



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:48 AM GMT

PDB ID : 3G45  
Title : Crystal structure of human phosphodiesterase 4b with regulatory domain and d155988  
Authors : Staker, B.L.  
Deposited on : 2009-02-03  
Resolution : 2.63 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](mailto: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.

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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

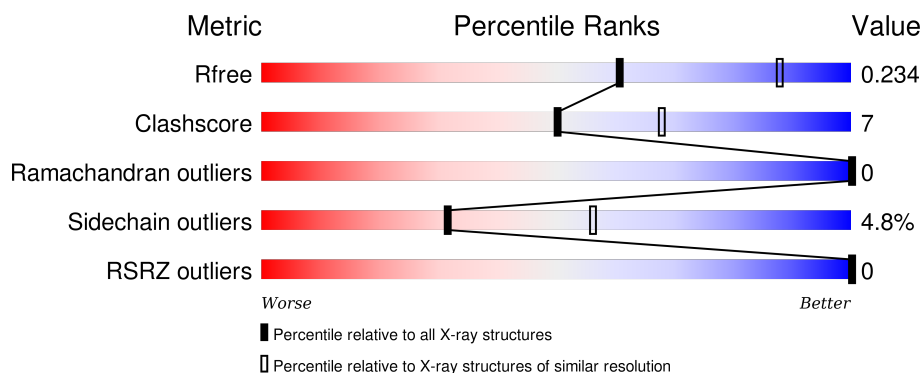
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.63 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	3377 (2.68-2.60)
Clashscore	102246	3781 (2.68-2.60)
Ramachandran outliers	100387	3722 (2.68-2.60)
Sidechain outliers	100360	3722 (2.68-2.60)
RSRZ outliers	91569	3388 (2.68-2.60)

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  $\geq 3$ , 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	421	 74% 13% 12%
1	B	421	 72% 15% • 12%

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
2	ZN	B	801	-	-	-	X
3	MG	A	802	-	-	-	X
3	MG	B	802	-	-	-	X
4	988	B	901	-	-	-	X

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 6133 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 cAMP-specific 3',5'-cyclic phosphodiesterase 4B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	371	Total	C	N	O	S	0	0	0
			2992	1881	509	581	21			
1	B	370	Total	C	N	O	S	0	0	0
			2985	1877	508	579	21			

There are 34 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	240	MET	-	expression tag	UNP Q07343
A	295	LYS	-	linker	UNP Q07343
A	296	VAL	-	linker	UNP Q07343
A	297	THR	-	linker	UNP Q07343
A	298	ALA	-	linker	UNP Q07343
A	299	GLU	-	linker	UNP Q07343
A	300	GLU	-	linker	UNP Q07343
A	301	ALA	-	linker	UNP Q07343
A	302	PRO	-	linker	UNP Q07343
A	303	GLN	-	linker	UNP Q07343
A	304	PRO	-	linker	UNP Q07343
A	660	HIS	-	expression tag	UNP Q07343
A	661	HIS	-	expression tag	UNP Q07343
A	662	HIS	-	expression tag	UNP Q07343
A	663	HIS	-	expression tag	UNP Q07343
A	664	HIS	-	expression tag	UNP Q07343
A	665	HIS	-	expression tag	UNP Q07343
B	240	MET	-	expression tag	UNP Q07343
B	295	LYS	-	linker	UNP Q07343
B	296	VAL	-	linker	UNP Q07343
B	297	THR	-	linker	UNP Q07343
B	298	ALA	-	linker	UNP Q07343
B	299	GLU	-	linker	UNP Q07343
B	300	GLU	-	linker	UNP Q07343
B	301	ALA	-	linker	UNP Q07343

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Chain	Residue	Modelled	Actual	Comment	Reference
B	302	PRO	-	linker	UNP Q07343
B	303	GLN	-	linker	UNP Q07343
B	304	PRO	-	linker	UNP Q07343
B	660	HIS	-	expression tag	UNP Q07343
B	661	HIS	-	expression tag	UNP Q07343
B	662	HIS	-	expression tag	UNP Q07343
B	663	HIS	-	expression tag	UNP Q07343
B	664	HIS	-	expression tag	UNP Q07343
B	665	HIS	-	expression tag	UNP Q07343

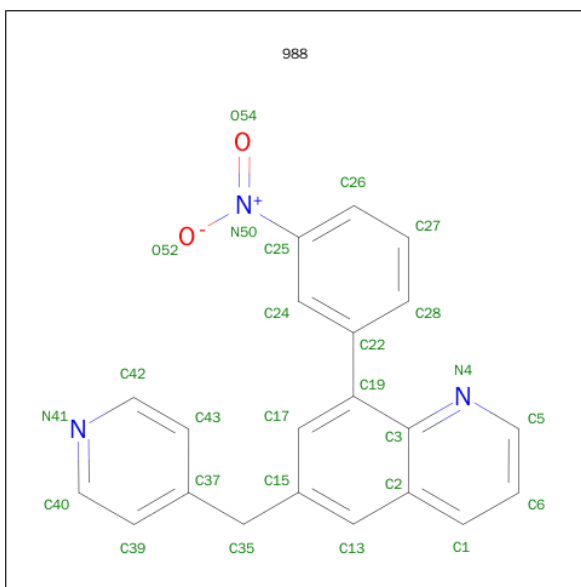
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

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 MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 4 is 8-(3-NITROPHENYL)-6-(PYRIDIN-4-YLMETHYL)QUINOLINE (three-letter code: 988) (formula: C<sub>21</sub>H<sub>15</sub>N<sub>3</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			26	21	3	2		
4	B	1	Total	C	N	O	0	0
			26	21	3	2		

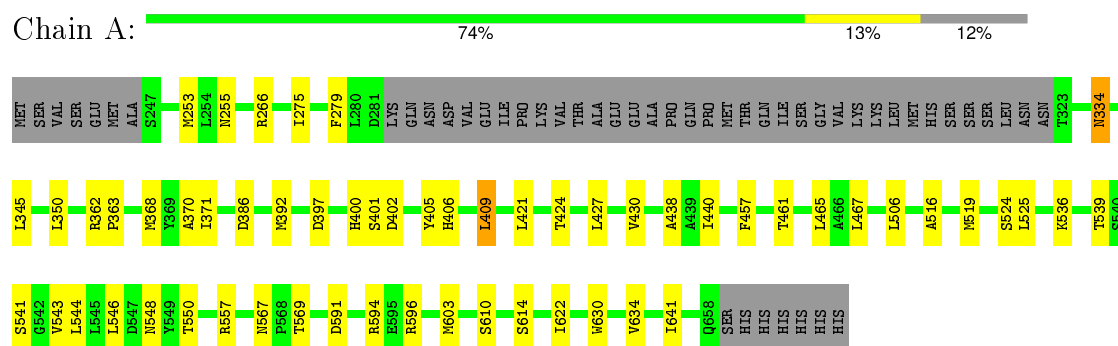
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	52	Total	O	0	0
			52	52		
5	B	48	Total	O	0	0
			48	48		

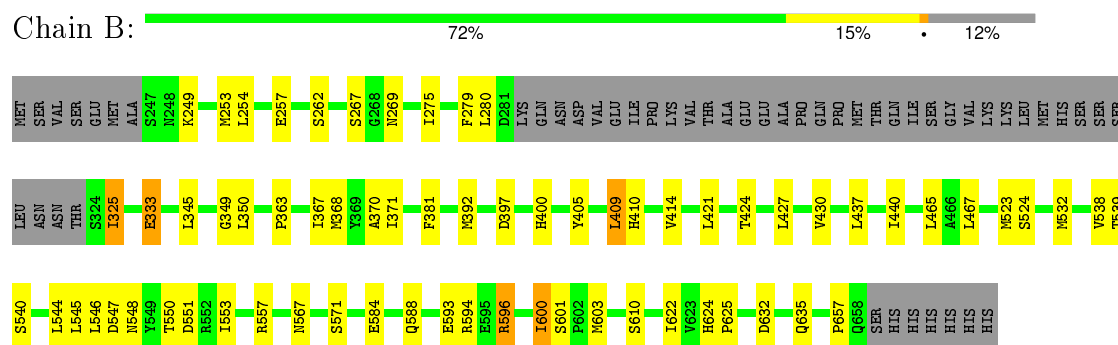
### 3 Residue-property plots

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: cAMP-specific 3',5'-cyclic phosphodiesterase 4B



- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4B



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	95.00 Å 95.00 Å 93.71 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.63 42.37 – 2.63	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.63) 99.7 (42.37-2.63)	Depositor EDS
$R_{merge}$	0.24	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.24 (at 2.65 Å)	Xtriage
Refinement program	REFMAC 5.5.0070	Depositor
R, $R_{free}$	0.179 , 0.233 0.185 , 0.234	Depositor DCC
$R_{free}$ test set	1413 reflections (5.31%)	DCC
Wilson B-factor (Å <sup>2</sup> )	34.8	Xtriage
Anisotropy	0.065	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 9.2	EDS
Estimated twinning fraction	0.022 for -h,-k,l 0.449 for h,-h-k,-l 0.024 for -k,-h,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 28022 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	6133	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.28% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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, MG, 988

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	0.63	0/3051	0.66	1/4133 (0.0%)
1	B	0.61	0/3044	0.69	1/4123 (0.0%)
All	All	0.62	0/6095	0.68	2/8256 (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	B	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	325	ILE	CG1-CB-CG2	6.45	125.59	111.40
1	A	362	ARG	NE-CZ-NH2	-5.09	117.75	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	540	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	2992	0	2898	41	0
1	B	2985	0	2891	43	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	26	0	15	4	0
4	B	26	0	15	1	0
5	A	52	0	0	1	0
5	B	48	0	0	1	0
All	All	6133	0	5819	83	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 7.

All (83) 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:421:LEU:O	1:B:424:THR:HG22	1.71	0.90
1:B:538:VAL:HG12	1:B:539:THR:O	1.72	0.90
1:A:421:LEU:O	1:A:424:THR:HG22	1.81	0.80
1:B:279:PHE:CD1	1:B:622:ILE:HD13	2.19	0.77
1:B:539:THR:HG22	1:B:545:LEU:HD13	1.68	0.75
1:B:596:ARG:HD3	5:B:55:HOH:O	1.87	0.73
1:B:424:THR:CG2	1:B:427:LEU:HD12	2.19	0.72
1:B:280:LEU:HD23	1:B:523:MET:HG3	1.72	0.71
1:B:424:THR:HG21	1:B:427:LEU:HD12	1.75	0.68
1:B:280:LEU:CD2	1:B:523:MET:HG3	2.24	0.68
1:B:368:MET:HG3	1:B:392:MET:HE1	1.76	0.67
1:B:594:ARG:HG3	1:B:600:ILE:HD11	1.78	0.64
1:A:400:HIS:HB3	1:A:402:ASP:OD1	1.98	0.64
1:B:567:ASN:HD22	4:B:901:988:H1	1.62	0.63
1:A:279:PHE:CD1	1:A:622:ILE:HD13	2.34	0.63
1:B:279:PHE:CD1	1:B:622:ILE:CD1	2.83	0.62
1:B:603:MET:HE3	1:B:603:MET:HA	1.81	0.62
1:A:334:ASN:OD1	1:B:657:PRO:HG2	2.00	0.62
1:A:279:PHE:CE1	1:A:622:ILE:HD13	2.35	0.61
1:A:519:MET:HA	1:A:519:MET:CE	2.30	0.61
1:B:280:LEU:HD23	1:B:523:MET:CG	2.31	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:519:MET:HE3	1:A:519:MET:HA	1.84	0.60
1:A:548:ASN:HD22	1:A:550:THR:HB	1.66	0.60
1:B:584:GLU:OE1	1:B:588:GLN:NE2	2.34	0.59
1:B:368:MET:HG3	1:B:392:MET:CE	2.33	0.58
1:A:525:LEU:HD21	1:A:557:ARG:HD2	1.85	0.58
1:A:539:THR:HG22	1:A:543:VAL:O	2.03	0.58
1:B:371:ILE:HG21	1:B:440:ILE:HD13	1.85	0.58
1:A:591:ASP:OD1	1:A:594:ARG:NH1	2.35	0.57
1:B:279:PHE:CE1	1:B:622:ILE:HD13	2.39	0.57
1:A:424:THR:CG2	1:A:427:LEU:HD12	2.35	0.57
1:B:548:ASN:ND2	1:B:550:THR:HB	2.20	0.56
1:A:548:ASN:ND2	1:A:550:THR:HB	2.20	0.56
1:A:603:MET:HE1	4:A:901:988:H26	1.87	0.56
1:A:567:ASN:HD22	4:A:901:988:H1	1.71	0.55
1:B:345:LEU:HD22	1:B:370:ALA:HB1	1.88	0.54
1:A:630:TRP:O	1:A:634:VAL:HG22	2.08	0.54
1:B:430:VAL:HG11	1:B:546:LEU:HD12	1.90	0.53
1:A:368:MET:HG3	1:A:392:MET:HE1	1.92	0.52
1:A:275:ILE:HG12	1:A:622:ILE:HD11	1.91	0.52
1:A:438:ALA:HB2	1:A:506:LEU:HD12	1.92	0.52
1:A:279:PHE:CD1	1:A:622:ILE:CD1	2.94	0.51
1:A:368:MET:HG3	1:A:392:MET:CE	2.41	0.51
1:A:371:ILE:HG21	1:A:440:ILE:HD13	1.94	0.50
1:A:397:ASP:HB3	5:A:94:HOH:O	2.12	0.50
1:B:405:TYR:OH	1:B:567:ASN:ND2	2.42	0.50
1:A:603:MET:HE1	1:A:614:SER:HB3	1.94	0.49
1:B:624:HIS:HB3	1:B:625:PRO:HD3	1.94	0.49
1:B:603:MET:CE	1:B:603:MET:HA	2.43	0.48
1:A:424:THR:HG21	1:A:427:LEU:HD12	1.95	0.48
1:B:253:MET:O	1:B:257:GLU:HG3	2.14	0.48
1:B:548:ASN:HD22	1:B:550:THR:HB	1.79	0.47
1:A:430:VAL:HG11	1:A:546:LEU:HD12	1.98	0.46
1:A:427:LEU:HD21	1:A:544:LEU:HD12	1.98	0.45
1:A:350:LEU:HD23	1:A:350:LEU:C	2.36	0.45
1:B:381:PHE:CD2	1:B:437:LEU:HD22	2.51	0.45
1:B:275:ILE:HG12	1:B:622:ILE:HD12	1.99	0.45
1:A:427:LEU:CD2	1:A:544:LEU:HD12	2.47	0.45
1:A:406:HIS:CE1	4:A:901:988:H40	2.52	0.45
1:B:363:PRO:HG3	1:B:409:LEU:HD13	1.98	0.45
1:B:553:ILE:O	1:B:557:ARG:HG2	2.17	0.44
1:A:402:ASP:OD1	1:A:402:ASP:N	2.44	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:569:THR:HB	1:A:641:ILE:HG23	1.99	0.44
1:B:593:GLU:OE2	1:B:601:SER:OG	2.29	0.44
1:A:457:PHE:O	1:A:461:THR:HG23	2.17	0.44
1:B:427:LEU:CD2	1:B:544:LEU:HD12	2.48	0.43
1:A:516:ALA:HB2	1:A:557:ARG:HD3	2.01	0.43
1:B:254:LEU:HD11	1:B:280:LEU:HD21	1.99	0.43
1:A:345:LEU:HD22	1:A:370:ALA:HB1	2.01	0.43
1:B:262:SER:HB2	1:B:269:ASN:ND2	2.34	0.43
1:A:525:LEU:HD21	1:A:557:ARG:CD	2.49	0.42
1:A:405:TYR:OH	1:A:567:ASN:ND2	2.52	0.42
1:B:349:GLY:O	1:B:350:LEU:C	2.57	0.42
1:A:603:MET:CE	4:A:901:988:H26	2.49	0.42
1:B:371:ILE:CG2	1:B:440:ILE:HD13	2.49	0.42
1:B:367:ILE:HA	1:B:367:ILE:HD12	1.93	0.41
1:B:333:GLU:H	1:B:333:GLU:CD	2.23	0.41
1:A:275:ILE:HG12	1:A:622:ILE:CD1	2.50	0.41
1:A:363:PRO:HG3	1:A:409:LEU:HD13	2.02	0.41
1:B:262:SER:HB2	1:B:269:ASN:HD22	1.86	0.41
1:B:410:HIS:O	1:B:414:VAL:HG23	2.21	0.41
1:A:334:ASN:N	1:A:334:ASN:HD22	2.19	0.41
1:B:548:ASN:ND2	1:B:551:ASP:H	2.19	0.40

There are no symmetry-related clashes.

## 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	367/421 (87%)	361 (98%)	6 (2%)	0	100	100
1	B	366/421 (87%)	357 (98%)	9 (2%)	0	100	100
All	All	733/842 (87%)	718 (98%)	15 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	337/385 (88%)	323 (96%)	14 (4%)	36	63
1	B	336/385 (87%)	318 (95%)	18 (5%)	27	50
All	All	673/770 (87%)	641 (95%)	32 (5%)	31	56

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	253	MET
1	A	255	ASN
1	A	266	ARG
1	A	334	ASN
1	A	386	ASP
1	A	401	SER
1	A	409	LEU
1	A	465	LEU
1	A	467	LEU
1	A	524	SER
1	A	536	LYS
1	A	541	SER
1	A	596	ARG
1	A	610	SER
1	B	249	LYS
1	B	267	SER
1	B	325	ILE
1	B	333	GLU
1	B	397	ASP
1	B	400	HIS
1	B	409	LEU
1	B	465	LEU
1	B	467	LEU
1	B	524	SER
1	B	532	MET

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Mol	Chain	Res	Type
1	B	547	ASP
1	B	571	SER
1	B	596	ARG
1	B	600	ILE
1	B	610	SER
1	B	632	ASP
1	B	635	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	269	ASN
1	A	277	ASN
1	A	567	ASN
1	A	658	GLN
1	B	269	ASN
1	B	361	ASN
1	B	548	ASN
1	B	567	ASN
1	B	577	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](#)

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 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 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	$\# Z  > 2$
4	988	A	901	-	27,29,29	2.16	3 (11%)	37,40,40	1.47	7 (18%)
4	988	B	901	-	27,29,29	2.16	3 (11%)	37,40,40	1.65	7 (18%)

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
4	988	A	901	-	-	0/12/12/12	0/4/4/4
4	988	B	901	-	-	0/12/12/12	0/4/4/4

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	901	988	C19-C3	3.45	1.47	1.43
4	A	901	988	C2-C3	3.88	1.47	1.42
4	B	901	988	C19-C3	3.92	1.48	1.43
4	B	901	988	C2-C3	3.93	1.48	1.42
4	B	901	988	O54-N50	8.80	1.40	1.22
4	A	901	988	O54-N50	9.09	1.40	1.22

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	901	988	C19-C3-C2	-4.63	117.08	119.28
4	A	901	988	C19-C3-C2	-3.93	117.41	119.28
4	B	901	988	C22-C19-C3	-3.18	117.64	122.68
4	A	901	988	C22-C19-C3	-2.69	118.41	122.68
4	B	901	988	C35-C15-C13	-2.16	118.35	123.46
4	A	901	988	C35-C15-C13	-2.09	118.52	123.46
4	A	901	988	C2-C3-N4	-2.08	120.08	122.50
4	B	901	988	C2-C3-N4	-2.04	120.12	122.50
4	B	901	988	C5-N4-C3	2.07	119.82	117.37
4	A	901	988	C5-N4-C3	2.09	119.85	117.37
4	A	901	988	C13-C15-C17	2.30	120.96	118.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	901	988	C13-C15-C17	2.93	121.62	118.55
4	A	901	988	C19-C3-N4	3.96	122.51	118.76
4	B	901	988	C19-C3-N4	4.27	122.79	118.76

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	901	988	4	0
4	B	901	988	1	0

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	371/421 (88%)	-0.40	0 100 100	21, 34, 53, 63	0
1	B	370/421 (87%)	-0.38	0 100 100	22, 34, 56, 61	0
All	All	741/842 (88%)	-0.39	0 100 100	21, 34, 54, 63	0

There are no RSRZ outliers to report.

### 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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
3	MG	B	802	1/1	0.96	0.30	15.46	14,14,14,14	0
3	MG	A	802	1/1	0.91	0.35	12.05	22,22,22,22	0
2	ZN	B	801	1/1	0.99	0.17	5.22	31,31,31,31	0
4	988	B	901	26/26	0.96	0.19	2.79	31,37,44,47	0
2	ZN	A	801	1/1	0.99	0.15	1.25	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	988	A	901	26/26	0.95	0.18	1.13	32,37,44,49	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.