



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 05:21 PM UTC

PDB ID : 9Z3B / pdb_00009z3b
Title : Structure C-terminal human Mesothelin Peptide bound to MSLNB703 Fab
Authors : Shaffer, P.L.; Ember, S.
Deposited on : 2025-11-06
Resolution : 1.96 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

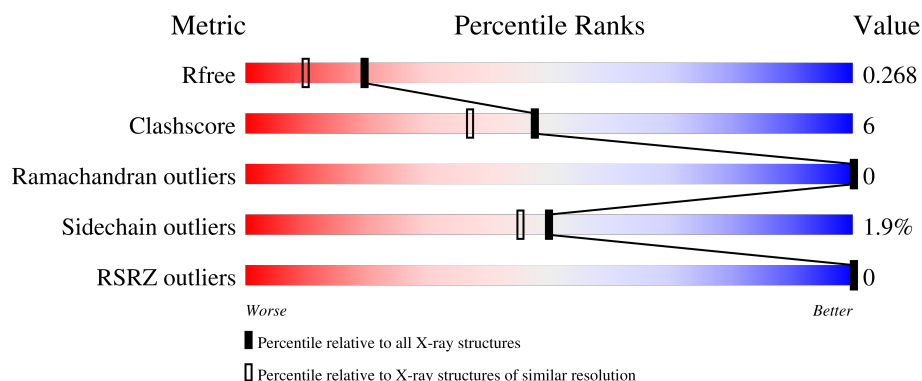
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.96 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.



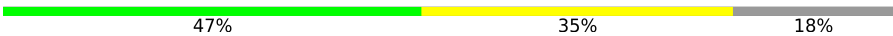
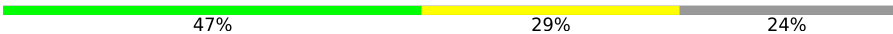
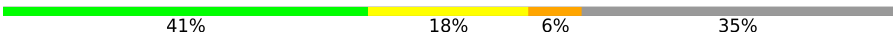
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	220	
1	C	220	
1	E	220	
1	G	220	
2	B	231	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	D	231	 82% 14% ..
2	F	231	 84% 13% .
2	H	231	 81% 16% .
3	I	17	 71% 6% 6% 18%
3	J	17	 47% 35% 18%
3	K	17	 47% 29% 24%
3	L	17	 41% 18% 6% 35%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 13677 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 MSLNB703 Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	220	Total	C	N	O	S	0	0	0
			1642	1032	269	336	5			
1	C	218	Total	C	N	O	S	0	1	0
			1628	1028	268	328	4			
1	E	218	Total	C	N	O	S	0	1	0
			1662	1042	273	343	4			
1	G	216	Total	C	N	O	S	0	1	0
			1582	996	257	325	4			

- Molecule 2 is a protein called MSLNB703 Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	223	Total	C	N	O	S	0	0	0
			1646	1035	274	333	4			
2	D	226	Total	C	N	O	S	0	0	0
			1649	1037	276	332	4			
2	F	222	Total	C	N	O	S	0	1	0
			1644	1033	273	334	4			
2	H	223	Total	C	N	O	S	0	0	0
			1640	1033	276	327	4			

- Molecule 3 is a protein called Mesothelin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	I	14	Total	C	N	O	S	0	0	0
			107	68	15	23	1			
3	J	14	Total	C	N	O	S	0	0	0
			100	62	15	22	1			
3	K	13	Total	C	N	O	S	0	0	0
			100	65	14	20	1			
3	L	11	Total	C	N	O	S	0	0	0
			72	42	12	17	1			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	35	Total 35	O 35	0	0
4	B	30	Total 30	O 30	0	0
4	C	26	Total 26	O 26	0	0
4	D	24	Total 24	O 24	0	0
4	E	23	Total 23	O 23	0	0
4	F	25	Total 25	O 25	0	0
4	G	9	Total 9	O 9	0	0
4	H	31	Total 31	O 31	0	0
4	I	1	Total 1	O 1	0	0
4	J	1	Total 1	O 1	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.

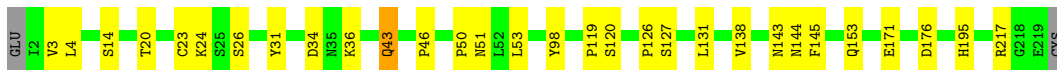
- Molecule 1: MSLNB703 Light Chain

Chain A: 



- Molecule 1: MSLNB703 Light Chain

Chain C: 



- Molecule 1: MSLNB703 Light Chain

Chain E: 



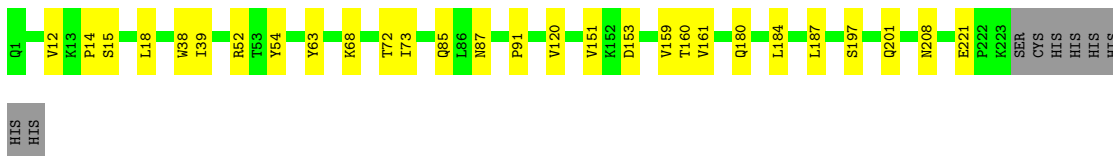
- Molecule 1: MSLNB703 Light Chain

Chain G: 



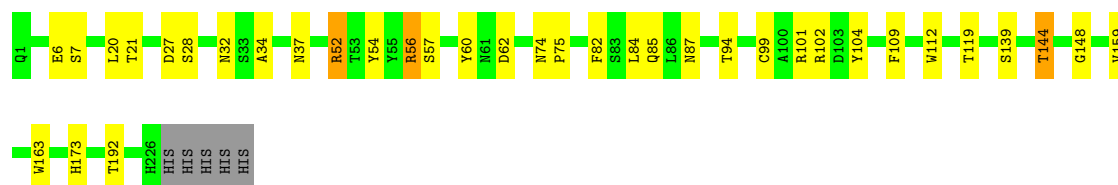
- Molecule 2: MSLNB703 Heavy Chain

Chain B: 



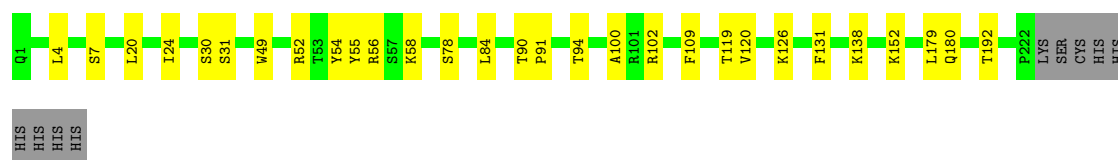
- Molecule 2: MSLNB703 Heavy Chain

Chain D:  82% 14% ..



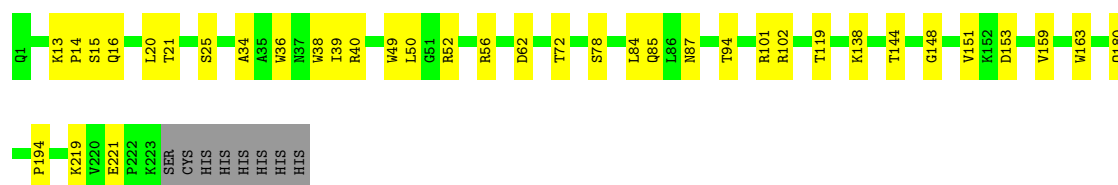
• Molecule 2: MSLNB703 Heavy Chain

Chain F:  84% 13% .



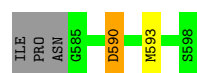
• Molecule 2: MSLNB703 Heavy Chain

Chain H:  81% 16% .

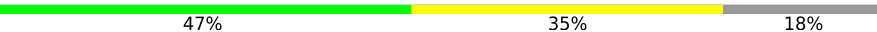


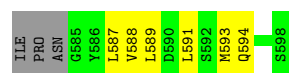
• Molecule 3: Mesothelin

Chain I:  71% 6% 6% 18%

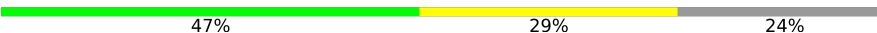


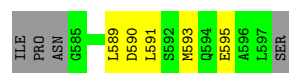
• Molecule 3: Mesothelin

Chain J:  47% 35% 18%



• Molecule 3: Mesothelin

Chain K:  47% 29% 24%



• Molecule 3: Mesothelin



ILE	Y586	S592	A596
PRO	L587	M593	LEU
ASN	V588		SER
GLY	L589		

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	60.15Å 79.74Å 86.77Å 77.18° 89.73° 89.84°	Depositor
Resolution (Å)	44.21 – 1.96 44.21 – 1.96	Depositor EDS
% Data completeness (in resolution range)	75.3 (44.21-1.96) 74.6 (44.21-1.96)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 1.97Å)	Xtriage
Refinement program	PHENIX (1.19.2_4158: ???)	Depositor
R, R_{free}	0.227 , 0.278 0.229 , 0.268	Depositor DCC
R_{free} test set	4286 reflections (3.82%)	wwPDB-VP
Wilson B-factor (Å ²)	31.0	Xtriage
Anisotropy	0.017	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 28.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.237 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	13677	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 5.73% 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	A	0.24	0/1681	0.46	0/2301
1	C	0.26	0/1670	0.52	0/2289
1	E	0.29	0/1710	0.53	0/2335
1	G	0.27	0/1624	0.49	0/2233
2	B	0.26	0/1689	0.48	0/2318
2	D	0.58	0/1692	0.83	3/2326 (0.1%)
2	F	0.24	0/1690	0.47	0/2321
2	H	0.23	0/1683	0.46	0/2310
3	I	0.57	0/107	1.01	0/142
3	J	0.25	0/99	0.54	0/131
3	K	0.20	0/100	0.38	0/134
3	L	0.21	0/71	0.56	0/95
All	All	0.32	0/13816	0.55	3/18935 (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
2	D	0	1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	57	SER	N-CA-C	-9.29	102.76	114.56
2	D	56	ARG	N-CA-C	-5.23	103.07	111.02
2	D	34	ALA	N-CA-C	5.21	116.91	109.14

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	52	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	1642	0	1497	17	0
1	C	1628	0	1483	19	0
1	E	1662	0	1547	13	0
1	G	1582	0	1404	19	0
2	B	1646	0	1553	16	0
2	D	1649	0	1534	24	0
2	F	1644	0	1545	17	0
2	H	1640	0	1544	23	0
3	I	107	0	106	2	0
3	J	100	0	99	9	0
3	K	100	0	101	4	0
3	L	72	0	53	6	0
4	A	35	0	0	1	0
4	B	30	0	0	1	0
4	C	26	0	0	2	0
4	D	24	0	0	1	0
4	E	23	0	0	0	0
4	F	25	0	0	0	0
4	G	9	0	0	1	0
4	H	31	0	0	1	0
4	I	1	0	0	0	0
4	J	1	0	0	0	0
All	All	13677	0	12466	145	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 6.

The worst 5 of 145 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)
3:J:588:VAL:HG11	3:J:594:GLN:HG2	1.60	0.82

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:31:TYR:OH	3:J:594:GLN:NE2	2.16	0.79
2:D:102:ARG:HG3	3:J:589:LEU:HD13	1.64	0.79
2:F:152:LYS:NZ	2:F:180:GLN:OE1	2.20	0.73
1:G:121:VAL:HG21	1:G:202:VAL:HG11	1.73	0.70

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	218/220 (99%)	214 (98%)	4 (2%)	0	100	100
1	C	217/220 (99%)	211 (97%)	6 (3%)	0	100	100
1	E	217/220 (99%)	210 (97%)	7 (3%)	0	100	100
1	G	215/220 (98%)	208 (97%)	7 (3%)	0	100	100
2	B	221/231 (96%)	216 (98%)	5 (2%)	0	100	100
2	D	224/231 (97%)	219 (98%)	5 (2%)	0	100	100
2	F	221/231 (96%)	214 (97%)	7 (3%)	0	100	100
2	H	221/231 (96%)	215 (97%)	6 (3%)	0	100	100
3	I	12/17 (71%)	11 (92%)	1 (8%)	0	100	100
3	J	12/17 (71%)	12 (100%)	0	0	100	100
3	K	11/17 (65%)	11 (100%)	0	0	100	100
3	L	9/17 (53%)	8 (89%)	1 (11%)	0	100	100
All	All	1798/1872 (96%)	1749 (97%)	49 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	174/195 (89%)	173 (99%)	1 (1%)	78	79
1	C	170/195 (87%)	165 (97%)	5 (3%)	37	29
1	E	185/195 (95%)	183 (99%)	2 (1%)	65	64
1	G	164/195 (84%)	162 (99%)	2 (1%)	63	61
2	B	183/202 (91%)	181 (99%)	2 (1%)	65	64
2	D	179/202 (89%)	174 (97%)	5 (3%)	38	30
2	F	183/202 (91%)	178 (97%)	5 (3%)	39	32
2	H	179/202 (89%)	176 (98%)	3 (2%)	53	49
3	I	12/15 (80%)	11 (92%)	1 (8%)	10	3
3	J	11/15 (73%)	11 (100%)	0	100	100
3	K	11/15 (73%)	10 (91%)	1 (9%)	9	2
3	L	6/15 (40%)	5 (83%)	1 (17%)	2	0
All	All	1457/1648 (88%)	1429 (98%)	28 (2%)	50	45

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	208	SER
3	L	588	VAL
2	F	78	SER
2	H	144	THR
2	F	31	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
2	H	87	ASN
2	H	16	GLN
1	E	161	GLN
1	G	43	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	E	153	GLN

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	A	220/220 (100%)	-1.05	0 100 100	17, 33, 50, 86	0
1	C	218/220 (99%)	-1.04	0 100 100	18, 35, 49, 68	1 (0%)
1	E	218/220 (99%)	-1.05	0 100 100	22, 35, 47, 68	1 (0%)
1	G	216/220 (98%)	-0.91	0 100 100	25, 46, 70, 83	1 (0%)
2	B	223/231 (96%)	-1.10	0 100 100	18, 27, 42, 60	0
2	D	226/231 (97%)	-1.07	0 100 100	18, 28, 47, 77	0
2	F	222/231 (96%)	-1.07	0 100 100	18, 32, 45, 64	1 (0%)
2	H	223/231 (96%)	-1.00	0 100 100	21, 33, 61, 77	0
3	I	14/17 (82%)	-0.67	0 100 100	40, 49, 81, 82	0
3	J	14/17 (82%)	-0.77	0 100 100	43, 52, 63, 67	0
3	K	13/17 (76%)	-0.93	0 100 100	41, 43, 54, 63	0
3	L	11/17 (64%)	-0.56	0 100 100	59, 65, 72, 87	0
All	All	1818/1872 (97%)	-1.03	0 100 100	17, 34, 58, 87	4 (0%)

There are no RSRZ outliers to report.

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.