	B	404	TYR	8.2
2	D	208	VAL	8.1
2	D	157	GLY	7.9
1	B	312	PRO	7.9
2	D	186	LEU	7.4
1	B	311	ALA	7.0
2	D	156	VAL	6.7
2	D	187	ALA	6.6
2	C	206	ILE	6.2
2	C	128	SER	5.9
2	C	214	ILE	5.7
2	D	133	MET	5.4
2	D	206	ILE	5.3
2	C	135	VAL	5.2
2	C	185	TYR	5.2
2	C	199	PRO	5.1

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Mol	Chain	Res	Type	RSRZ
2	D	188	LYS	5.0
2	D	185	TYR	5.0
2	C	208	VAL	4.8
1	A	43	ASN	4.8
2	C	169	ILE	4.7
2	C	137	LEU	4.6
1	A	385	ILE	4.6
2	C	200	LEU	4.4
2	C	191	VAL	4.3
1	B	141	TYR	4.3
2	C	129	TYR	4.2
2	C	155	LYS	4.2
1	A	100	ASP	4.1
2	C	184	GLY	4.1
2	C	159	LYS	4.1
1	A	310	THR	4.1
2	C	149	VAL	4.0
2	C	147	GLY	4.0
2	C	182	GLU	4.0
2	C	136	LEU	3.9
1	A	141	TYR	3.9
1	B	42	SER	3.8
2	C	203	PRO	3.8
1	A	146	VAL	3.8
1	A	106	HIS	3.8
2	C	134	GLN	3.7
2	C	148	THR	3.7
1	A	104	GLU	3.7
2	C	187	ALA	3.7
2	D	160	LEU	3.4
2	D	198	VAL	3.4
1	B	106	HIS	3.4
2	C	133	MET	3.3
2	C	158	GLU	3.3
2	C	178	PHE	3.3
1	A	147	SER	3.2
2	D	200	LEU	3.2
1	B	394	PRO	3.2
2	C	188	LYS	3.1
2	C	176	ILE	3.1
1	B	396	THR	3.1
2	D	155	LYS	3.1

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Mol	Chain	Res	Type	RSRZ
2	D	159	LYS	3.1
2	C	131	PRO	3.1
2	C	207	ILE	3.1
2	C	190	LEU	3.1
1	B	139	ASP	3.1
2	D	158	GLU	3.1
2	D	207	ILE	3.0
2	D	183	GLU	3.0
2	C	166	LEU	3.0
1	A	215	TYR	3.0
1	A	40	GLY	3.0
2	C	196	ARG	3.0
2	C	180	VAL	2.9
2	D	204	LEU	2.9
1	B	143	ASP	2.9
2	C	202	THR	2.9
2	C	204	LEU	2.8
2	C	195	THR	2.8
2	C	186	LEU	2.8
1	B	43	ASN	2.8
2	D	201	GLY	2.8
2	D	189	ILE	2.7
1	B	308	TYR	2.7
2	D	203	PRO	2.7
1	A	73	ASP	2.7
1	B	389	GLY	2.7
2	C	211	GLU	2.7
1	B	142	GLY	2.7
1	B	73	ASP	2.7
1	B	403	THR	2.7
2	C	212	ALA	2.7
1	A	142	GLY	2.7
2	C	138	PRO	2.7
1	A	95	ILE	2.6
1	B	100	ASP	2.6
1	A	140	THR	2.6
1	A	18	LYS	2.6
1	B	217	MET	2.6
1	A	302	ARG	2.5
2	C	132	HIS	2.5
2	C	209	GLU	2.5
1	B	215	TYR	2.5

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Mol	Chain	Res	Type	RSRZ
2	D	134	GLN	2.5
2	D	152	TRP	2.5
1	A	304	PHE	2.5
1	B	41	SER	2.5
2	C	160	LEU	2.5
2	C	130	PRO	2.4
1	A	107	ARG	2.4
2	C	181	GLN	2.4
2	D	172	ASP	2.4
2	C	140	LEU	2.4
1	B	75	VAL	2.4
2	C	198	VAL	2.4
1	A	69	ASN	2.4
1	A	44	ALA	2.4
2	C	174	ALA	2.4
1	B	95	ILE	2.4
2	C	154	LYS	2.4
1	B	234	GLN	2.4
2	D	190	LEU	2.3
2	D	191	VAL	2.3
2	D	195	THR	2.3
2	D	199	PRO	2.3
1	A	347	PHE	2.3
2	C	139	ALA	2.3
2	C	171	THR	2.3
1	B	98	PHE	2.3
2	D	171	THR	2.3
2	D	180	VAL	2.3
1	B	107	ARG	2.3
1	B	25	LYS	2.2
1	A	217	MET	2.2
1	B	137	TYR	2.2
2	D	141	SER	2.2
2	C	150	GLN	2.2
2	D	169	ILE	2.1
2	D	151	ARG	2.1
1	A	306	TYR	2.1
1	A	308	TYR	2.1
2	D	197	ASP	2.1
2	C	144	MET	2.1
2	C	145	THR	2.1
1	B	19	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
2	C	164	ASP	2.0
2	D	150	GLN	2.0
1	B	211	LEU	2.0
1	A	74	ARG	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
2	LA2	D	173	20/21	0.93	0.17	-	76,80,83,83	0
2	LA2	C	173	20/21	0.90	0.20	-	80,83,90,91	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
3	K	B	3002	1/1	0.92	0.28	1.49	67,67,67,67	0
3	K	A	3001	1/1	0.65	0.17	-0.38	75,75,75,75	0

6.5 Other polymers [i](#)

There are no such residues in this entry.