



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 12, 2026 – 02:27 AM UTC

PDB ID : 7R1O / pdb_00007r1o
Title : p62-ZZ domain of the human sequestosome in complex with dusquetide
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Deposited on : 2022-02-03
Resolution : 2.20 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
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

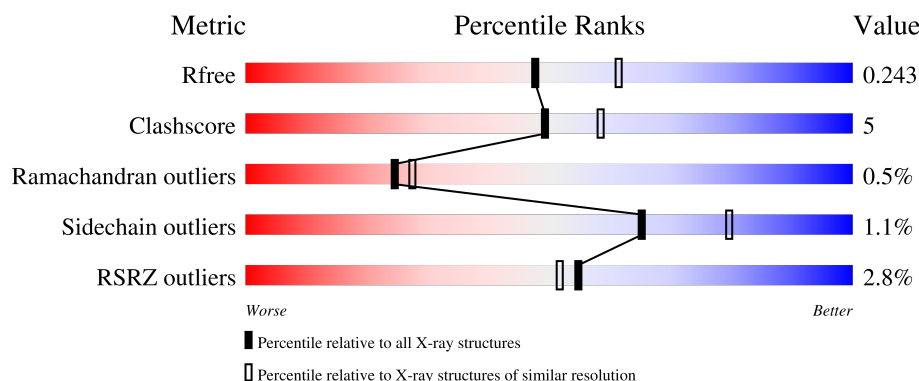
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	AAA	53	83% 17%
1	BBB	53	2% 79% 9% 9%
1	CCC	53	6% 83% 13%
1	DDD	53	2% 85% 15%
2	EEE	5	100%

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Mol	Chain	Length	Quality of chain
2	FFF	5	 A horizontal bar chart showing the quality of chain 2 (FFF) with a length of 5. The bar is divided into four segments: a red segment labeled '20%', a green segment labeled '60%', a yellow segment labeled '20%', and a grey segment labeled '20%'. The segments are stacked horizontally, with the red segment on the left, followed by green, yellow, and grey on the right.

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 1711 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 Sequestosome-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	53	Total	C	N	O	S	0	0	0
			397	247	71	72	7			
1	BBB	48	Total	C	N	O	S	0	0	0
			351	218	63	64	6			
1	CCC	51	Total	C	N	O	S	0	0	0
			377	234	68	68	7			
1	DDD	53	Total	C	N	O	S	0	2	0
			404	252	71	74	7			

- Molecule 2 is a protein called Dusquetide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	EEE	5	Total	C	N	O	0	0	0
			39	25	8	6			
2	FFF	4	Total	C	N	O	0	0	0
			33	22	7	4			

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	AAA	2	Total	Zn	0	0
			2	2		
3	BBB	2	Total	Zn	0	0
			2	2		
3	CCC	2	Total	Zn	0	0
			2	2		
3	DDD	2	Total	Zn	0	0
			2	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	AAA	34	Total 34	O 34	0	0
4	BBB	20	Total 20	O 20	0	0
4	CCC	11	Total 11	O 11	0	0
4	DDD	32	Total 32	O 32	0	0
4	EEE	3	Total 3	O 3	0	0
4	FFF	2	Total 2	O 2	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: Sequestosome-1

Chain AAA:  83% 17%



- Molecule 1: Sequestosome-1

Chain BBB:  79% 9% 9% 2%



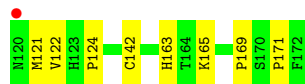
- Molecule 1: Sequestosome-1

Chain CCC:  83% 13% 6%

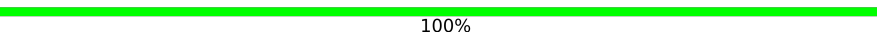


- Molecule 1: Sequestosome-1

Chain DDD:  85% 15% 2%



- Molecule 2: Dusquetide

Chain EEE:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: Dusquetide

Chain FFF:  60% 20% 20% 20%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	124.07Å 25.15Å 77.53Å 90.00° 124.92° 90.00°	Depositor
Resolution (Å)	24.63 – 2.20 24.63 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.9 (24.63-2.20) 98.9 (24.63-2.20)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.45 (at 2.21Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.178 , 0.243 0.184 , 0.243	Depositor DCC
R_{free} test set	491 reflections (4.74%)	wwPDB-VP
Wilson B-factor (Å ²)	26.9	Xtriage
Anisotropy	0.153	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 47.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	1711	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.09% 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 ⓘ

5.1 Standard geometry ⓘ

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

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	AAA	1.20	1/408 (0.2%)	1.42	0/552
1	BBB	1.15	0/360	1.54	1/488 (0.2%)
1	CCC	1.10	0/387	1.38	1/525 (0.2%)
1	DDD	1.25	1/421 (0.2%)	1.38	0/570
2	EEE	1.17	0/39	1.29	0/51
2	FFF	0.90	0/33	1.07	0/44
All	All	1.17	2/1648 (0.1%)	1.42	2/2230 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AAA	159	LEU	C-O	6.01	1.31	1.23
1	DDD	171	PRO	C-O	-5.58	1.17	1.24

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CCC	123	HIS	CB-CA-C	5.43	116.32	110.08
1	BBB	147	ASP	CA-CB-CG	5.39	117.99	112.60

There are no chirality outliers.

There are no planarity outliers.

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	AAA	397	0	375	7	0
1	BBB	351	0	336	5	0
1	CCC	377	0	360	5	0
1	DDD	404	0	387	4	0
2	EEE	39	0	47	0	0
2	FFF	33	0	42	2	0
3	AAA	2	0	0	0	0
3	BBB	2	0	0	0	0
3	CCC	2	0	0	0	0
3	DDD	2	0	0	0	0
4	AAA	34	0	0	0	0
4	BBB	20	0	0	0	0
4	CCC	11	0	0	0	0
4	DDD	32	0	0	0	0
4	EEE	3	0	0	0	0
4	FFF	2	0	0	0	0
All	All	1711	0	1547	17	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 17 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:DDD:122:VAL:O	1:DDD:124:PRO:HD3	2.06	0.55
1:CCC:150:LEU:HD12	1:CCC:165:LYS:HE2	1.87	0.55
1:BBB:137:GLY:O	1:BBB:170:SER:HB3	2.07	0.54
1:BBB:166:LEU:HD23	1:BBB:166:LEU:N	2.24	0.52
1:AAA:127:ILE:HD12	2:FFF:3:VAL:HG11	1.96	0.48

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	AAA	51/53 (96%)	50 (98%)	1 (2%)	0	100	100
1	BBB	46/53 (87%)	42 (91%)	3 (6%)	1 (2%)	5	3
1	CCC	49/53 (92%)	47 (96%)	2 (4%)	0	100	100
1	DDD	53/53 (100%)	47 (89%)	6 (11%)	0	100	100
2	EEE	3/5 (60%)	3 (100%)	0	0	100	100
2	FFF	2/5 (40%)	2 (100%)	0	0	100	100
All	All	204/222 (92%)	191 (94%)	12 (6%)	1 (0%)	24	27

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	BBB	125	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	AAA	46/46 (100%)	46 (100%)	0	100	100
1	BBB	41/46 (89%)	40 (98%)	1 (2%)	43	58
1	CCC	44/46 (96%)	44 (100%)	0	100	100
1	DDD	48/46 (104%)	47 (98%)	1 (2%)	47	63
2	EEE	4/4 (100%)	4 (100%)	0	100	100
2	FFF	4/4 (100%)	4 (100%)	0	100	100
All	All	187/192 (97%)	185 (99%)	2 (1%)	65	79

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	BBB	166	LEU
1	DDD	121	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are

no such sidechains identified.

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 8 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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	AAA	53/53 (100%)	-0.53	0 100 100	19, 23, 39, 44	0
1	BBB	48/53 (90%)	0.15	1 (2%) 63 60	28, 40, 64, 74	0
1	CCC	51/53 (96%)	0.28	3 (5%) 28 25	24, 45, 81, 106	0
1	DDD	53/53 (100%)	-0.45	1 (1%) 66 63	15, 25, 41, 66	2 (3%)
2	EEE	5/5 (100%)	-0.41	0 100 100	23, 28, 38, 41	0
2	FFF	4/5 (80%)	0.32	1 (25%) 2 1	20, 33, 52, 62	0
All	All	214/222 (96%)	-0.15	6 (2%) 55 52	15, 31, 69, 106	2 (0%)

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BBB	171	PRO	2.9
1	CCC	121	MET	2.8
1	CCC	171	PRO	2.7
1	CCC	127	ILE	2.4
1	DDD	120	ASN	2.3

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($\text{\AA}^2$)	Q<0.9
3	ZN	BBB	901	1/1	0.99	0.03	43,43,43,43	0
3	ZN	CCC	901	1/1	0.99	0.03	54,54,54,54	0
3	ZN	CCC	902	1/1	0.99	0.02	35,35,35,35	0
3	ZN	BBB	902	1/1	1.00	0.01	29,29,29,29	0
3	ZN	AAA	902	1/1	1.00	0.01	19,19,19,19	0
3	ZN	AAA	901	1/1	1.00	0.01	22,22,22,22	0
3	ZN	DDD	901	1/1	1.00	0.02	26,26,26,26	0
3	ZN	DDD	902	1/1	1.00	0.02	23,23,23,23	0

6.5 Other polymers [i](#)

There are no such residues in this entry.