



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 28, 2026 – 02:08 PM EDT

PDB ID : 35SB / pdb_000035sb
Title : Polar Interface Homodimer - S4A
Authors : Harvey, B.T.
Deposited on : 2026-05-14
Resolution : 1.83 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 Phenix2.2
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.2
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.51

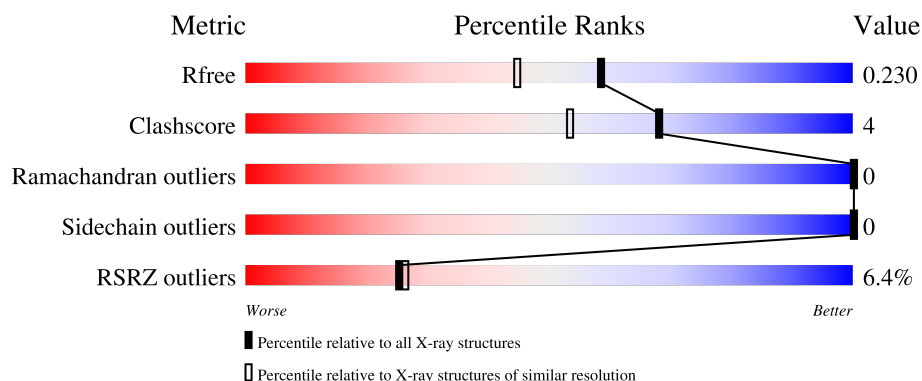
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.83 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	1296 (1.84-1.84)
Clashscore	190562	1329 (1.84-1.84)
Ramachandran outliers	187476	1318 (1.84-1.84)
Sidechain outliers	187428	1318 (1.84-1.84)
RSRZ outliers	180081	1296 (1.84-1.84)

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	83	2% 99% .
1	B	83	2% 92% 7% .
1	C	83	% 87% 12% .
1	D	83	6% 89% 11% .
1	E	83	7% 87% 11% ..

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Mol	Chain	Length	Quality of chain
1	F	83	% 89% 8% ..
1	G	83	28% 80% 19% .
1	H	83	2% 90% 10%

2 Entry composition

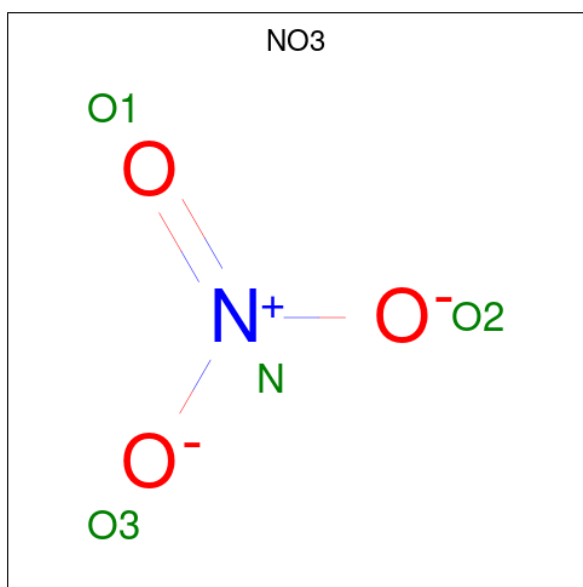
There are 3 unique types of molecules in this entry. The entry contains 11840 atoms, of which 5895 are hydrogens and 0 are deuteriums.

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 S4A.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	83	Total	C	H	N	O	S	0	7	0
			1440	453	737	106	143	1			
1	B	82	Total	C	H	N	O	S	0	8	0
			1435	453	731	107	143	1			
1	C	82	Total	C	H	N	O	S	0	8	0
			1469	458	759	110	141	1			
1	D	83	Total	C	H	N	O	S	0	13	0
			1521	474	784	113	149	1			
1	E	82	Total	C	H	N	O	S	0	8	0
			1414	449	719	105	140	1			
1	F	82	Total	C	H	N	O	S	0	11	0
			1490	468	764	110	147	1			
1	G	83	Total	C	H	N	O	S	0	0	0
			1306	418	658	99	130	1			
1	H	83	Total	C	H	N	O	S	0	4	0
			1437	449	743	106	138	1			

- Molecule 2 is NITRATE ION (CCD ID: NO3) (formula: NO₃).



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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	30	Total	O	0	0
			30	30		
3	B	32	Total	O	0	0
			32	32		
3	C	47	Total	O	0	0
			47	47		
3	D	49	Total	O	0	0
			49	49		
3	E	24	Total	O	0	0
			24	24		
3	F	59	Total	O	0	0
			59	59		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	G	18	Total	O	0	0
			18	18		
3	H	45	Total	O	0	0
			45	45		

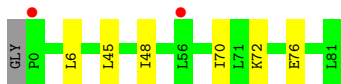
3 Residue-property plots [i](#)

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.

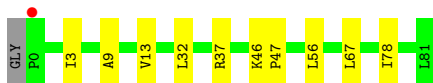
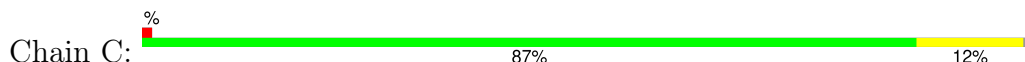
- Molecule 1: S4A



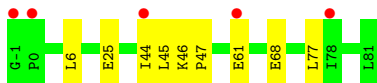
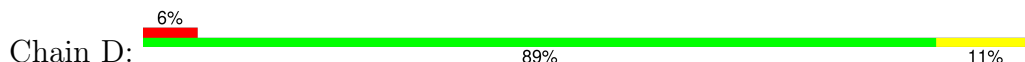
- Molecule 1: S4A



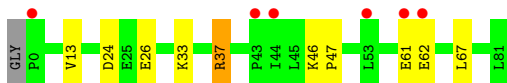
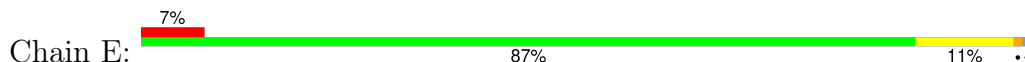
- Molecule 1: S4A



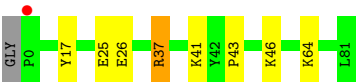
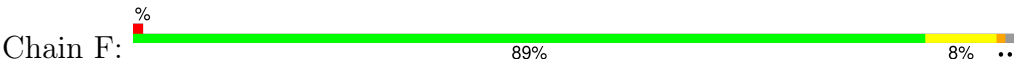
- Molecule 1: S4A



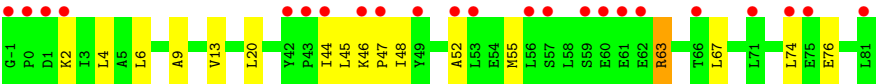
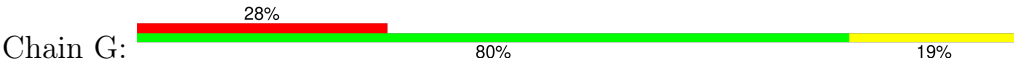
- Molecule 1: S4A



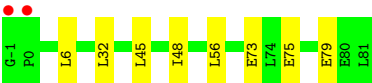
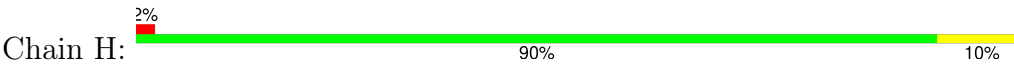
- Molecule 1: S4A



• Molecule 1: S4A



• Molecule 1: S4A



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	82.53Å 82.53Å 187.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.31 – 1.83 40.31 – 1.83	Depositor EDS
% Data completeness (in resolution range)	99.8 (40.31-1.83) 99.8 (40.31-1.83)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.12 (at 1.83Å)	Xtriage
Refinement program	PHENIX 2.0_5936	Depositor
R, R_{free}	0.196 , 0.229 0.196 , 0.230	Depositor DCC
R_{free} test set	2000 reflections (3.44%)	wwPDB-VP
Wilson B-factor (Å ²)	27.6	Xtriage
Anisotropy	0.137	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 44.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	11840	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 49.08 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 7.8457e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: NO3

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	0.30	0/736	0.47	0/985
1	B	0.30	0/741	0.50	0/992
1	C	0.38	0/750	0.53	0/1000
1	D	0.32	0/792	0.54	0/1055
1	E	0.29	0/733	0.44	0/983
1	F	0.38	0/773	0.55	0/1033
1	G	0.42	0/654	0.69	1/879 (0.1%)
1	H	0.35	0/722	0.55	0/966
All	All	0.34	0/5901	0.54	1/7893 (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	A	0	1
1	C	0	1
1	E	0	1
1	F	0	1
1	G	0	1
All	All	0	5

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	2	LYS	N-CA-C	-5.20	105.79	111.82

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	73[A]	GLU	Mainchain
1	C	37[A]	ARG	Sidechain
1	E	37[A]	ARG	Sidechain
1	F	37[A]	ARG	Sidechain
1	G	63	ARG	Sidechain

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	703	737	699	0	0
1	B	704	731	696	3	0
1	C	710	759	716	5	0
1	D	737	784	731	5	1
1	E	695	719	673	8	1
1	F	726	764	713	7	0
1	G	648	658	658	12	1
1	H	694	743	726	4	0
2	A	4	0	0	0	0
2	B	4	0	0	0	0
2	C	8	0	0	0	0
2	D	4	0	0	0	0
2	H	4	0	0	0	0
3	A	30	0	0	0	0
3	B	32	0	0	0	0
3	C	47	0	0	0	0
3	D	49	0	0	1	0
3	E	24	0	0	2	0
3	F	59	0	0	1	0
3	G	18	0	0	1	0
3	H	45	0	0	0	0
All	All	5945	5895	5612	41	2

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.

The worst 5 of 41 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:H:32:LEU:HD11	1:H:56:LEU:HD21	1.94	0.49
1:E:26:GLU:HB3	1:F:37[B]:ARG:HH21	1.77	0.49
1:E:13:VAL:HG12	1:E:67:LEU:CD1	2.43	0.49
1:G:76:GLU:CA	3:G:112:HOH:O	2.60	0.48
1:G:44:ILE:O	1:G:47:PRO:HD2	2.13	0.48

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:62:GLU:OE2	1:E:62:GLU:OE2[7_465]	1.87	0.33
1:D:61[A]:GLU:OE2	1:G:20:LEU:O[3_455]	2.03	0.17

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	88/83 (106%)	88 (100%)	0	0	100	100
1	B	88/83 (106%)	88 (100%)	0	0	100	100
1	C	88/83 (106%)	88 (100%)	0	0	100	100
1	D	94/83 (113%)	94 (100%)	0	0	100	100
1	E	88/83 (106%)	88 (100%)	0	0	100	100
1	F	91/83 (110%)	91 (100%)	0	0	100	100
1	G	81/83 (98%)	81 (100%)	0	0	100	100
1	H	85/83 (102%)	83 (98%)	2 (2%)	0	100	100
All	All	703/664 (106%)	701 (100%)	2 (0%)	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	A	79/74 (107%)	79 (100%)	0	100	100
1	B	79/74 (107%)	79 (100%)	0	100	100
1	C	82/74 (111%)	82 (100%)	0	100	100
1	D	85/74 (115%)	85 (100%)	0	100	100
1	E	77/74 (104%)	77 (100%)	0	100	100
1	F	84/74 (114%)	84 (100%)	0	100	100
1	G	66/74 (89%)	66 (100%)	0	100	100
1	H	78/74 (105%)	78 (100%)	0	100	100
All	All	630/592 (106%)	630 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

6 ligands 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	$\# Z > 2$
2	NO3	C	102	-	1,3,3	0.05	0	0,3,3	-	-
2	NO3	C	101	-	1,3,3	0.40	0	0,3,3	-	-
2	NO3	B	101	-	1,3,3	0.17	0	0,3,3	-	-
2	NO3	A	101	-	1,3,3	0.28	0	0,3,3	-	-
2	NO3	H	101	-	1,3,3	0.01	0	0,3,3	-	-
2	NO3	D	101	-	1,3,3	0.09	0	0,3,3	-	-

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](#)

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	83/83 (100%)	0.10	2 (2%) 59 66	16, 39, 60, 86	4 (4%)
1	B	82/83 (98%)	0.14	2 (2%) 59 66	19, 41, 65, 87	4 (4%)
1	C	82/83 (98%)	-0.10	1 (1%) 76 82	16, 34, 53, 65	4 (4%)
1	D	83/83 (100%)	0.14	5 (6%) 27 29	14, 36, 59, 99	7 (8%)
1	E	82/83 (98%)	0.37	6 (7%) 21 22	18, 42, 68, 83	4 (4%)
1	F	82/83 (98%)	-0.29	1 (1%) 76 82	15, 28, 46, 71	7 (8%)
1	G	83/83 (100%)	1.30	23 (27%) 1 1	25, 64, 84, 115	0
1	H	83/83 (100%)	-0.13	2 (2%) 59 66	17, 34, 58, 87	2 (2%)
All	All	660/664 (99%)	0.19	42 (6%) 25 26	14, 38, 72, 115	32 (4%)

The worst 5 of 42 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	-1	GLY	5.6
1	G	1	ASP	4.7
1	G	56	LEU	4.3
1	H	-1	GLY	3.9
1	G	2	LYS	3.8

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](#)

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(Å ²)	Q<0.9
2	NO3	A	101	4/4	0.81	0.09	64,65,67,78	0
2	NO3	D	101	4/4	0.82	0.12	57,59,59,63	0
2	NO3	H	101	4/4	0.84	0.11	40,43,51,56	0
2	NO3	C	101	4/4	0.92	0.09	32,38,39,41	0
2	NO3	B	101	4/4	0.93	0.09	39,43,47,50	0
2	NO3	C	102	4/4	0.93	0.12	36,44,45,58	0

6.5 Other polymers [i](#)

There are no such residues in this entry.