



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 09:00 pm GMT

PDB ID : 5CM8  
Title : Structural Basis for the Selectivity of Guanine Nucleotide Exchange Factors  
for the small G-protein Ral  
Authors : Popovic, M.; Schouten, A.; Rehmann, H.  
Deposited on : 2015-07-16  
Resolution : 2.60 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  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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) : recalc28949

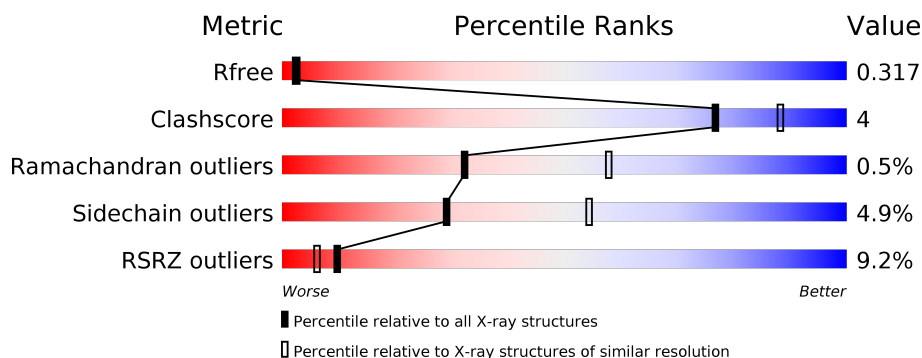
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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))
$R_{free}$	100719	2542 (2.60-2.60)
Clashscore	112137	2895 (2.60-2.60)
Ramachandran outliers	110173	2848 (2.60-2.60)
Sidechain outliers	110143	2848 (2.60-2.60)
RSRZ outliers	101464	2550 (2.60-2.60)

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	473	<div> <div>2%</div> <div> <div></div> <div>77%</div> <div>10%</div> <div>11%</div> </div> </div>
2	B	203	<div> <div>22%</div> <div> <div></div> <div>71%</div> <div>11%</div> <div>17%</div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4634 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 Ral guanine nucleotide dissociation stimulator-like 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	419	Total	C	N	O	S	0	0	0
			3278	2060	594	615	9			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	42	GLY	-	expression tag	UNP Q61193
A	43	PRO	-	expression tag	UNP Q61193
A	44	LEU	-	expression tag	UNP Q61193
A	45	GLY	-	expression tag	UNP Q61193
A	46	SER	-	expression tag	UNP Q61193
A	47	PRO	-	expression tag	UNP Q61193
A	48	ASN	-	expression tag	UNP Q61193
A	49	SER	-	expression tag	UNP Q61193
A	147	TYR	HIS	conflict	UNP Q61193
A	402	THR	MET	conflict	UNP Q61193

- Molecule 2 is a protein called Ras-related protein Ral-a.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	169	Total	C	N	O	S	0	0	0
			1311	825	223	258	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	GLY	-	expression tag	UNP P48555
B	0	SER	-	expression tag	UNP P48555

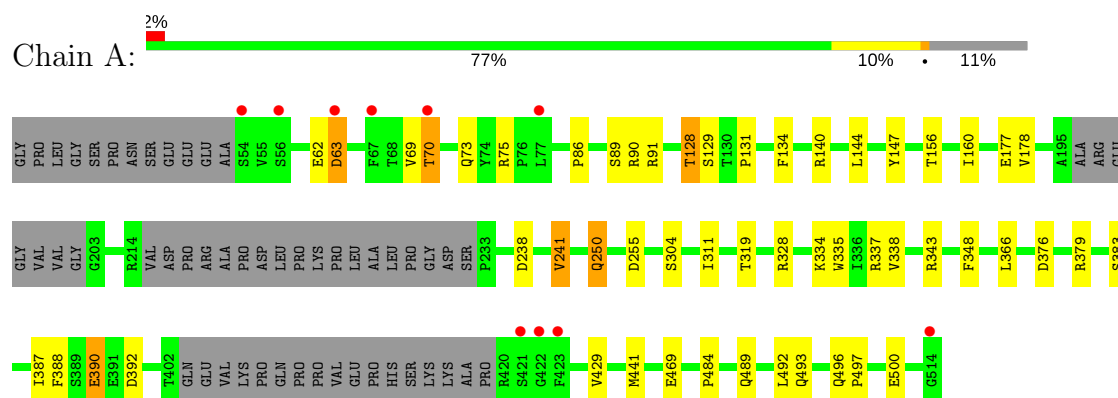
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	39	Total 39	O 39	0	0
3	B	6	Total 6	O 6	0	0

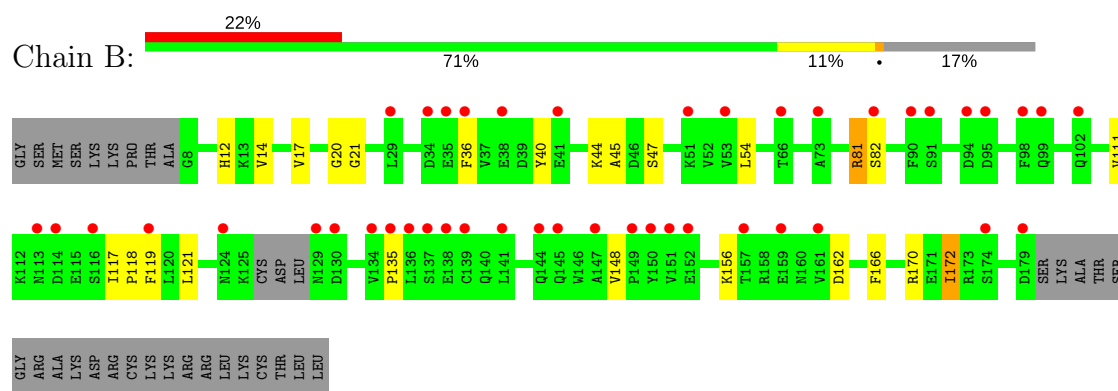
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Ral guanine nucleotide dissociation stimulator-like 2



- Molecule 2: Ras-related protein Ral-a



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	111.11Å 98.49Å 71.32Å 90.00° 91.61° 90.00°	Depositor
Resolution (Å)	44.42 – 2.60 44.42 – 2.60	Depositor EDS
% Data completeness (in resolution range)	100.0 (44.42-2.60) 97.7 (44.42-2.60)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.35 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.259 , 0.322 0.253 , 0.317	Depositor DCC
$R_{free}$ test set	1159 reflections (5.27%)	DCC
Wilson B-factor (Å <sup>2</sup> )	54.9	Xtriage
Anisotropy	0.437	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 32.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.032 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	4634	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.02% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	0.33	0/3345	0.50	0/4538
2	B	0.35	0/1332	0.49	1/1798 (0.1%)
All	All	0.33	0/4677	0.49	1/6336 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	135	PRO	N-CA-CB	5.91	110.39	103.30

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	3278	0	3269	23	0
2	B	1311	0	1227	11	0
3	A	39	0	0	0	0
3	B	6	0	0	0	0
All	All	4634	0	4496	32	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 4.

All (32) 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:73:GLN:HG2	1:A:86:PRO:HB3	1.78	0.65
1:A:128:THR:HG22	1:A:129:SER:H	1.63	0.63
2:B:12:HIS:ND1	2:B:172:ILE:HD11	2.16	0.60
2:B:81:ARG:HB2	2:B:111:VAL:CG1	2.33	0.58
1:A:348:PHE:HB3	1:A:388:PHE:HZ	1.68	0.57
2:B:81:ARG:HB2	2:B:111:VAL:HG12	1.86	0.56
1:A:255:ASP:HB3	1:A:429:VAL:HG11	1.88	0.56
1:A:376:ASP:OD1	1:A:379:ARG:NH2	2.38	0.52
1:A:250:GLN:HG3	1:A:489:GLN:HE21	1.76	0.51
2:B:119:PHE:HD2	2:B:148:VAL:HG11	1.76	0.51
2:B:117:ILE:HG13	2:B:118:PRO:HD2	1.93	0.50
2:B:54:LEU:HD11	2:B:170:ARG:HG3	1.93	0.49
1:A:334:LYS:O	1:A:338:VAL:HG23	2.13	0.49
2:B:81:ARG:HA	2:B:82:SER:HA	1.60	0.48
1:A:144:LEU:HA	1:A:147:TYR:CD1	2.49	0.48
1:A:311:ILE:HD11	1:A:319:THR:HG23	1.96	0.48
1:A:69:VAL:HG22	1:A:90:ARG:HG3	1.95	0.47
1:A:328:ARG:HD3	1:A:366:LEU:HD13	1.97	0.47
1:A:441:MET:HG2	2:B:40:TYR:OH	2.16	0.45
1:A:156:THR:O	1:A:160:ILE:HG12	2.17	0.44
1:A:304:SER:HB3	1:A:335:TRP:HE1	1.83	0.44
1:A:70:THR:HG23	1:A:89:SER:HB3	1.99	0.44
1:A:238:ASP:O	1:A:241:VAL:HG12	2.17	0.44
1:A:250:GLN:OE1	1:A:484:PRO:HA	2.18	0.43
1:A:392:ASP:HB3	2:B:45:ALA:HB1	2.00	0.43
1:A:383:SER:O	1:A:387:ILE:HG12	2.19	0.43
1:A:129:SER:HB2	1:A:131:PRO:HD2	2.01	0.42
2:B:162:ASP:O	2:B:166:PHE:HD1	2.02	0.42
2:B:44:LYS:O	2:B:47:SER:HB2	2.19	0.41
1:A:390:GLU:H	1:A:390:GLU:CD	2.24	0.41
1:A:62:GLU:O	1:A:63:ASP:C	2.58	0.41
1:A:496:GLN:HA	1:A:497:PRO:HD2	1.94	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	411/473 (87%)	401 (98%)	9 (2%)	1 (0%)	51	76
2	B	165/203 (81%)	152 (92%)	11 (7%)	2 (1%)	15	32
All	All	576/676 (85%)	553 (96%)	20 (4%)	3 (0%)	32	58

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	63	ASP
2	B	21	GLY
2	B	20	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	355/399 (89%)	338 (95%)	17 (5%)	30	55
2	B	134/178 (75%)	127 (95%)	7 (5%)	27	52
All	All	489/577 (85%)	465 (95%)	24 (5%)	29	54

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	70	THR
1	A	75	ARG
1	A	91	ARG
1	A	128	THR
1	A	134	PHE
1	A	140	ARG
1	A	177	GLU
1	A	178	VAL
1	A	241	VAL
1	A	250	GLN

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Mol	Chain	Res	Type
1	A	337	ARG
1	A	343	ARG
1	A	390	GLU
1	A	469	GLU
1	A	492	LEU
1	A	493	GLN
1	A	500	GLU
2	B	14	VAL
2	B	17	VAL
2	B	36	PHE
2	B	81	ARG
2	B	121	LEU
2	B	156	LYS
2	B	172	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	30	GLN
2	B	69	GLN

### 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 ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

## 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, 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	419/473 (88%)	0.30	10 (2%) 59 52	36, 54, 76, 84	0
2	B	169/203 (83%)	1.36	44 (26%) 1 0	51, 89, 119, 121	0
All	All	588/676 (86%)	0.60	54 (9%) 10 6	36, 59, 102, 121	0

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	91	SER	7.0
2	B	150	TYR	6.0
2	B	161	VAL	5.4
2	B	139	CYS	5.2
2	B	102	GLN	5.0
1	A	423	PHE	4.2
1	A	54	SER	4.2
1	A	514	GLY	4.0
2	B	35	GLU	3.8
2	B	124	ASN	3.7
2	B	129	ASN	3.7
2	B	90	PHE	3.6
2	B	135	PRO	3.6
2	B	157	THR	3.5
2	B	130	ASP	3.4
2	B	137	SER	3.3
1	A	421	SER	3.3
2	B	151	VAL	3.2
2	B	136	LEU	2.9
2	B	82	SER	2.9
2	B	113	ASN	2.9
2	B	134	VAL	2.8
2	B	147	ALA	2.8
1	A	63	ASP	2.8

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Mol	Chain	Res	Type	RSRZ
2	B	159	GLU	2.8
1	A	77	LEU	2.8
2	B	141	LEU	2.7
2	B	53	VAL	2.7
1	A	422	GLY	2.7
2	B	66	THR	2.7
2	B	36	PHE	2.6
2	B	145	GLN	2.5
2	B	29	LEU	2.5
2	B	34	ASP	2.5
2	B	149	PRO	2.5
2	B	116	SER	2.5
2	B	99	GLN	2.4
2	B	119	PHE	2.4
1	A	70	THR	2.4
2	B	144	GLN	2.4
2	B	98	PHE	2.4
2	B	179	ASP	2.2
1	A	67	PHE	2.2
2	B	41	GLU	2.2
2	B	152	GLU	2.2
2	B	38	GLU	2.2
2	B	114	ASP	2.2
1	A	56	SER	2.1
2	B	174	SER	2.1
2	B	94	ASP	2.1
2	B	51	LYS	2.1
2	B	73	ALA	2.1
2	B	95	ASP	2.0
2	B	138	GLU	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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.