



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 25, 2026 – 02:04 AM EDT

PDB ID : 1SOJ / pdb_00001soj
Title : CATALYTIC DOMAIN OF HUMAN PHOSPHODIESTERASE 3B IN COMPLEX WITH IBMX
Authors : Scapin, G.; Patel, S.B.; Chung, C.; Varnerin, J.P.; Edmondson, S.D.; Mastracchio, A.; Parmee, E.R.; Becker, J.W.; Singh, S.B.; Van Der Ploeg, L.H.; Tota, M.R.
Deposited on : 2004-03-15
Resolution : 2.90 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

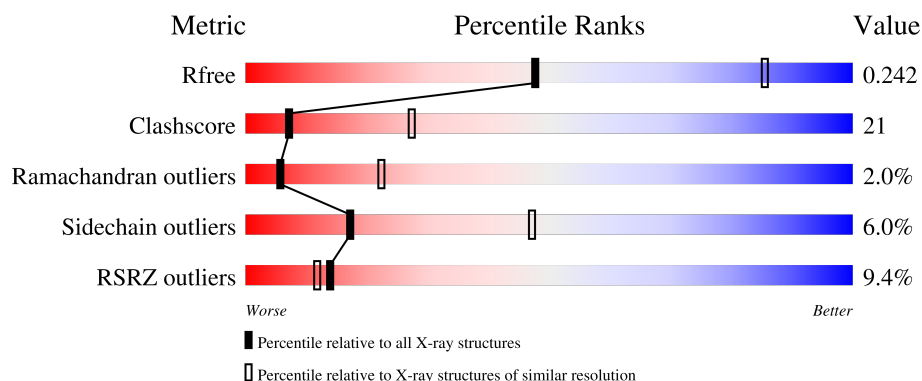
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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}	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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 $\leq 5\%$. 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	420	6% 56% 28% • 13%
1	B	420	8% 53% 32% 5% 9%
1	C	420	6% 53% 29% • 13%
1	D	420	9% 53% 32% 5% 9%

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Mol	Chain	Length	Quality of chain
1	E	420	
1	F	420	
1	G	420	
1	H	420	
1	I	420	
1	J	420	
1	K	420	
1	L	420	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 36048 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 cGMP-inhibited 3',5'-cyclic phosphodiesterase B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	364	Total	C	N	O	S	0	0	0
			2907	1862	496	535	14			
1	B	381	Total	C	N	O	S	0	0	0
			3017	1922	519	562	14			
1	C	364	Total	C	N	O	S	0	0	0
			2907	1862	496	535	14			
1	D	381	Total	C	N	O	S	0	0	0
			3017	1922	519	562	14			
1	E	364	Total	C	N	O	S	0	0	0
			2907	1862	496	535	14			
1	F	381	Total	C	N	O	S	0	0	0
			3017	1922	519	562	14			
1	G	364	Total	C	N	O	S	0	0	0
			2907	1862	496	535	14			
1	H	381	Total	C	N	O	S	0	0	0
			3017	1922	519	562	14			
1	I	364	Total	C	N	O	S	0	0	0
			2907	1862	496	535	14			
1	J	381	Total	C	N	O	S	0	0	0
			3017	1922	519	562	14			
1	K	364	Total	C	N	O	S	0	0	0
			2907	1862	496	535	14			
1	L	381	Total	C	N	O	S	0	0	0
			3017	1922	519	562	14			

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

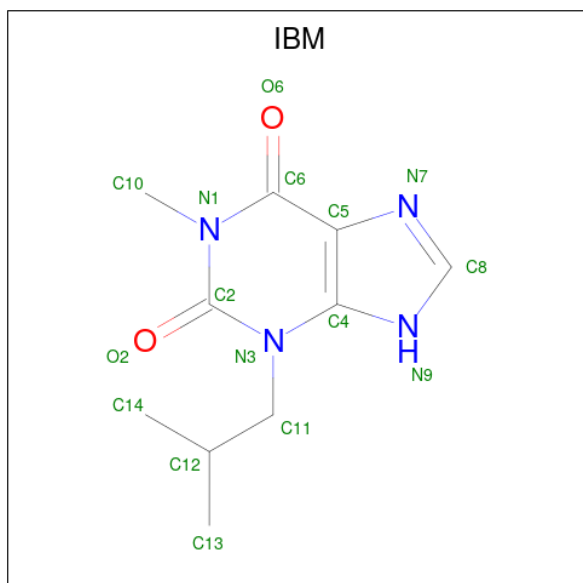
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Mg	0	0
			2	2		
2	B	2	Total	Mg	0	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	2	Total	Mg	0	0
			2	2		
2	D	2	Total	Mg	0	0
			2	2		
2	E	2	Total	Mg	0	0
			2	2		
2	F	2	Total	Mg	0	0
			2	2		
2	G	2	Total	Mg	0	0
			2	2		
2	H	2	Total	Mg	0	0
			2	2		
2	I	2	Total	Mg	0	0
			2	2		
2	J	2	Total	Mg	0	0
			2	2		
2	K	2	Total	Mg	0	0
			2	2		
2	L	2	Total	Mg	0	0
			2	2		

- Molecule 3 is 3-ISOBUTYL-1-METHYLNANTHINE (CCD ID: IBM) (formula: $C_{10}H_{14}N_4O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			16	10	4	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			16	10	4	2		
3	C	1	Total	C	N	O	0	0
			16	10	4	2		
3	D	1	Total	C	N	O	0	0
			16	10	4	2		
3	E	1	Total	C	N	O	0	0
			16	10	4	2		
3	F	1	Total	C	N	O	0	0
			16	10	4	2		
3	G	1	Total	C	N	O	0	0
			16	10	4	2		
3	H	1	Total	C	N	O	0	0
			16	10	4	2		
3	I	1	Total	C	N	O	0	0
			16	10	4	2		
3	J	1	Total	C	N	O	0	0
			16	10	4	2		
3	K	1	Total	C	N	O	0	0
			16	10	4	2		
3	L	1	Total	C	N	O	0	0
			16	10	4	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	24	Total	O	0	0
			24	24		
4	B	24	Total	O	0	0
			24	24		
4	C	24	Total	O	0	0
			24	24		
4	D	24	Total	O	0	0
			24	24		
4	E	23	Total	O	0	0
			23	23		
4	F	25	Total	O	0	0
			25	25		
4	G	23	Total	O	0	0
			23	23		
4	H	25	Total	O	0	0
			25	25		

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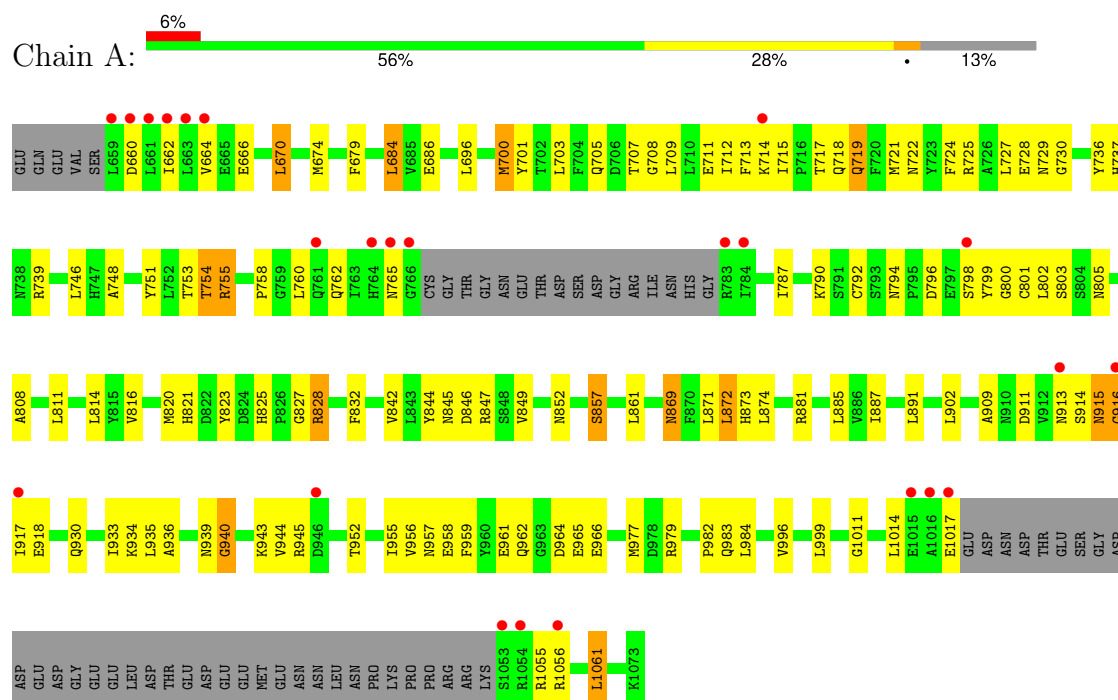
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	I	24	Total 24	O 24	0	0
4	J	24	Total 24	O 24	0	0
4	K	24	Total 24	O 24	0	0
4	L	24	Total 24	O 24	0	0

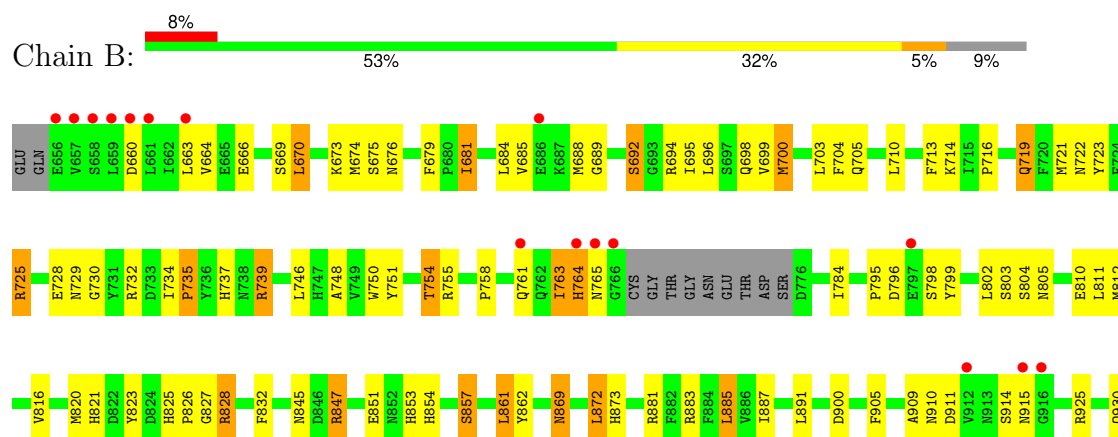
3 Residue-property plots

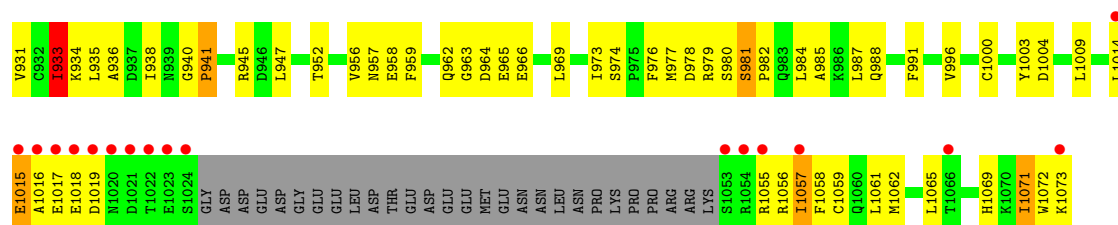
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: cGMP-inhibited 3',5'-cyclic phosphodiesterase B

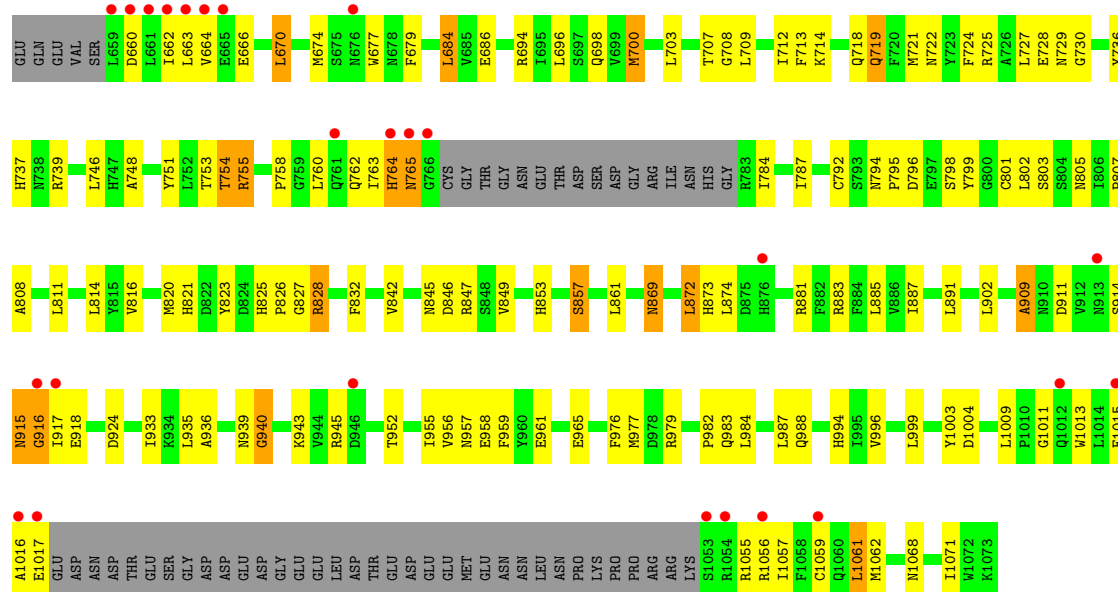


• Molecule 1: cGMP-inhibited 3',5'-cyclic phosphodiesterase B

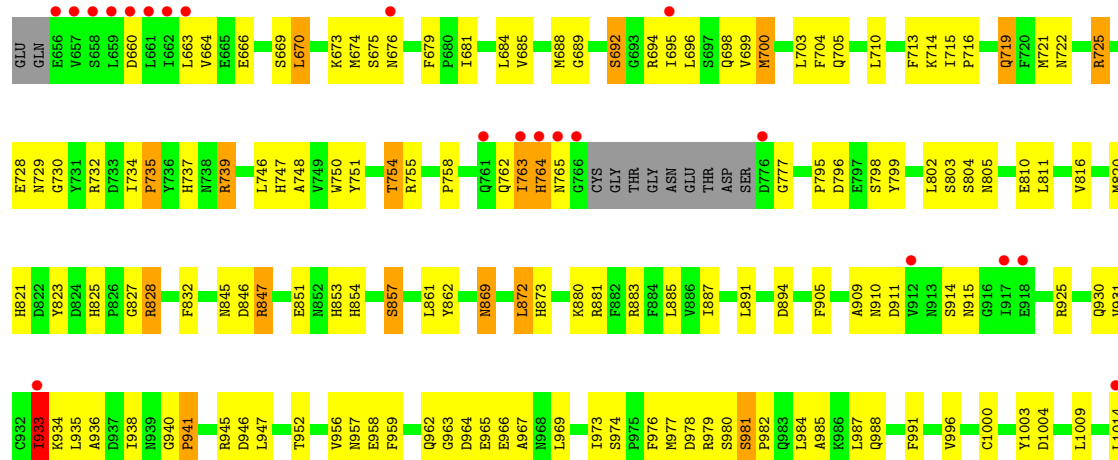


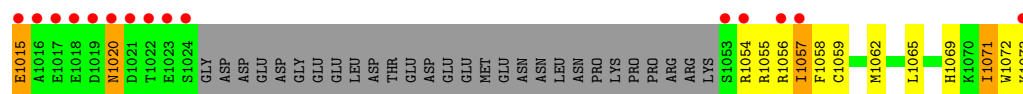


• Molecule 1: cGMP-inhibited 3',5'-cyclic phosphodiesterase B

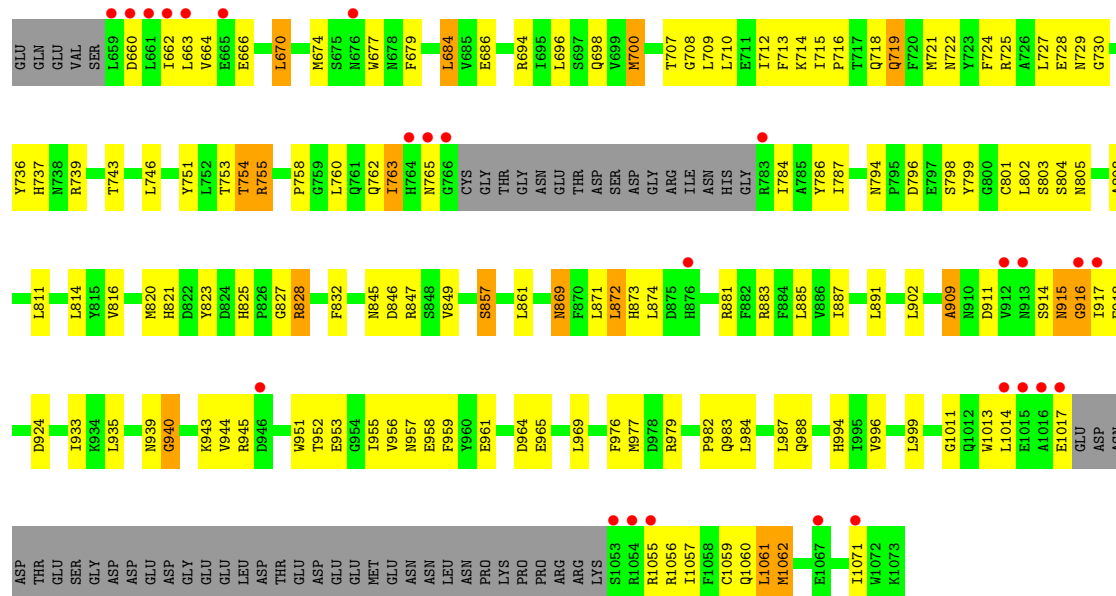


• Molecule 1: cGMP-inhibited 3',5'-cyclic phosphodiesterase B

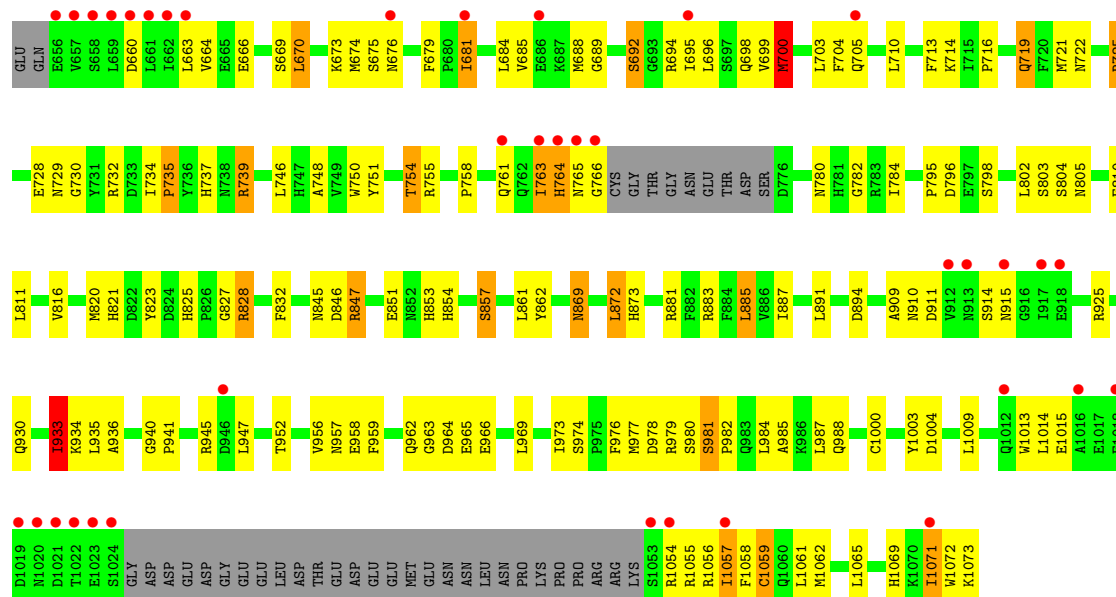




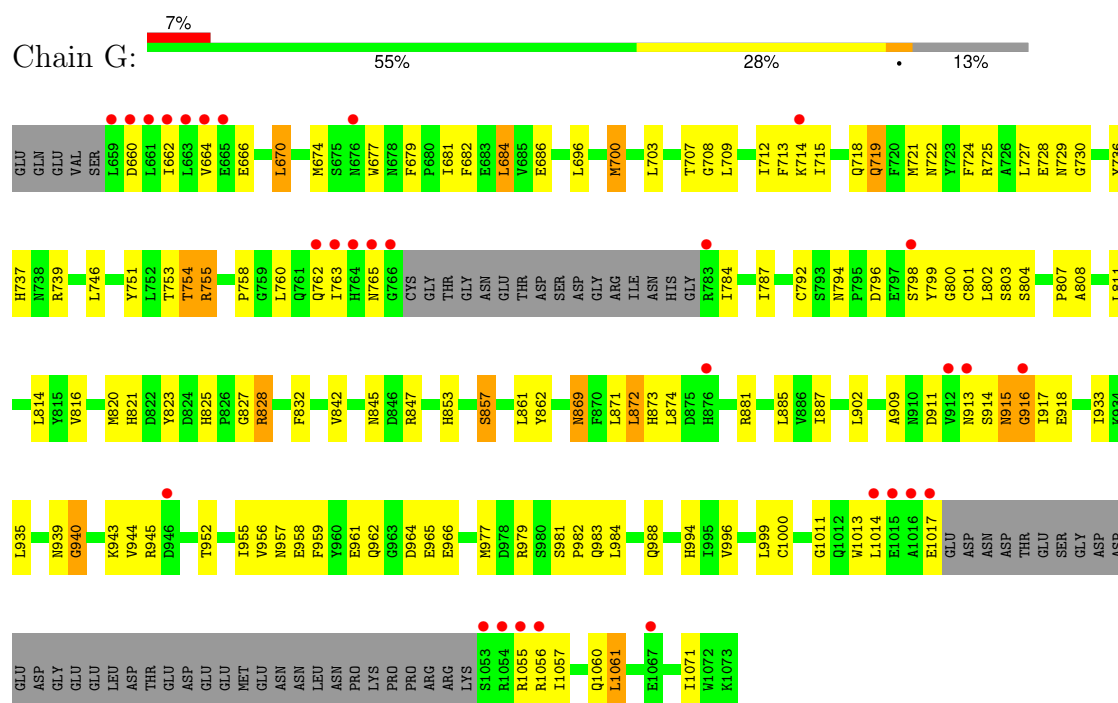
- Molecule 1: cGMP-inhibited 3',5'-cyclic phosphodiesterase B



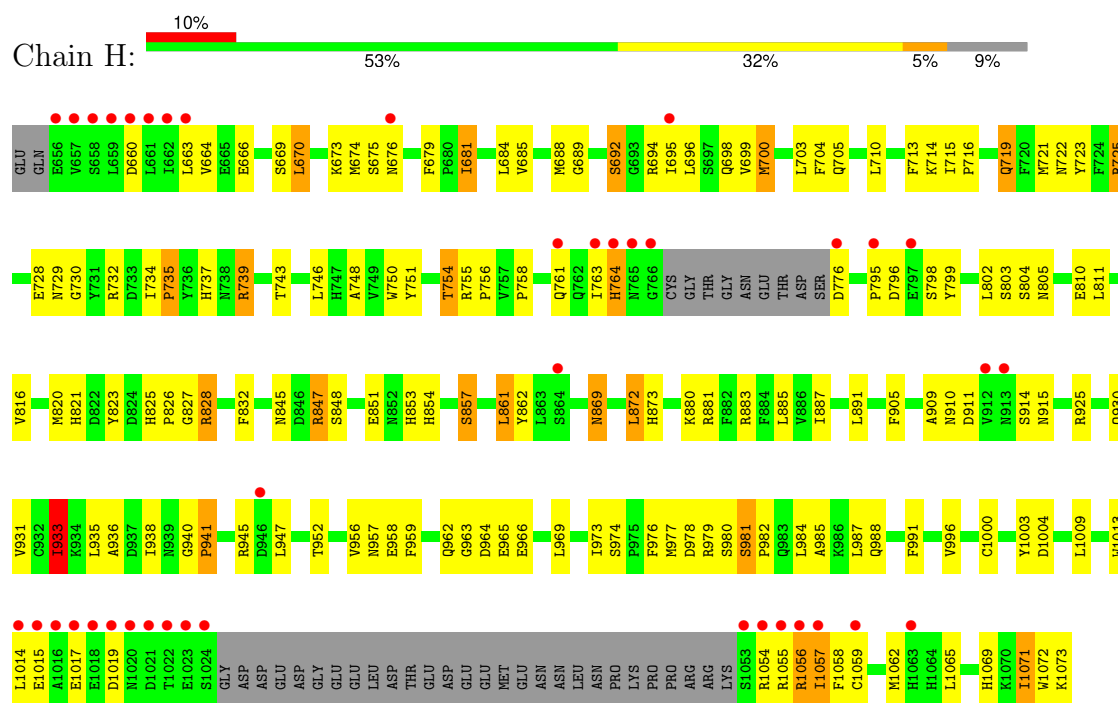
- Molecule 1: cGMP-inhibited 3',5'-cyclic phosphodiesterase B



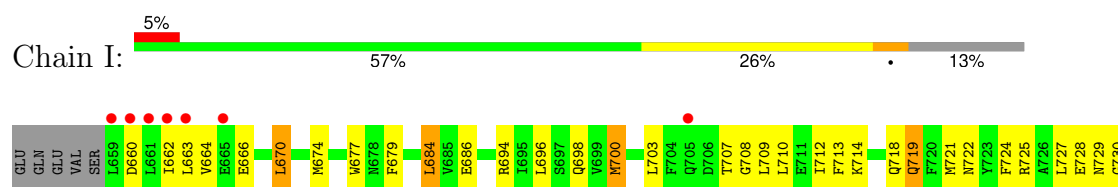
- Molecule 1: cGMP-inhibited 3',5'-cyclic phosphodiesterase B

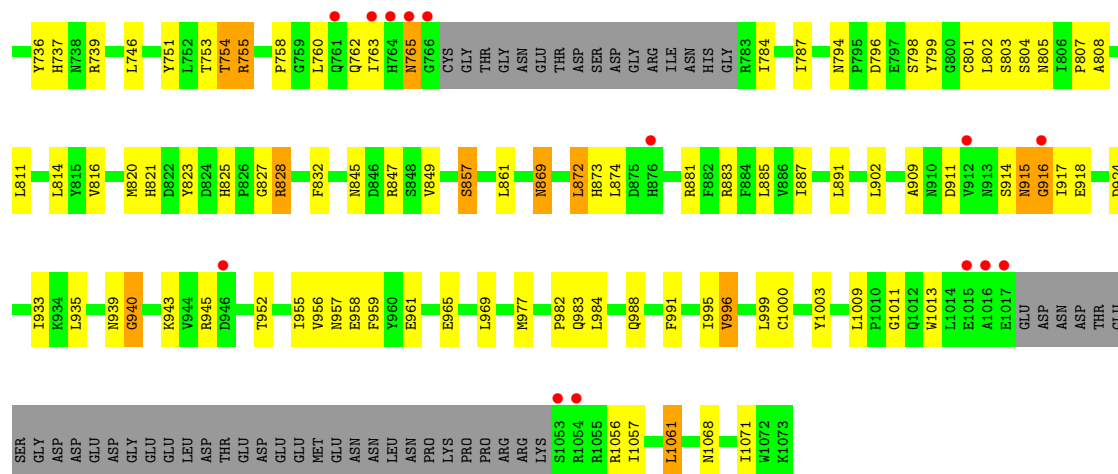


- Molecule 1: cGMP-inhibited 3',5'-cyclic phosphodiesterase B

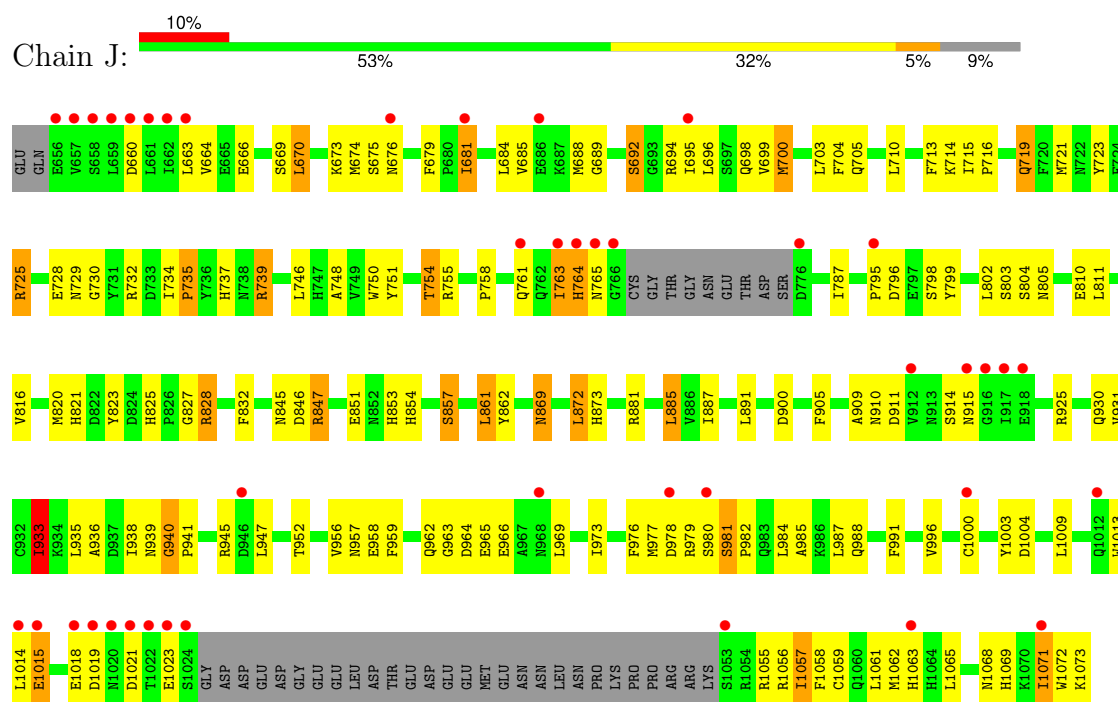


- Molecule 1: cGMP-inhibited 3',5'-cyclic phosphodiesterase B

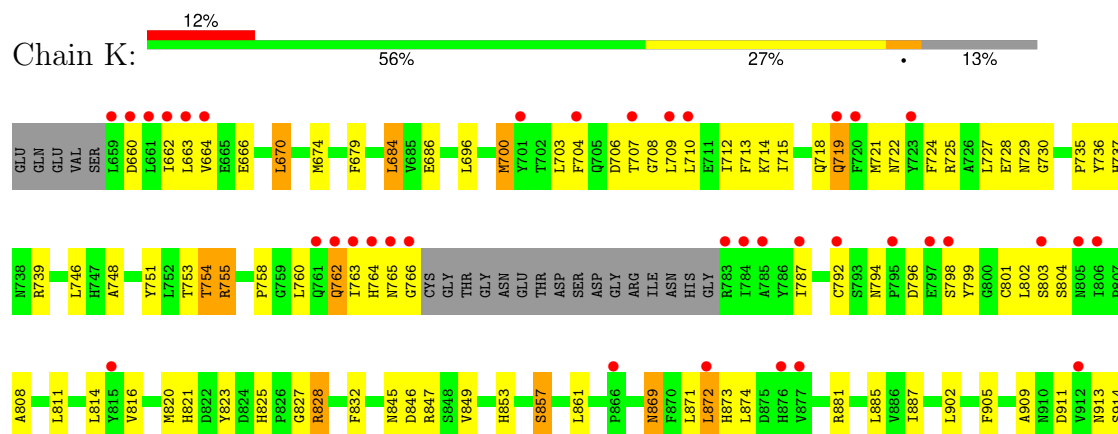


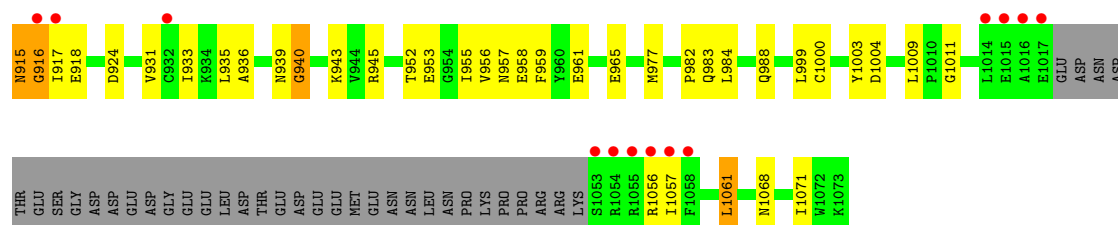


• Molecule 1: cGMP-inhibited 3',5'-cyclic phosphodiesterase B

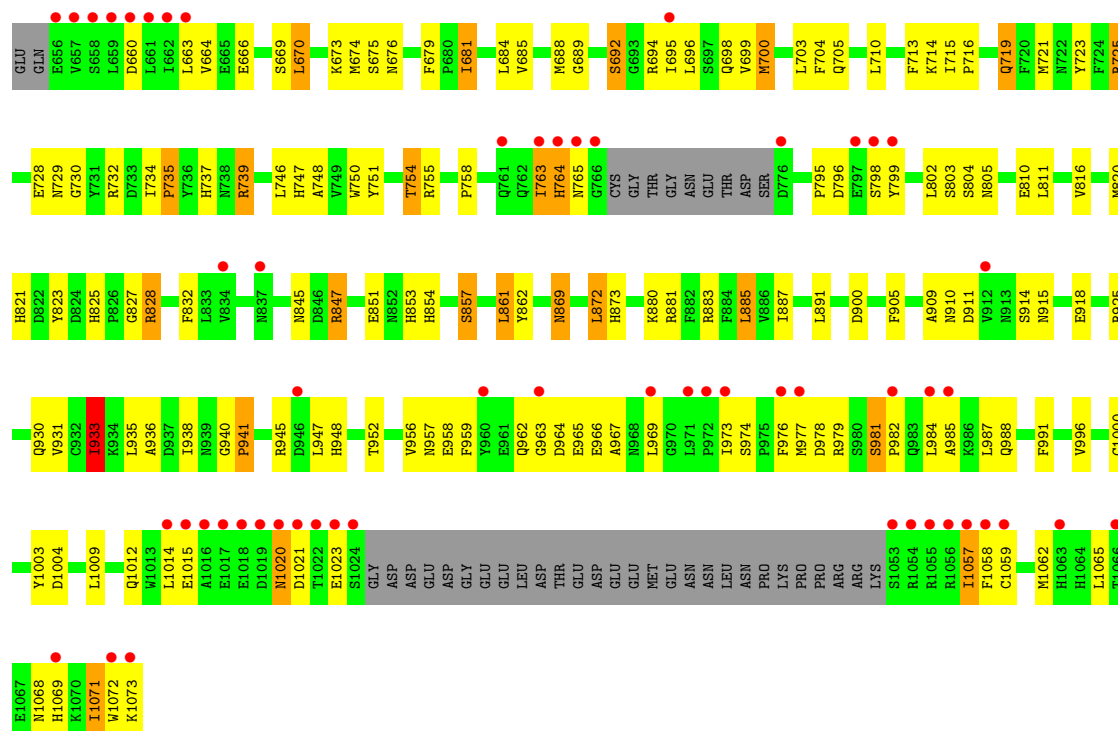


• Molecule 1: cGMP-inhibited 3',5'-cyclic phosphodiesterase B





● Molecule 1: cGMP-inhibited 3',5'-cyclic phosphodiesterase B



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	275.05Å 147.08Å 253.49Å 90.00° 109.84° 90.00°	Depositor
Resolution (Å)	30.00 – 2.90 30.00 – 2.90	Depositor EDS
% Data completeness (in resolution range)	97.7 (30.00-2.90) 96.6 (30.00-2.90)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.14 (at 2.91Å)	Xtriage
Refinement program	CNX	Depositor
R, R_{free}	0.231 , 0.249 0.228 , 0.242	Depositor DCC
R_{free} test set	10128 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	49.3	Xtriage
Anisotropy	0.691	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 54.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	36048	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.30% 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 ⓘ

5.1 Standard geometry ⓘ

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

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	0.57	0/2982	0.91	5/4053 (0.1%)
1	B	0.52	0/3092	0.89	7/4203 (0.2%)
1	C	0.56	0/2982	0.90	6/4053 (0.1%)
1	D	0.59	0/3092	0.89	7/4203 (0.2%)
1	E	0.61	0/2982	0.91	8/4053 (0.2%)
1	F	0.61	1/3092 (0.0%)	0.90	7/4203 (0.2%)
1	G	0.55	0/2982	0.90	9/4053 (0.2%)
1	H	0.53	0/3092	0.88	6/4203 (0.1%)
1	I	0.57	0/2982	0.91	4/4053 (0.1%)
1	J	0.58	0/3092	0.90	8/4203 (0.2%)
1	K	0.52	0/2982	0.90	4/4053 (0.1%)
1	L	0.53	0/3092	0.89	6/4203 (0.1%)
All	All	0.56	1/36444 (0.0%)	0.90	77/49536 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	700	MET	SD-CE	-6.35	1.63	1.79

The worst 5 of 77 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	909	ALA	N-CA-C	8.06	119.76	110.97
1	F	909	ALA	N-CA-C	7.93	119.61	110.97
1	J	909	ALA	N-CA-C	7.87	119.55	110.97
1	B	909	ALA	N-CA-C	7.84	119.51	110.97
1	H	909	ALA	N-CA-C	7.79	119.46	110.97

There are no chirality outliers.

There are no planarity outliers.

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	2907	0	2772	114	0
1	B	3017	0	2834	143	0
1	C	2907	0	2772	130	0
1	D	3017	0	2834	141	0
1	E	2907	0	2772	122	0
1	F	3017	0	2834	132	0
1	G	2907	0	2772	115	0
1	H	3017	0	2834	133	0
1	I	2907	0	2772	114	0
1	J	3017	0	2834	152	0
1	K	2907	0	2772	116	0
1	L	3017	0	2834	131	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
2	E	2	0	0	0	0
2	F	2	0	0	0	0
2	G	2	0	0	0	0
2	H	2	0	0	0	0
2	I	2	0	0	0	0
2	J	2	0	0	0	0
2	K	2	0	0	0	0
2	L	2	0	0	0	0
3	A	16	0	14	0	0
3	B	16	0	14	0	0
3	C	16	0	14	0	0
3	D	16	0	14	0	0
3	E	16	0	14	0	0
3	F	16	0	14	0	0
3	G	16	0	14	0	0
3	H	16	0	14	0	0
3	I	16	0	14	0	0
3	J	16	0	14	0	0
3	K	16	0	14	0	0
3	L	16	0	14	0	0
4	A	24	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	24	0	0	3	0
4	C	24	0	0	1	0
4	D	24	0	0	1	0
4	E	23	0	0	2	0
4	F	25	0	0	1	0
4	G	23	0	0	1	0
4	H	25	0	0	0	0
4	I	24	0	0	1	0
4	J	24	0	0	0	0
4	K	24	0	0	1	0
4	L	24	0	0	1	0
All	All	36048	0	33804	1450	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 21.

The worst 5 of 1450 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:719:GLN:H	1:A:719:GLN:HE21	1.04	1.00
1:E:825:HIS:HD2	1:E:827:GLY:H	1.10	1.00
1:I:719:GLN:H	1:I:719:GLN:HE21	1.06	0.98
1:K:762:GLN:HE22	1:K:804:SER:HB2	1.28	0.98
1:K:719:GLN:H	1:K:719:GLN:HE21	1.06	0.98

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	358/420 (85%)	332 (93%)	21 (6%)	5 (1%)	9 30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	375/420 (89%)	337 (90%)	28 (8%)	10 (3%)	4	16
1	C	358/420 (85%)	330 (92%)	22 (6%)	6 (2%)	7	26
1	D	375/420 (89%)	334 (89%)	31 (8%)	10 (3%)	4	16
1	E	358/420 (85%)	334 (93%)	18 (5%)	6 (2%)	7	26
1	F	375/420 (89%)	335 (89%)	31 (8%)	9 (2%)	4	18
1	G	358/420 (85%)	333 (93%)	22 (6%)	3 (1%)	16	44
1	H	375/420 (89%)	339 (90%)	28 (8%)	8 (2%)	5	21
1	I	358/420 (85%)	332 (93%)	20 (6%)	6 (2%)	7	26
1	J	375/420 (89%)	338 (90%)	28 (8%)	9 (2%)	4	18
1	K	358/420 (85%)	327 (91%)	25 (7%)	6 (2%)	7	26
1	L	375/420 (89%)	334 (89%)	30 (8%)	11 (3%)	3	15
All	All	4398/5040 (87%)	4005 (91%)	304 (7%)	89 (2%)	6	22

5 of 89 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	869	ASN
1	C	765	ASN
1	C	869	ASN
1	D	764	HIS
1	E	763	ILE

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	306/370 (83%)	291 (95%)	15 (5%)	22	54
1	B	313/370 (85%)	292 (93%)	21 (7%)	15	43
1	C	306/370 (83%)	291 (95%)	15 (5%)	22	54
1	D	313/370 (85%)	292 (93%)	21 (7%)	15	43
1	E	306/370 (83%)	292 (95%)	14 (5%)	24	57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	313/370 (85%)	292 (93%)	21 (7%)	15	43
1	G	306/370 (83%)	290 (95%)	16 (5%)	21	52
1	H	313/370 (85%)	290 (93%)	23 (7%)	13	38
1	I	306/370 (83%)	291 (95%)	15 (5%)	22	54
1	J	313/370 (85%)	292 (93%)	21 (7%)	15	43
1	K	306/370 (83%)	287 (94%)	19 (6%)	16	46
1	L	313/370 (85%)	293 (94%)	20 (6%)	16	44
All	All	3714/4440 (84%)	3493 (94%)	221 (6%)	17	47

5 of 221 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	857	SER
1	H	1017	GLU
1	L	1015	GLU
1	K	1057	ILE
1	G	915	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 156 such sidechains are listed below:

Mol	Chain	Res	Type
1	I	957	ASN
1	K	957	ASN
1	J	719	GLN
1	K	718	GLN
1	L	825	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 36 ligands modelled in this entry, 24 are monoatomic - leaving 12 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	IBM	B	2112	-	17,17,17	2.44	4 (23%)	19,25,25	1.42	3 (15%)
3	IBM	F	2116	-	17,17,17	2.30	4 (23%)	19,25,25	1.45	3 (15%)
3	IBM	E	2115	-	17,17,17	2.42	4 (23%)	19,25,25	1.42	3 (15%)
3	IBM	L	2122	-	17,17,17	2.55	4 (23%)	19,25,25	1.47	4 (21%)
3	IBM	D	2114	-	17,17,17	2.54	4 (23%)	19,25,25	1.41	4 (21%)
3	IBM	A	2111	-	17,17,17	2.56	4 (23%)	19,25,25	1.41	3 (15%)
3	IBM	K	2121	-	17,17,17	2.48	4 (23%)	19,25,25	1.36	3 (15%)
3	IBM	H	2118	-	17,17,17	2.47	4 (23%)	19,25,25	1.34	3 (15%)
3	IBM	J	2120	-	17,17,17	2.37	4 (23%)	19,25,25	1.30	3 (15%)
3	IBM	G	2117	-	17,17,17	2.38	4 (23%)	19,25,25	1.40	3 (15%)
3	IBM	C	2113	-	17,17,17	2.47	4 (23%)	19,25,25	1.36	3 (15%)
3	IBM	I	2119	-	17,17,17	2.43	4 (23%)	19,25,25	1.37	3 (15%)

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	IBM	B	2112	-	-	0/4/4/4	0/2/2/2
3	IBM	F	2116	-	-	0/4/4/4	0/2/2/2
3	IBM	E	2115	-	-	0/4/4/4	0/2/2/2
3	IBM	L	2122	-	-	0/4/4/4	0/2/2/2
3	IBM	D	2114	-	-	0/4/4/4	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	IBM	A	2111	-	-	0/4/4/4	0/2/2/2
3	IBM	K	2121	-	-	0/4/4/4	0/2/2/2
3	IBM	H	2118	-	-	0/4/4/4	0/2/2/2
3	IBM	J	2120	-	-	0/4/4/4	0/2/2/2
3	IBM	G	2117	-	-	0/4/4/4	0/2/2/2
3	IBM	C	2113	-	-	0/4/4/4	0/2/2/2
3	IBM	I	2119	-	-	0/4/4/4	0/2/2/2

The worst 5 of 48 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	2114	IBM	C4-N9	6.64	1.47	1.36
3	L	2122	IBM	C4-N9	6.58	1.47	1.36
3	A	2111	IBM	C4-N9	6.56	1.47	1.36
3	E	2115	IBM	C4-N9	6.48	1.47	1.36
3	H	2118	IBM	C4-N9	6.48	1.47	1.36

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	2116	IBM	O6-C6-C5	-3.47	115.66	124.59
3	B	2112	IBM	O6-C6-C5	-3.45	115.69	124.59
3	F	2116	IBM	O6-C6-N1	3.42	126.61	120.36
3	A	2111	IBM	O6-C6-C5	-3.38	115.88	124.59
3	B	2112	IBM	O6-C6-N1	3.36	126.50	120.36

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	364/420 (86%)	0.29	24 (6%)	24 19	24, 42, 80, 100	0
1	B	381/420 (90%)	0.50	33 (8%)	16 13	25, 50, 92, 100	0
1	C	364/420 (86%)	0.24	25 (6%)	23 18	26, 43, 81, 100	0
1	D	381/420 (90%)	0.50	36 (9%)	14 12	22, 47, 89, 100	0
1	E	364/420 (86%)	0.21	26 (7%)	22 17	23, 42, 81, 100	0
1	F	381/420 (90%)	0.52	37 (9%)	13 11	21, 45, 79, 100	0
1	G	364/420 (86%)	0.27	30 (8%)	17 14	24, 44, 83, 100	0
1	H	381/420 (90%)	0.65	40 (10%)	11 10	29, 52, 92, 100	0
1	I	364/420 (86%)	0.16	21 (5%)	29 22	23, 42, 81, 100	0
1	J	381/420 (90%)	0.53	42 (11%)	10 9	22, 46, 77, 100	0
1	K	364/420 (86%)	0.96	50 (13%)	6 5	28, 51, 87, 100	0
1	L	381/420 (90%)	0.94	56 (14%)	6 4	28, 54, 91, 100	0
All	All	4470/5040 (88%)	0.48	420 (9%)	14 12	21, 46, 85, 100	0

The worst 5 of 420 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	1016	ALA	11.1
1	D	1016	ALA	10.7
1	D	1021	ASP	10.4
1	B	1016	ALA	10.4
1	A	766	GLY	10.2

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no oligosaccharides 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, 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($\text{\AA}^2$)	Q<0.9
3	IBM	L	2122	16/16	0.91	0.17	68,77,78,79	0
3	IBM	H	2118	16/16	0.92	0.18	72,78,79,80	0
3	IBM	B	2112	16/16	0.94	0.13	54,56,59,59	0
3	IBM	D	2114	16/16	0.95	0.10	35,53,56,57	0
3	IBM	G	2117	16/16	0.95	0.10	44,49,50,51	0
3	IBM	C	2113	16/16	0.96	0.09	36,42,48,48	0
3	IBM	A	2111	16/16	0.96	0.09	36,38,42,42	0
3	IBM	K	2121	16/16	0.96	0.10	54,59,60,61	0
3	IBM	E	2115	16/16	0.96	0.10	28,32,35,37	0
3	IBM	J	2120	16/16	0.97	0.09	31,35,40,41	0
3	IBM	F	2116	16/16	0.97	0.07	28,37,40,40	0
3	IBM	I	2119	16/16	0.97	0.08	35,38,39,39	0
2	MG	H	2138	1/1	0.98	0.04	32,32,32,32	0
2	MG	C	2128	1/1	0.99	0.02	29,29,29,29	0
2	MG	D	2130	1/1	0.99	0.03	22,22,22,22	0
2	MG	E	2132	1/1	0.99	0.03	29,29,29,29	0
2	MG	B	2126	1/1	0.99	0.03	56,56,56,56	0
2	MG	K	2144	1/1	0.99	0.03	40,40,40,40	0
2	MG	L	2146	1/1	0.99	0.06	30,30,30,30	0
2	MG	J	2142	1/1	1.00	0.03	39,39,39,39	0
2	MG	K	2143	1/1	1.00	0.02	20,20,20,20	0
2	MG	A	2124	1/1	1.00	0.01	41,41,41,41	0
2	MG	L	2145	1/1	1.00	0.03	23,23,23,23	0
2	MG	D	2129	1/1	1.00	0.04	9,9,9,9	0
2	MG	B	2125	1/1	1.00	0.01	4,4,4,4	0
2	MG	E	2131	1/1	1.00	0.03	1,1,1,1	0
2	MG	A	2123	1/1	1.00	0.01	2,2,2,2	0
2	MG	F	2133	1/1	1.00	0.03	1,1,1,1	0
2	MG	F	2134	1/1	1.00	0.03	19,19,19,19	0
2	MG	G	2135	1/1	1.00	0.00	1,1,1,1	0
2	MG	G	2136	1/1	1.00	0.01	28,28,28,28	0
2	MG	H	2137	1/1	1.00	0.02	12,12,12,12	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MG	C	2127	1/1	1.00	0.02	5,5,5,5	0
2	MG	I	2139	1/1	1.00	0.03	5,5,5,5	0
2	MG	I	2140	1/1	1.00	0.02	27,27,27,27	0
2	MG	J	2141	1/1	1.00	0.02	6,6,6,6	0

6.5 Other polymers [i](#)

There are no such residues in this entry.