



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:22 PM GMT

PDB ID : 4LEV
Title : Structure of human cGAS
Authors : Li, P.
Deposited on : 2013-06-26
Resolution : 1.95 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

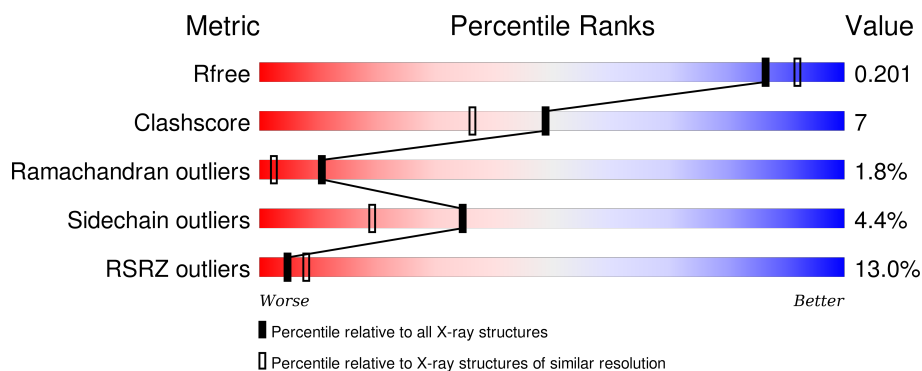
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	1833 (1.96-1.96)
Clashscore	102246	1953 (1.96-1.96)
Ramachandran outliers	100387	1936 (1.96-1.96)
Sidechain outliers	100360	1936 (1.96-1.96)
RSRZ outliers	91569	1835 (1.96-1.96)

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	369	
1	B	369	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6567 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 Cyclic GMP-AMP synthase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	369	Total	C	N	O	S	Se	0	3	0
			3057	1955	525	561	10	6			
1	B	369	Total	C	N	O	S	Se	0	3	0
			3057	1954	525	561	10	7			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	154	PHE	-	EXPRESSION TAG	UNP Q8N884
A	155	GLU	-	EXPRESSION TAG	UNP Q8N884
A	156	LEU	-	EXPRESSION TAG	UNP Q8N884
B	154	PHE	-	EXPRESSION TAG	UNP Q8N884
B	155	GLU	-	EXPRESSION TAG	UNP Q8N884
B	156	LEU	-	EXPRESSION TAG	UNP Q8N884

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

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

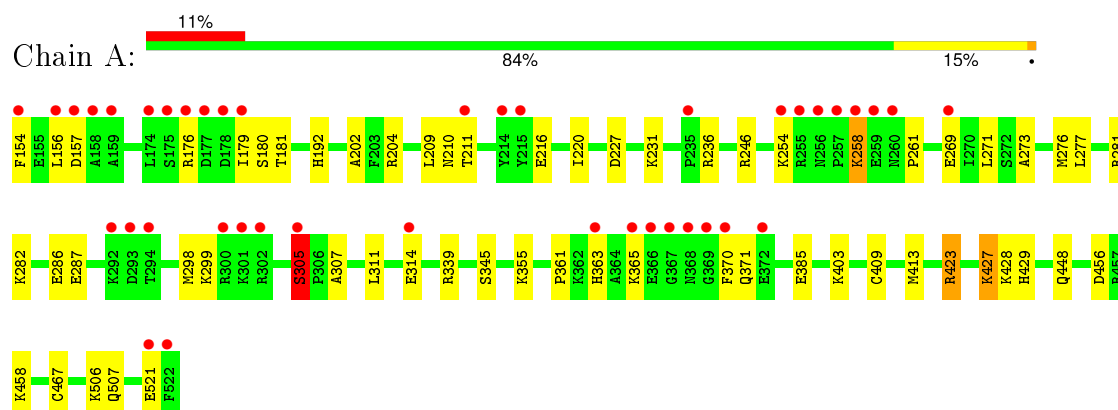
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	241	Total	O	0	0
			241	241		
3	B	210	Total	O	0	0
			210	210		

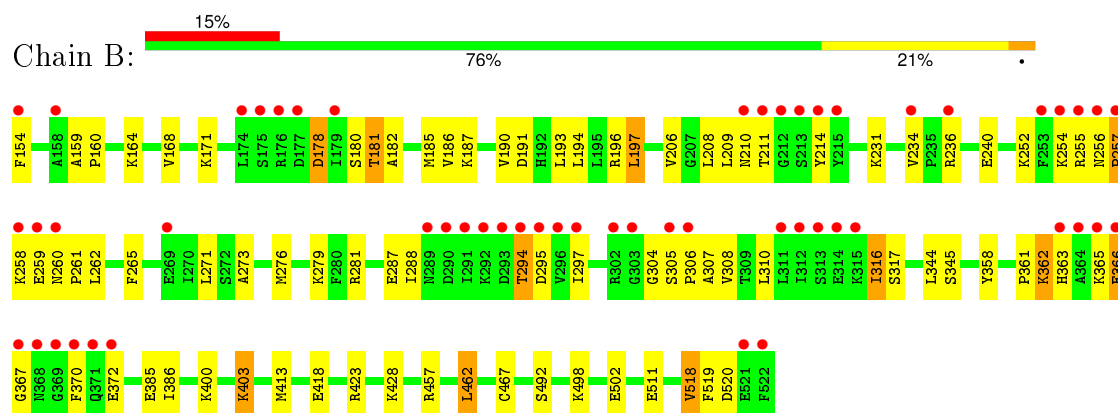
3 Residue-property plots

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: Cyclic GMP-AMP synthase



• Molecule 1: Cyclic GMP-AMP synthase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	212.98Å 47.72Å 86.87Å 90.00° 113.89° 90.00°	Depositor
Resolution (Å)	38.45 – 1.95 38.45 – 1.95	Depositor EDS
% Data completeness (in resolution range)	97.8 (38.45-1.95) 93.5 (38.45-1.95)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.59 (at 1.95Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.167 , 0.202 0.166 , 0.201	Depositor DCC
R_{free} test set	3870 reflections (3.48%)	DCC
Wilson B-factor (Å ²)	28.5	Xtriage
Anisotropy	0.366	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 53.3	EDS
Estimated twinning fraction	0.018 for -h-2*k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 57244 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6567	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.23% 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

5.1 Standard geometry

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	0.52	0/3114	0.63	1/4169 (0.0%)
1	B	0.50	0/3114	0.62	0/4168
All	All	0.51	0/6228	0.63	1/8337 (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	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	305	SER	C-N-CA	-5.47	99.04	122.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	305	SER	Peptide

5.2 Too-close contacts

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	3057	0	3088	36	2
1	B	3057	0	3086	52	1
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	241	0	0	9	0
3	B	210	0	0	5	0
All	All	6567	0	6174	88	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 (88) 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:164:LYS:NZ	3:B:836:HOH:O	2.08	0.85
1:A:458:LYS:NZ	3:A:875:HOH:O	2.16	0.79
1:B:418:GLU:OE2	3:B:811:HOH:O	2.03	0.75
1:A:236:ARG:HB2	1:A:254:LYS:HD2	1.69	0.73
1:A:365:LYS:HB3	1:A:370:PHE:HB3	1.72	0.71
1:A:271:LEU:HD21	1:A:276:MSE:HE1	1.73	0.70
1:B:236:ARG:HB2	1:B:254:LYS:HG3	1.74	0.70
1:A:204:ARG:HH21	1:A:261:PRO:HB3	1.60	0.67
1:A:286:GLU:OE1	3:A:869:HOH:O	2.12	0.67
1:B:294:THR:OG1	1:B:295:ASP:N	2.22	0.67
1:A:157:ASP:OD2	3:A:837:HOH:O	2.13	0.67
1:B:193:LEU:HD11	1:B:310:LEU:HD11	1.78	0.66
1:A:507:GLN:NE2	3:A:818:HOH:O	2.21	0.66
1:B:191:ASP:OD1	1:B:214:TYR:OH	2.14	0.65
1:B:255:ARG:HD2	1:B:259:GLU:OE2	1.98	0.64
1:B:164:LYS:HE3	1:B:520:ASP:HB3	1.83	0.60
1:A:273:ALA:HB1	1:A:361:PRO:HB3	1.83	0.60
1:B:365:LYS:HB3	1:B:370:PHE:HB3	1.83	0.60
1:A:448:GLN:NE2	3:A:913:HOH:O	2.32	0.60
1:B:305:SER:OG	1:B:361:PRO:O	2.19	0.60
1:A:209:LEU:O	1:A:211:THR:N	2.37	0.58
1:B:168:VAL:HG21	1:B:519:PHE:HB3	1.85	0.58
1:A:423:ARG:NH1	3:A:818:HOH:O	2.37	0.57
1:B:194:LEU:HD11	1:B:208:LEU:HG	1.88	0.55
1:B:186:VAL:HG23	1:B:316:ILE:HD11	1.90	0.54
1:A:202:ALA:HA	1:A:261:PRO:HB2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:288:ILE:HD11	1:B:310:LEU:HD22	1.89	0.54
1:B:240:GLU:OE1	1:B:252:LYS:NZ	2.25	0.53
1:A:427:LYS:O	1:A:429:HIS:N	2.42	0.53
1:A:339:ARG:NH1	3:A:825:HOH:O	2.41	0.52
1:B:273:ALA:HB1	1:B:361:PRO:HB3	1.90	0.52
1:A:281:ARG:HH12	1:A:298:MSE:HE3	1.74	0.52
1:B:257:PRO:O	1:B:259:GLU:N	2.43	0.51
1:A:176:ARG:HH11	1:A:176:ARG:HG3	1.75	0.51
1:A:192:HIS:NE2	1:A:287:GLU:OE2	2.43	0.50
1:B:428:LYS:HA	3:B:839:HOH:O	2.12	0.50
1:A:299:LYS:O	3:A:762:HOH:O	2.20	0.49
1:B:187:LYS:HA	1:B:214:TYR:CE1	2.48	0.49
1:B:363:HIS:CE1	1:B:372:GLU:HG3	2.47	0.49
1:B:178:ASP:O	1:B:181:THR:HG23	2.13	0.48
1:B:413[A]:MSE:SE	1:B:467:CYS:HB3	2.63	0.48
1:A:409:CYS:O	1:A:413[A]:MSE:HG3	2.14	0.48
1:A:176:ARG:HH22	1:A:220:ILE:HA	1.79	0.48
1:B:265:PHE:HZ	1:B:279:LYS:HD3	1.79	0.47
1:B:498:LYS:HE3	1:B:502:GLU:OE2	2.13	0.47
1:B:281:ARG:HG3	1:B:308:VAL:HG22	1.97	0.47
1:A:236:ARG:HG2	1:A:236:ARG:HH11	1.79	0.47
1:B:385:GLU:HG2	3:B:767:HOH:O	2.15	0.47
1:A:281:ARG:NH1	1:A:298:MSE:HE3	2.31	0.46
1:B:403:LYS:HG2	1:B:457:ARG:HD2	1.97	0.46
1:A:423:ARG:NH2	1:A:521:GLU:OE1	2.50	0.45
1:B:260:ASN:C	1:B:262:LEU:H	2.19	0.45
1:A:236:ARG:HG2	1:A:236:ARG:NH1	2.32	0.45
1:B:305:SER:HB2	1:B:362:LYS:NZ	2.30	0.45
1:A:413[A]:MSE:SE	1:A:467:CYS:HB3	2.66	0.45
1:A:176:ARG:NH1	1:A:176:ARG:HG3	2.32	0.44
1:B:181:THR:OG1	1:B:182:ALA:N	2.50	0.44
1:B:260:ASN:O	1:B:262:LEU:N	2.50	0.44
1:A:282:LYS:O	1:A:286:GLU:HG3	2.18	0.44
1:A:258:LYS:H	1:A:258:LYS:HG3	1.42	0.43
1:B:181:THR:O	1:B:185[A]:MSE:HG3	2.17	0.43
1:B:209:LEU:HG	1:B:210:ASN:N	2.34	0.43
1:A:307:ALA:HB2	3:A:849:HOH:O	2.18	0.43
1:B:196:ARG:HE	1:B:287:GLU:CD	2.22	0.43
1:B:186:VAL:CG2	1:B:316:ILE:HD11	2.49	0.43
1:B:197:LEU:HA	1:B:197:LEU:HD12	1.85	0.43
1:A:355:LYS:HE3	1:A:385:GLU:OE2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:344:LEU:CD1	1:B:386:ILE:HD12	2.49	0.42
1:A:176:ARG:NH2	1:A:220:ILE:HD12	2.34	0.42
1:B:423:ARG:NH1	3:B:794:HOH:O	2.52	0.42
1:B:305:SER:OG	1:B:362:LYS:HG2	2.20	0.42
1:B:209:LEU:HD13	1:B:358:TYR:CZ	2.53	0.42
1:A:277:LEU:O	1:A:281:ARG:HG3	2.18	0.42
1:B:511:GLU:OE1	1:B:518:VAL:HB	2.20	0.42
1:B:366:GLU:HB3	1:B:367:GLY:H	1.67	0.42
1:A:403:LYS:HD2	1:A:403:LYS:HA	1.80	0.41
1:B:159:ALA:HA	1:B:160:PRO:HD3	1.90	0.41
1:B:271:LEU:HD21	1:B:276:MSE:HE1	2.01	0.41
1:B:462:LEU:HA	1:B:462:LEU:HD12	1.75	0.41
1:B:197:LEU:HB3	1:B:206:VAL:HG11	2.02	0.41
1:B:256:ASN:CB	1:B:257:PRO:HD2	2.51	0.41
1:B:305:SER:HB2	1:B:362:LYS:HZ3	1.85	0.40
1:A:179:ILE:O	1:A:181:THR:N	2.53	0.40
1:B:190:VAL:HB	1:B:214:TYR:HE1	1.85	0.40
1:B:168:VAL:CG2	1:B:519:PHE:HB3	2.51	0.40
1:B:210:ASN:HD22	1:B:210:ASN:HA	1.70	0.40
1:B:344:LEU:HD11	1:B:386:ILE:HG23	2.03	0.40
1:A:156:LEU:HD23	1:A:156:LEU:HA	1.94	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)
1:A:314:GLU:O	1:A:506:LYS:NZ[4_655]	2.16	0.04
1:A:456:ASP:OD2	1:B:400:LYS:NZ[4_656]	2.17	0.03

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	370/369 (100%)	348 (94%)	17 (5%)	5 (1%)	14	4
1	B	370/369 (100%)	342 (92%)	20 (5%)	8 (2%)	8	2
All	All	740/738 (100%)	690 (93%)	37 (5%)	13 (2%)	11	2

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	428	LYS
1	B	257	PRO
1	B	258	LYS
1	B	307	ALA
1	A	180	SER
1	A	210	ASN
1	A	216	GLU
1	A	345	SER
1	B	345	SER
1	B	366	GLU
1	B	304	GLY
1	B	306	PRO
1	B	261	PRO

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	342/334 (102%)	330 (96%)	12 (4%)	43	29
1	B	342/334 (102%)	324 (95%)	18 (5%)	28	13
All	All	684/668 (102%)	654 (96%)	30 (4%)	35	19

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	154	PHE
1	A	227	ASP
1	A	231	LYS

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Mol	Chain	Res	Type
1	A	246	ARG
1	A	258	LYS
1	A	269	GLU
1	A	305	SER
1	A	311	LEU
1	A	363	HIS
1	A	371	GLN
1	A	423	ARG
1	A	427	LYS
1	B	154	PHE
1	B	171	LYS
1	B	178	ASP
1	B	180	SER
1	B	181	THR
1	B	197	LEU
1	B	211	THR
1	B	231	LYS
1	B	234	VAL
1	B	294	THR
1	B	297	ILE
1	B	316	ILE
1	B	317	SER
1	B	362	LYS
1	B	403	LYS
1	B	462	LEU
1	B	492	SER
1	B	518	VAL

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

Mol	Chain	Res	Type
1	A	210	ASN
1	A	224	ASN
1	B	210	ASN

5.3.3 RNA ⓘ

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 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	364/369 (98%)	0.40	41 (11%) 7 11	18, 40, 118, 165	0
1	B	364/369 (98%)	0.65	54 (14%) 3 5	18, 46, 126, 174	0
All	All	728/738 (98%)	0.52	95 (13%) 5 8	18, 42, 123, 174	0

All (95) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	367	GLY	17.4
1	B	370	PHE	12.3
1	B	368	ASN	12.2
1	A	368	ASN	10.8
1	A	367	GLY	10.3
1	A	257	PRO	9.3
1	A	258	LYS	9.0
1	A	366	GLU	7.6
1	B	366	GLU	7.4
1	A	256	ASN	7.3
1	B	369	GLY	7.0
1	B	522	PHE	7.0
1	B	211	THR	6.9
1	A	154	PHE	6.7
1	A	369	GLY	6.6
1	A	156	LEU	6.6
1	B	292	LYS	6.4
1	A	370	PHE	6.4
1	B	214	TYR	6.4
1	B	294	THR	5.7
1	B	303	GLY	5.6
1	B	305	SER	5.6
1	B	256	ASN	5.4
1	A	255	ARG	5.4

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Mol	Chain	Res	Type	RSRZ
1	B	297	ILE	5.2
1	A	214	TYR	5.2
1	B	255	ARG	5.2
1	B	254	LYS	5.2
1	A	211	THR	5.1
1	B	296	VAL	5.0
1	B	258	LYS	4.9
1	B	176	ARG	4.9
1	B	175	SER	4.9
1	B	291	ILE	4.8
1	B	215	TYR	4.8
1	B	212	GLY	4.6
1	B	260	ASN	4.5
1	A	176	ARG	4.5
1	B	315	LYS	4.4
1	B	521	GLU	4.4
1	B	179	ILE	4.4
1	A	305	SER	4.3
1	B	253	PHE	4.3
1	A	260	ASN	4.3
1	B	314	GLU	4.2
1	B	365	LYS	4.0
1	A	158	ALA	4.0
1	A	522	PHE	4.0
1	B	364	ALA	3.9
1	A	365	LYS	3.9
1	B	306	PRO	3.9
1	A	157	ASP	3.8
1	A	314	GLU	3.8
1	B	293	ASP	3.7
1	A	179	ILE	3.7
1	A	178	ASP	3.7
1	B	174	LEU	3.6
1	B	313	SER	3.6
1	A	292	LYS	3.5
1	A	174	LEU	3.5
1	A	259	GLU	3.5
1	B	154	PHE	3.4
1	A	254	LYS	3.3
1	B	213	SER	3.2
1	B	289	ASN	3.2
1	A	235	PRO	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	257	PRO	3.2
1	B	259	GLU	3.1
1	B	312	ILE	3.0
1	A	269	GLU	3.0
1	B	311	LEU	3.0
1	B	372	GLU	2.9
1	A	293	ASP	2.9
1	B	269	GLU	2.8
1	B	302	ARG	2.7
1	A	302	ARG	2.7
1	B	295	ASP	2.6
1	B	363	HIS	2.6
1	A	372	GLU	2.6
1	B	210	ASN	2.5
1	A	300	ARG	2.5
1	A	159	ALA	2.5
1	A	363	HIS	2.4
1	A	294	THR	2.4
1	A	521	GLU	2.4
1	B	236	ARG	2.4
1	A	177	ASP	2.4
1	B	234	VAL	2.2
1	B	290	ASP	2.2
1	B	371	GLN	2.2
1	A	301	LYS	2.2
1	B	177	ASP	2.1
1	A	175	SER	2.0
1	A	215	TYR	2.0
1	B	158	ALA	2.0

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 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(\AA^2)	Q<0.9
2	ZN	A	601	1/1	0.99	0.09	0.99	23,23,23,23	0
2	ZN	B	601	1/1	0.99	0.07	-0.87	20,20,20,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.