



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 17, 2026 – 06:05 PM UTC

PDB ID : 3PQZ / pdb_00003pqz
Title : Grb7 SH2 with peptide
Authors : Wilce, J.A.
Deposited on : 2010-11-29
Resolution : 2.41 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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (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

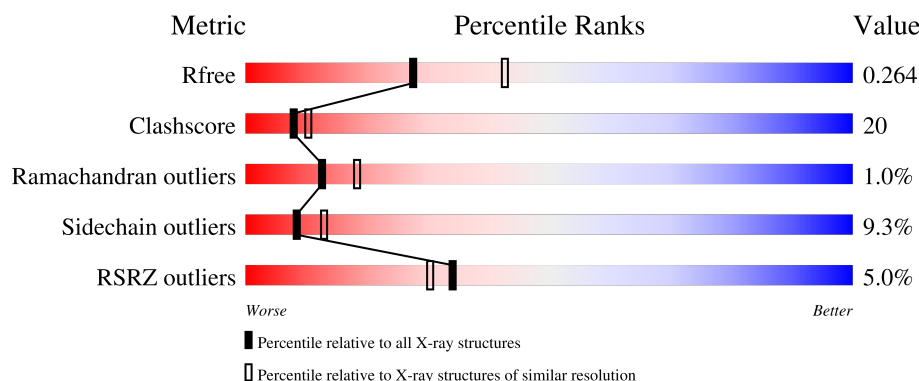
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.41 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	6062 (2.44-2.40)
Clashscore	190562	6562 (2.44-2.40)
Ramachandran outliers	187476	6481 (2.44-2.40)
Sidechain outliers	187428	6482 (2.44-2.40)
RSRZ outliers	180081	6066 (2.44-2.40)

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	117	3% 64% 23% • 11%
1	B	117	4% 56% 26% 5% • 10%
1	C	117	6% 50% 27% • • 17%
1	D	117	4% 51% 24% 7% • 17%
2	L	11	64% 36%

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Mol	Chain	Length	Quality of chain
2	M	11	 64% 36%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 3537 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 Growth factor receptor-bound protein 7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	104	Total	C	N	O	S	0	0	0
			841	534	157	145	5			
1	B	105	Total	C	N	O	S	0	0	0
			848	538	161	144	5			
1	C	97	Total	C	N	O	S	0	0	0
			791	505	145	136	5			
1	D	97	Total	C	N	O	S	0	0	0
			754	484	134	131	5			

- Molecule 2 is a protein called cyclic peptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	11	Total	C	N	O	S	0	0	0
			100	67	13	19	1			
2	M	11	Total	C	N	O	S	0	0	0
			100	67	13	19	1			

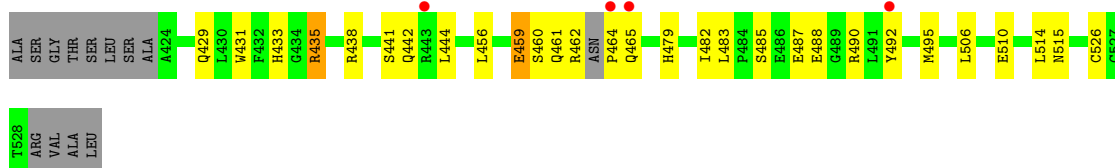
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	28	Total	O	0	0
			28	28		
3	B	32	Total	O	0	0
			32	32		
3	C	21	Total	O	0	0
			21	21		
3	D	21	Total	O	0	0
			21	21		
3	L	1	Total	O	0	0
			1	1		

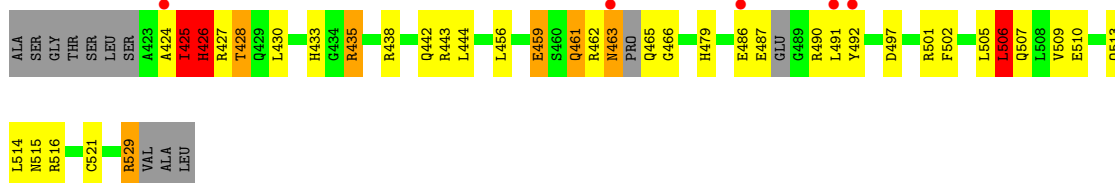
3 Residue-property plots [i](#)

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.

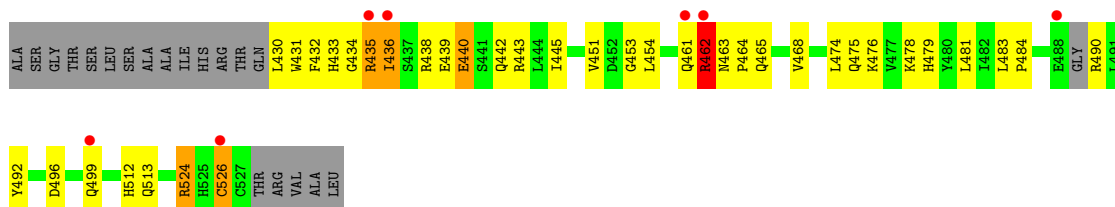
- Molecule 1: Growth factor receptor-bound protein 7



- Molecule 1: Growth factor receptor-bound protein 7

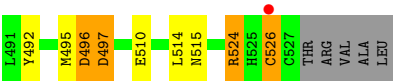


- Molecule 1: Growth factor receptor-bound protein 7

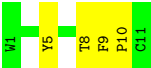


- Molecule 1: Growth factor receptor-bound protein 7

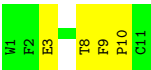




● Molecule 2: cyclic peptide



● Molecule 2: cyclic peptide



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	52.66Å 79.11Å 54.69Å 90.00° 104.40° 90.00°	Depositor
Resolution (Å)	32.88 – 2.41 32.88 – 2.41	Depositor EDS
% Data completeness (in resolution range)	92.8 (32.88-2.41) 92.8 (32.88-2.41)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.27 (at 2.42Å)	Xtriage
Refinement program	PHENIX 1.7 _650	Depositor
R, R_{free}	0.238 , 0.277 0.233 , 0.264	Depositor DCC
R_{free} test set	781 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	27.7	Xtriage
Anisotropy	0.726	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 67.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.000 for l,-k,h	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3537	wwPDB-VP
Average B, all atoms (Å ²)	33.0	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 47.78 % 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 9.4551e-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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CCS

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	0.83	2/858 (0.2%)	1.01	4/1154 (0.3%)
1	B	1.01	10/863 (1.2%)	0.96	3/1159 (0.3%)
1	C	0.68	0/807	0.86	0/1086
1	D	0.88	2/770 (0.3%)	0.94	4/1040 (0.4%)
2	L	0.21	0/96	0.47	0/131
2	M	0.22	0/96	0.46	0/131
All	All	0.84	14/3490 (0.4%)	0.93	11/4701 (0.2%)

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
1	D	0	1
All	All	0	2

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	426	HIS	C-O	-7.50	1.14	1.24
1	D	496	ASP	C-O	-7.49	1.16	1.24
1	B	442	GLN	CD-NE2	-7.20	1.18	1.33
1	B	506	LEU	C-O	-6.21	1.16	1.24
1	A	441	SER	C-O	-5.75	1.17	1.24

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	488	GLU	N-CA-C	7.83	122.22	111.17
1	B	425	ILE	CB-CA-C	-6.44	100.73	111.29
1	D	497	ASP	N-CA-C	6.29	120.06	111.39
1	D	463	ASN	N-CA-C	-5.80	97.00	109.81
1	A	483	LEU	CA-C-N	5.76	126.25	120.14

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	425	ILE	Peptide
1	D	462	ARG	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	841	0	830	21	0
1	B	848	0	842	36	0
1	C	791	0	783	45	0
1	D	754	0	715	29	0
2	L	100	0	76	5	0
2	M	100	0	76	4	0
3	A	28	0	0	3	0
3	B	32	0	0	6	0
3	C	21	0	0	2	0
3	D	21	0	0	2	0
3	L	1	0	0	0	0
All	All	3537	0	3322	133	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 20.

The worst 5 of 133 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:C:496:ASP:HB2	1:C:499:GLN:NE2	1.40	1.36

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:433:HIS:HB3	1:D:436:ILE:HD11	1.21	1.18
1:C:496:ASP:CB	1:C:499:GLN:NE2	2.07	1.15
1:C:433:HIS:HB3	1:C:436:ILE:HD11	1.24	1.12
1:B:463:ASN:HD22	1:B:465:GLN:CB	1.68	1.06

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	A	100/117 (86%)	97 (97%)	3 (3%)	0	100	100
1	B	99/117 (85%)	96 (97%)	1 (1%)	2 (2%)	6	7
1	C	93/117 (80%)	88 (95%)	4 (4%)	1 (1%)	11	16
1	D	93/117 (80%)	89 (96%)	3 (3%)	1 (1%)	11	16
2	L	9/11 (82%)	9 (100%)	0	0	100	100
2	M	9/11 (82%)	9 (100%)	0	0	100	100
All	All	403/490 (82%)	388 (96%)	11 (3%)	4 (1%)	12	18

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	425	ILE
1	B	426	HIS
1	C	462	ARG
1	D	463	ASN

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	91/104 (88%)	87 (96%)	4 (4%)	25	41
1	B	91/104 (88%)	81 (89%)	10 (11%)	6	8
1	C	87/104 (84%)	76 (87%)	11 (13%)	4	6
1	D	78/104 (75%)	69 (88%)	9 (12%)	5	7
2	L	9/9 (100%)	9 (100%)	0	100	100
2	M	9/9 (100%)	9 (100%)	0	100	100
All	All	365/434 (84%)	331 (91%)	34 (9%)	8	13

5 of 34 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	445	ILE
1	D	460	SER
1	D	524	ARG
1	B	506	LEU
1	B	490	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	442	GLN
1	D	442	GLN
1	B	463	ASN
1	B	513	GLN
1	B	515	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 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	$\# Z > 2$
2	CCS	M	11	2	7,8,10	0.80	0	4,8,12	0.55	0
2	CCS	L	11	2	7,8,10	0.73	0	4,8,12	0.51	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
2	CCS	M	11	2	-	0/4/7/10	-
2	CCS	L	11	2	-	0/4/7/10	-

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.

5.5 Carbohydrates ⓘ

There are no oligosaccharides 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 [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	104/117 (88%)	0.21	4 (3%) 44 40	13, 26, 62, 75	0
1	B	105/117 (89%)	0.25	5 (4%) 35 32	14, 26, 57, 95	0
1	C	97/117 (82%)	0.50	7 (7%) 21 18	14, 33, 67, 89	0
1	D	97/117 (82%)	0.35	5 (5%) 33 29	18, 33, 59, 80	0
2	L	10/11 (90%)	0.01	0 100 100	19, 23, 33, 45	0
2	M	10/11 (90%)	-0.04	0 100 100	20, 23, 33, 46	0
All	All	423/490 (86%)	0.31	21 (4%) 34 30	13, 29, 61, 95	0

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	492	TYR	5.6
1	C	462	ARG	4.4
1	C	526	CYS	4.0
1	C	461	GLN	3.6
1	A	492	TYR	3.5

6.2 Non-standard residues in protein, DNA, RNA chains [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	CCS	L	11	9/11	0.94	0.09	18,21,29,34	0
2	CCS	M	11	9/11	0.94	0.09	17,22,33,34	0

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.