



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 04:19 AM UTC

PDB ID : 2NYL / pdb\_00002nyl  
Title : Crystal structure of Protein Phosphatase 2A (PP2A) holoenzyme with the catalytic subunit carboxyl terminus truncated  
Authors : Xing, Y.; Xu, Y.; Chen, Y.; Chao, Y.; Lin, Z.; Shi, Y.  
Deposited on : 2006-11-20  
Resolution : 3.80 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](mailto: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>.

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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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

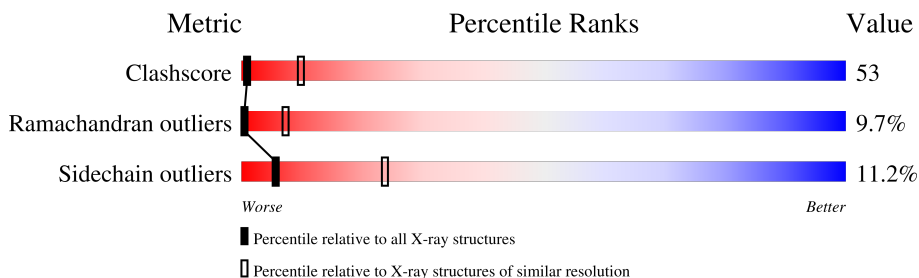
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.80 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))
Clashscore	190562	1012 (3.94-3.66)
Ramachandran outliers	187476	1048 (3.96-3.64)
Sidechain outliers	187428	1043 (3.96-3.64)

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  $\geq 3$ , 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  $\leq 5\%$ .

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	582	
1	D	582	
2	B	388	
2	E	388	
3	C	293	
3	F	293	
4	G	7	
4	H	7	

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 20212 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 Protein phosphatase 2, regulatory subunit A (PR 65), alpha isoform.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	582	Total	C	N	O	S	Se	0	0	0
			4535	2881	764	863	14	13			
1	D	582	Total	C	N	O	S	Se	0	0	0
			4535	2881	764	863	14	13			

- Molecule 2 is a protein called Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	388	Total	C	N	O	S	Se	0	0	0
			3131	2043	513	561	3	11			
2	E	388	Total	C	N	O	S	Se	0	0	0
			3131	2043	513	561	3	11			

- Molecule 3 is a protein called Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	293	Total	C	N	O	S	0	0	0
			2367	1497	405	450	15			
3	F	293	Total	C	N	O	S	0	0	0
			2367	1497	405	450	15			

- Molecule 4 is a protein called microcystin LR.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	G	7	Total	C	N	O	0	0	0
			71	49	10	12			
4	H	7	Total	C	N	O	0	0	0
			71	49	10	12			

- Molecule 5 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	2	Total 2	Mn 2	0	0
5	F	2	Total 2	Mn 2	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. 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. 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.

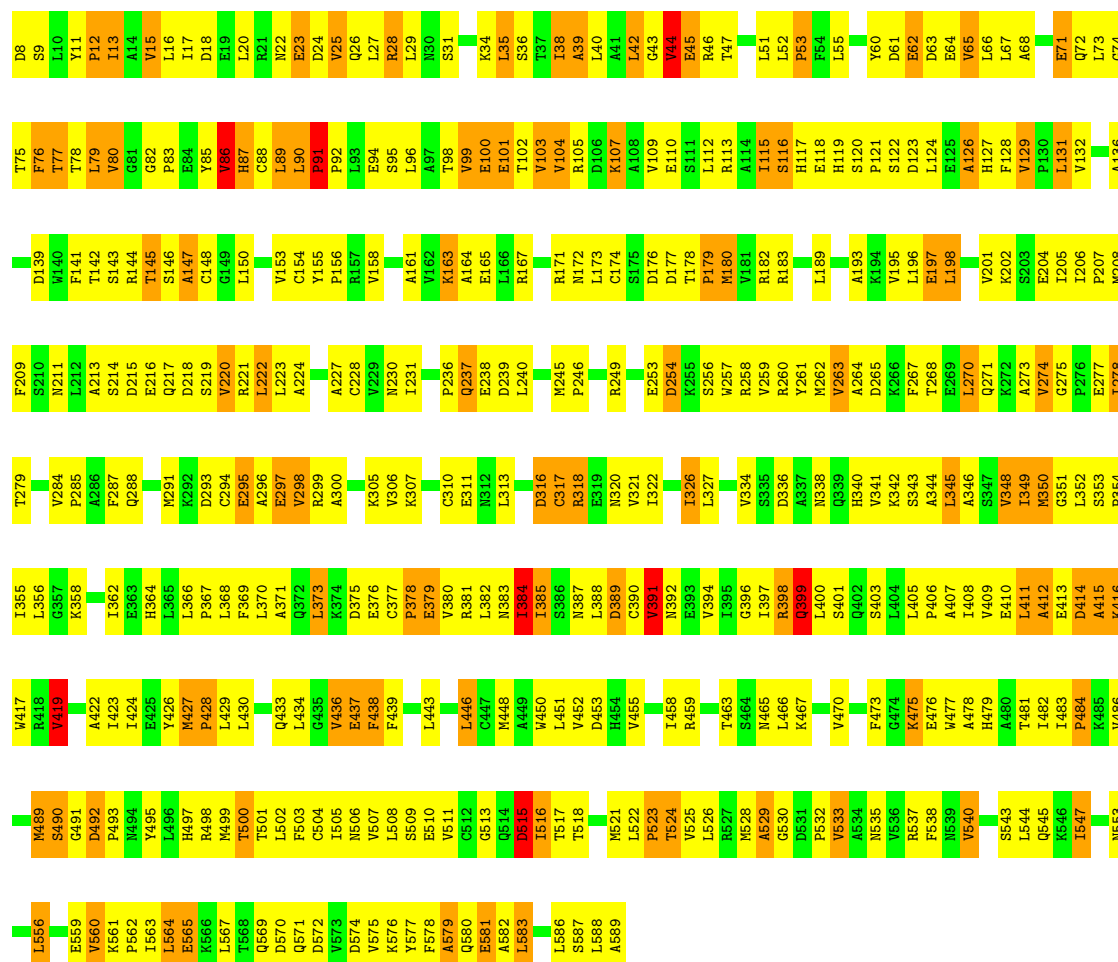
Note EDS was not executed.

- Molecule 1: Protein phosphatase 2, regulatory subunit A (PR 65), alpha isoform



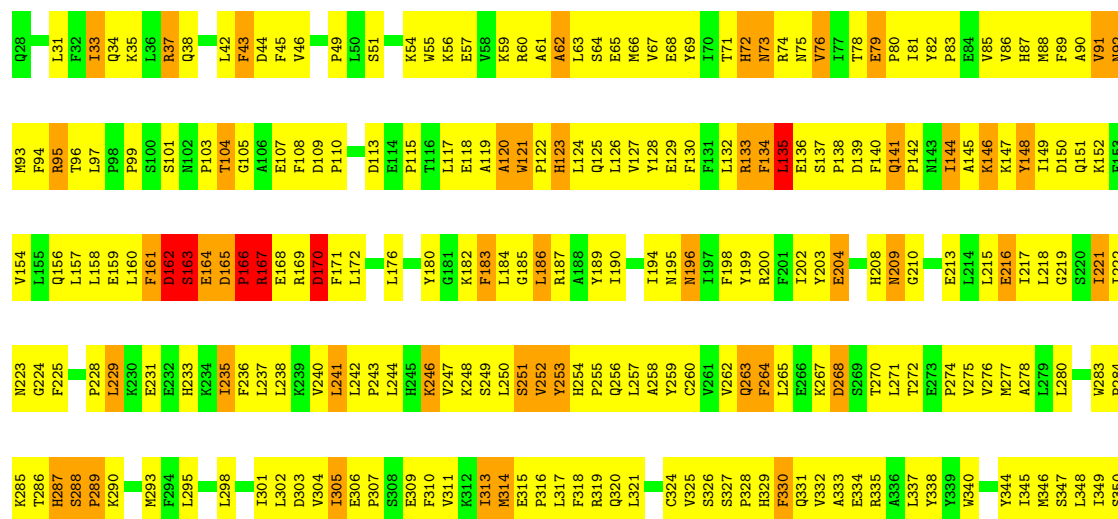
- Molecule 1: Protein phosphatase 2, regulatory subunit A (PR 65), alpha isoform





• Molecule 2: Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform

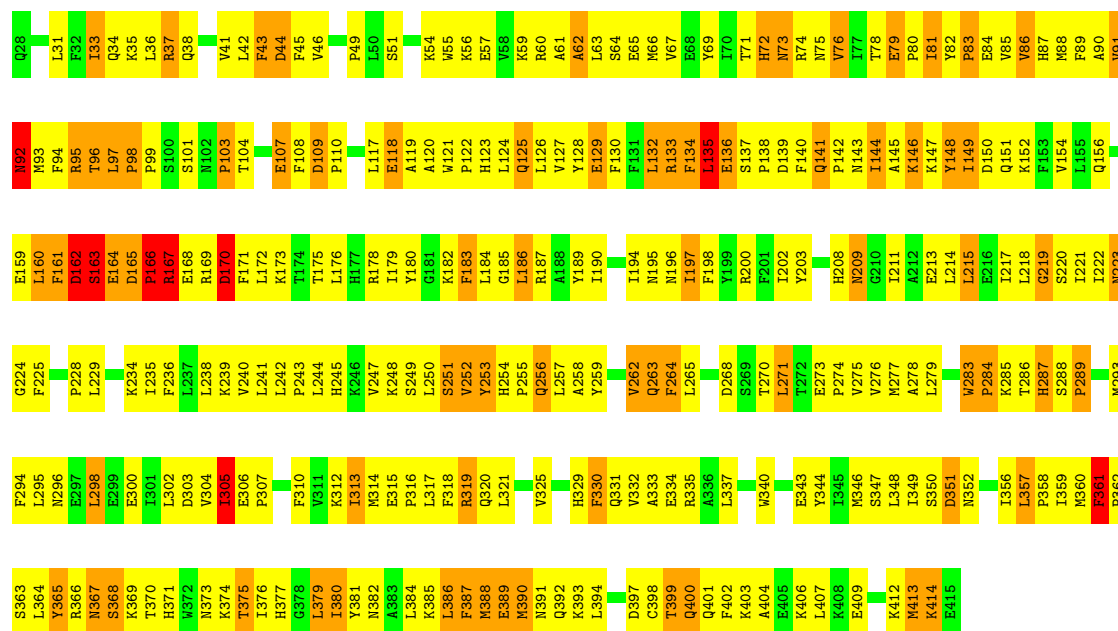
Chain B: 25% 56% 17%





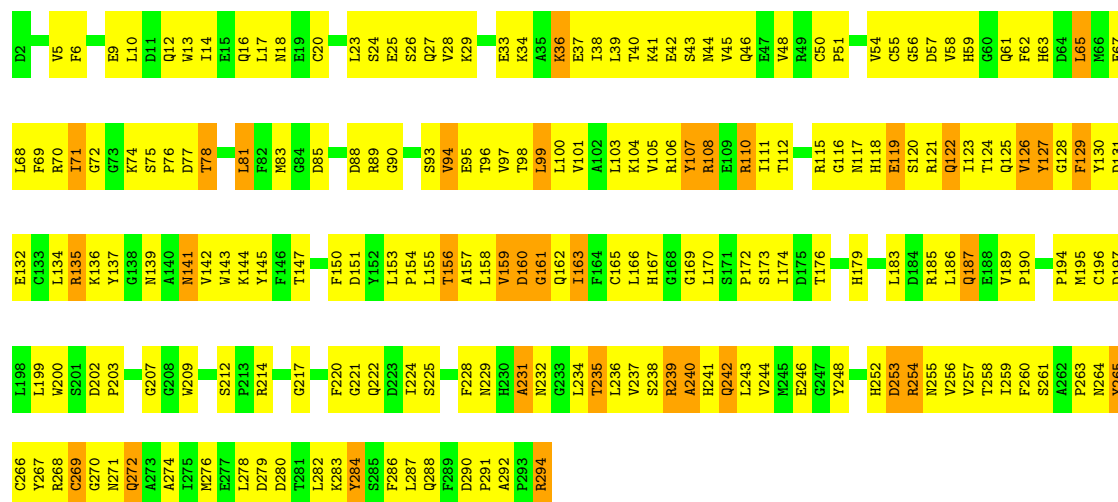
- Molecule 2: Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform

Chain E: 25% 53% 20%



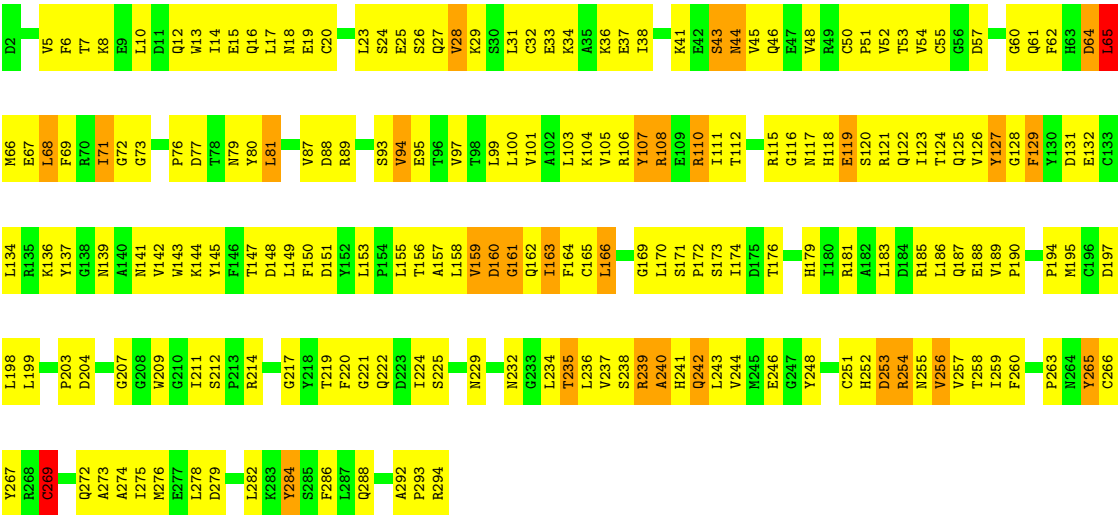
- Molecule 3: Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform

Chain C: 29% 59% 12%



- Molecule 3: Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform

Chain F: 32% 58% 10%



● Molecule 4: microcystin LR



● Molecule 4: microcystin LR





## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	108.48Å 159.85Å 270.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	100.00 – 3.80	Depositor
% Data completeness (in resolution range)	99.6 (100.00-3.80)	Depositor
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	CNS	Depositor
R, $R_{free}$	0.282 , 0.335	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	20212	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	80.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MN, ACB, DAL, FGA, 1ZN, DAM

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	0.60	0/4596	1.11	38/6218 (0.6%)
1	D	0.77	0/4596	1.13	36/6218 (0.6%)
2	B	0.62	0/3202	1.11	28/4326 (0.6%)
2	E	0.70	1/3202 (0.0%)	1.11	30/4326 (0.7%)
3	C	0.59	0/2424	1.04	11/3285 (0.3%)
3	F	0.61	0/2424	1.06	12/3285 (0.4%)
4	G	0.32	0/17	0.90	0/19
4	H	0.35	0/17	0.96	0/19
All	All	0.66	1/20478 (0.0%)	1.10	155/27696 (0.6%)

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
4	G	0	3
4	H	0	3
All	All	0	6

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	252	VAL	CA-CB	-5.48	1.49	1.55

The worst 5 of 155 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	220	VAL	N-CA-C	-14.09	100.28	112.12
1	A	38	ILE	N-CA-C	-11.54	102.42	112.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	38	ILE	N-CA-C	-11.22	102.54	113.53
2	B	144	ILE	N-CA-C	-11.20	99.92	112.80
1	A	220	VAL	N-CA-C	-10.42	101.68	111.48

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	G	4	ARG	Peptide
4	G	5	1ZN	Peptide,Mainchain
4	H	4	ARG	Peptide
4	H	5	1ZN	Peptide,Mainchain

## 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	4535	0	4637	491	0
1	D	4535	0	4637	469	0
2	B	3131	0	3050	359	0
2	E	3131	0	3050	381	0
3	C	2367	0	2268	234	0
3	F	2367	0	2268	234	0
4	G	71	0	61	1	0
4	H	71	0	61	3	0
5	C	2	0	0	0	0
5	F	2	0	0	0	0
All	All	20212	0	20032	2146	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 53.

The worst 5 of 2146 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:D:278:ILE:H	1:D:278:ILE:HD12	1.10	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:325:VAL:HG13	2:E:337:LEU:HD11	1.29	1.11
3:C:276:MET:HE3	3:C:278:LEU:HD21	1.33	1.10
1:D:350:MSE:HE1	1:D:391:VAL:HG13	1.24	1.10
2:B:277:MSE:HE1	2:B:316:PRO:HG3	1.35	1.08

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	580/582 (100%)	411 (71%)	124 (21%)	45 (8%)	1	11
1	D	580/582 (100%)	411 (71%)	119 (20%)	50 (9%)	0	9
2	B	386/388 (100%)	234 (61%)	97 (25%)	55 (14%)	0	3
2	E	386/388 (100%)	234 (61%)	95 (25%)	57 (15%)	0	2
3	C	291/293 (99%)	203 (70%)	69 (24%)	19 (6%)	1	14
3	F	291/293 (99%)	210 (72%)	63 (22%)	18 (6%)	1	14
4	G	1/7 (14%)	1 (100%)	0	0	100	100
4	H	1/7 (14%)	1 (100%)	0	0	100	100
All	All	2516/2540 (99%)	1705 (68%)	567 (22%)	244 (10%)	0	7

5 of 244 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	25	VAL
1	A	35	LEU
1	A	44	VAL
1	A	317	CYS
1	A	391	VAL

### 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	509/496 (103%)	438 (86%)	71 (14%)	3	18
1	D	509/496 (103%)	440 (86%)	69 (14%)	3	18
2	B	331/351 (94%)	297 (90%)	34 (10%)	7	27
2	E	331/351 (94%)	290 (88%)	41 (12%)	4	21
3	C	259/259 (100%)	243 (94%)	16 (6%)	16	42
3	F	259/259 (100%)	244 (94%)	15 (6%)	18	44
4	G	2/2 (100%)	2 (100%)	0	100	100
4	H	2/2 (100%)	2 (100%)	0	100	100
All	All	2202/2216 (99%)	1956 (89%)	246 (11%)	6	24

5 of 246 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	187	GLN
2	E	303	ASP
1	D	131	LEU
2	E	289	PRO
3	F	119	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 75 such sidechains are listed below:

Mol	Chain	Res	Type
2	E	177	HIS
3	F	141	ASN
2	E	209	ASN
3	F	12	GLN
2	B	254	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

10 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
4	DAM	H	7	4,3	4,5,6	1.90	1 (25%)	3,5,7	4.37	3 (100%)
4	DAM	G	7	4,3	4,5,6	1.86	1 (25%)	3,5,7	4.04	3 (100%)
4	ACB	H	3	-	7,8,9	1.30	0	8,10,12	0.91	0
4	ACB	G	3	-	7,8,9	1.17	0	8,10,12	0.79	0
4	1ZN	G	5	4	21,23,24	1.24	2 (9%)	25,29,31	0.92	1 (4%)
4	FGA	H	6	4	6,8,9	2.70	2 (33%)	6,9,11	0.57	0
4	1ZN	H	5	4	21,23,24	1.05	0	25,29,31	0.81	0
4	FGA	G	6	4	6,8,9	2.57	2 (33%)	6,9,11	0.58	0

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	DAM	H	7	4,3	-	0/0/4/6	-
4	DAM	G	7	4,3	-	0/0/4/6	-
4	ACB	H	3	-	-	2/10/10/12	-
4	ACB	G	3	-	-	2/10/10/12	-
4	1ZN	G	5	4	-	3/23/25/27	0/1/1/1
4	FGA	H	6	4	-	2/8/8/9	-
4	1ZN	H	5	4	-	3/23/25/27	0/1/1/1
4	FGA	G	6	4	-	3/8/8/9	-

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	H	6	FGA	O-C	5.45	1.38	1.22
4	G	6	FGA	O-C	5.32	1.37	1.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	7	DAM	C-CA	3.31	1.50	1.45
4	H	7	DAM	C-CA	3.30	1.50	1.45
4	H	6	FGA	OXT-C	-2.93	1.21	1.30

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	7	DAM	CM-N-CA	-5.25	116.01	123.98
4	G	7	DAM	CM-N-CA	-5.19	116.11	123.98
4	H	7	DAM	O-C-CA	-4.98	118.85	125.33
4	G	7	DAM	O-C-CA	-4.22	119.85	125.33
4	H	7	DAM	CB-CA-N	-2.23	120.35	125.84

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	G	3	ACB	CA-CB-CG-OD1
4	G	3	ACB	C4-CB-CG-OD1
4	H	3	ACB	C4-CB-CG-OD1
4	G	5	1ZN	C12-C13-C15-C16
4	G	5	1ZN	C14-C13-C15-C16

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	H	7	DAM	2	0
4	G	7	DAM	1	0
4	G	6	FGA	1	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 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 [i](#)

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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

### 6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.