



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 07:10 PM UTC

PDB ID : 8BE4 / pdb_00008be4
Title : Crystal structure of SOS1-KRasG12V-Nanobody14
Authors : Fischer, B.; Wohlkonig, A.; Steyaert, J.
Deposited on : 2022-10-21
Resolution : 1.90 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
Xtrriage (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

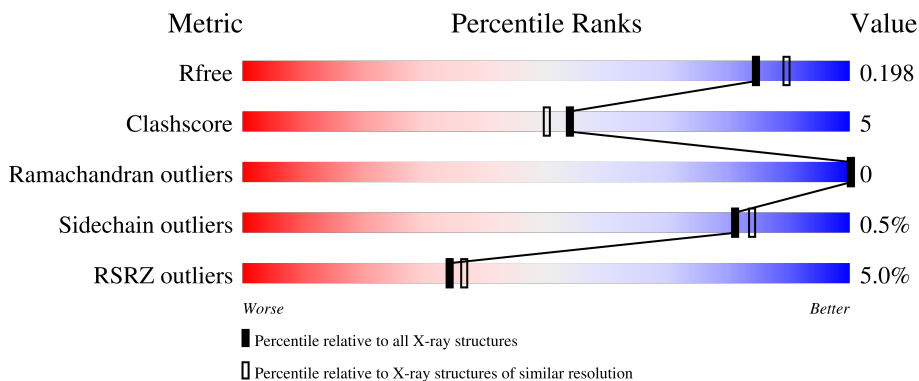
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	S	507	 4% 76% 11% 13%
2	R	190	 5% 73% 12% 13%
3	C000	128	 4% 93% 7%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6622 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 Son of sevenless homolog 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	S	440	3768	2421	645	688	14	0	12	0

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	543	MET	-	initiating methionine	UNP Q07889
S	544	GLY	-	expression tag	UNP Q07889
S	545	SER	-	expression tag	UNP Q07889
S	546	SER	-	expression tag	UNP Q07889
S	547	HIS	-	expression tag	UNP Q07889
S	548	HIS	-	expression tag	UNP Q07889
S	549	HIS	-	expression tag	UNP Q07889
S	550	HIS	-	expression tag	UNP Q07889
S	551	HIS	-	expression tag	UNP Q07889
S	552	HIS	-	expression tag	UNP Q07889
S	553	SER	-	expression tag	UNP Q07889
S	554	SER	-	expression tag	UNP Q07889
S	555	GLY	-	expression tag	UNP Q07889
S	556	LEU	-	expression tag	UNP Q07889
S	557	VAL	-	expression tag	UNP Q07889
S	558	PRO	-	expression tag	UNP Q07889
S	559	ARG	-	expression tag	UNP Q07889
S	560	GLY	-	expression tag	UNP Q07889
S	561	SER	-	expression tag	UNP Q07889
S	562	HIS	-	expression tag	UNP Q07889
S	563	MET	-	expression tag	UNP Q07889

- Molecule 2 is a protein called Isoform 2B of GTPase KRas.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	R	165	1385	865	243	271	6	0	7	0

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	-20	MET	-	initiating methionine	UNP P01116-2
R	-19	GLY	-	expression tag	UNP P01116-2
R	-18	SER	-	expression tag	UNP P01116-2
R	-17	SER	-	expression tag	UNP P01116-2
R	-16	HIS	-	expression tag	UNP P01116-2
R	-15	HIS	-	expression tag	UNP P01116-2
R	-14	HIS	-	expression tag	UNP P01116-2
R	-13	HIS	-	expression tag	UNP P01116-2
R	-12	HIS	-	expression tag	UNP P01116-2
R	-11	HIS	-	expression tag	UNP P01116-2
R	-10	SER	-	expression tag	UNP P01116-2
R	-9	SER	-	expression tag	UNP P01116-2
R	-8	GLY	-	expression tag	UNP P01116-2
R	-7	GLU	-	expression tag	UNP P01116-2
R	-6	ASN	-	expression tag	UNP P01116-2
R	-5	LEU	-	expression tag	UNP P01116-2
R	-4	TYR	-	expression tag	UNP P01116-2
R	-3	PHE	-	expression tag	UNP P01116-2
R	-2	GLN	-	expression tag	UNP P01116-2
R	-1	GLY	-	expression tag	UNP P01116-2
R	0	SER	-	expression tag	UNP P01116-2
R	12	VAL	GLY	engineered mutation	UNP P01116-2

- Molecule 3 is a protein called Nanobody14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C000	119	918	566	172	176	4	0	1	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	S	335	Total O 335 335	0	0
4	R	108	Total O 108 108	0	0

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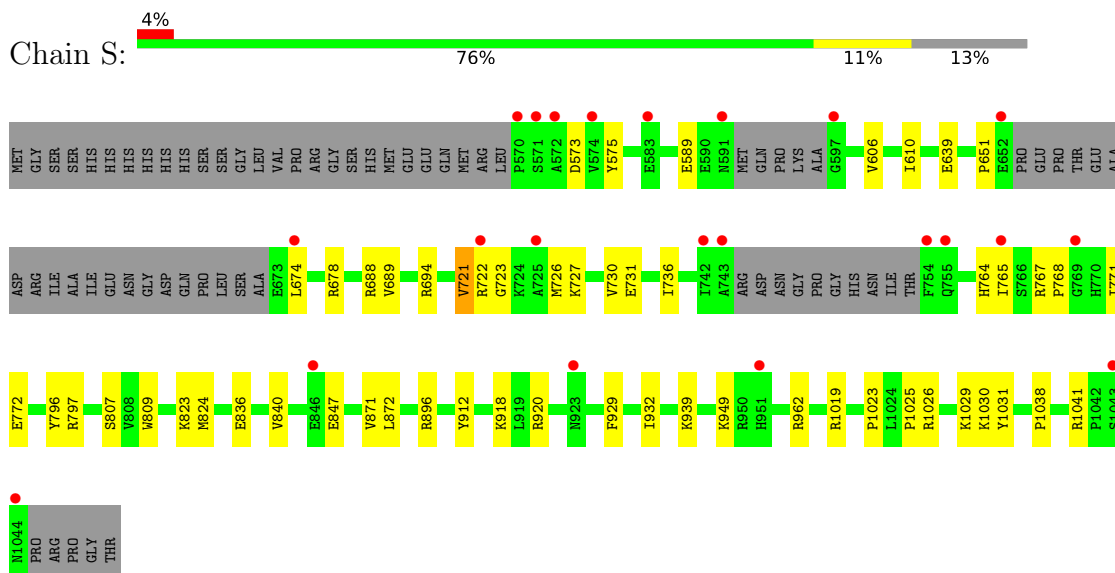
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C000	108	Total 108	O 108	0	0

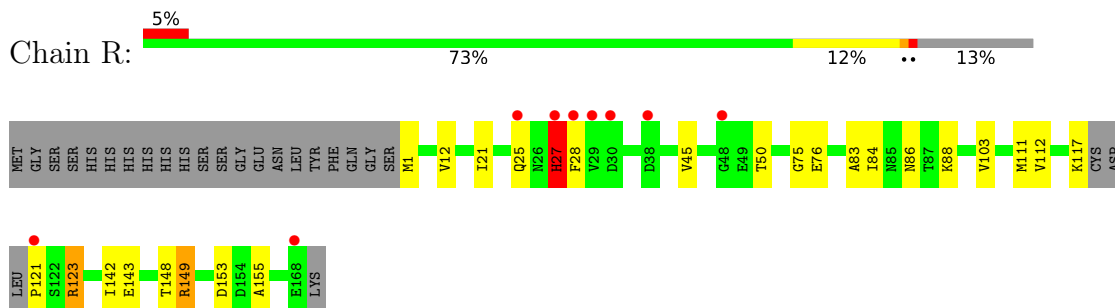
3 Residue-property plots [i](#)

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.

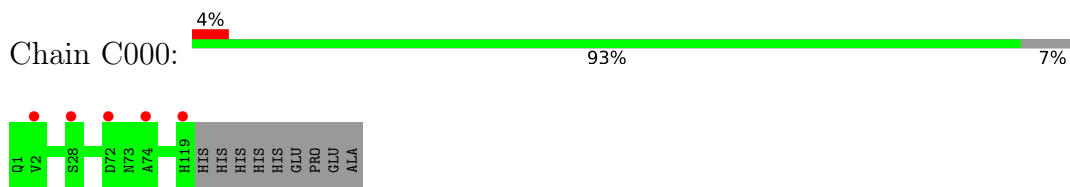
- Molecule 1: Son of sevenless homolog 1



- Molecule 2: Isoform 2B of GTPase KRas



- Molecule 3: Nanobody14



4 Data and refinement statistics i

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, α , β , γ	127.67Å 127.67Å 152.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.59 – 1.90 29.59 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.6 (29.59-1.90) 100.0 (29.59-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.33 (at 1.89Å)	Xtrriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.175 , 0.199 0.175 , 0.198	Depositor DCC
R_{free} test set	4795 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	35.8	Xtrriage
Anisotropy	0.048	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 39.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.021 for -h,k,-l	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	6622	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.87% 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 [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	S	0.90	3/3856 (0.1%)	0.81	4/5209 (0.1%)
2	R	0.87	2/1406 (0.1%)	0.86	5/1893 (0.3%)
3	C000	0.82	0/935	0.85	0/1265
All	All	0.88	5/6197 (0.1%)	0.83	9/8367 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	R	76	GLU	C-O	-5.99	1.16	1.24
1	S	871	VAL	C-O	-5.64	1.17	1.24
1	S	689	VAL	C-O	-5.52	1.17	1.24
2	R	103	VAL	C-O	-5.38	1.17	1.24
1	S	688	ARG	C-O	-5.09	1.18	1.24

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	R	123	ARG	N-CA-C	7.40	120.47	109.59
2	R	75	GLY	N-CA-C	6.19	124.54	112.04
2	R	27	HIS	N-CA-C	6.12	118.74	111.33
2	R	121	PRO	CA-C-N	-5.95	112.38	123.03
2	R	121	PRO	C-N-CA	-5.95	112.38	123.03

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	S	3768	0	3773	39	0
2	R	1385	0	1362	17	0
3	C000	918	0	0	0	0
4	C000	108	0	0	0	0
4	R	108	0	0	3	0
4	S	335	0	0	12	0
All	All	6622	0	5135	56	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 5.

The worst 5 of 56 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:S:847:GLU:OE2	1:S:1029:LYS:HE2	1.85	0.75
1:S:949:LYS:NZ	4:S:1102:HOH:O	2.22	0.73
2:R:142:ILE:HD13	2:R:155:ALA:HA	1.76	0.67
1:S:1030:LYS:HD2	1:S:1031:TYR:CZ	2.32	0.65
1:S:824[A]:MET:HE2	4:S:1206:HOH:O	1.96	0.65

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	S	444/507 (88%)	437 (98%)	7 (2%)	0	100	100
2	R	168/190 (88%)	167 (99%)	1 (1%)	0	100	100
3	C000	118/128 (92%)	115 (98%)	3 (2%)	0	100	100
All	All	730/825 (88%)	719 (98%)	11 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	S	424/469 (90%)	423 (100%)	1 (0%)	87	90
2	R	153/168 (91%)	151 (99%)	2 (1%)	61	61
3	C000	96/103 (93%)	96 (100%)	0	100	100
All	All	673/740 (91%)	670 (100%)	3 (0%)	81	87

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	S	721	VAL
2	R	27	HIS
2	R	149	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	S	905	HIS
1	S	973	GLN
2	R	70	GLN
2	R	61	GLN
1	S	879	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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 [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	S	440/507 (86%)	0.10	22 (5%) 34 36	14, 37, 68, 99	12 (2%)
2	R	165/190 (86%)	0.14	9 (5%) 30 32	16, 37, 62, 85	7 (4%)
3	C000	119/128 (92%)	0.12	5 (4%) 40 43	27, 36, 67, 89	1 (0%)
All	All	724/825 (87%)	0.11	36 (4%) 34 36	14, 37, 68, 99	20 (2%)

The worst 5 of 36 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	S	743	ALA	5.5
2	R	168	GLU	4.9
1	S	570	PRO	4.3
2	R	121	PRO	4.3
2	R	27	HIS	3.9

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 oligosaccharides 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.