



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 14, 2024 – 12:49 am GMT

PDB ID : 6SF2
Title : Ternary complex of human bone morphogenetic protein 9 (BMP9) growth factor domain, its prodomain and extracellular domain of activin receptor-like kinase 1 (ALK1).
Authors : Salmon, R.M.; Guo, J.; Yu, M.; Li, W.
Deposited on : 2019-07-31
Resolution : 3.30 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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

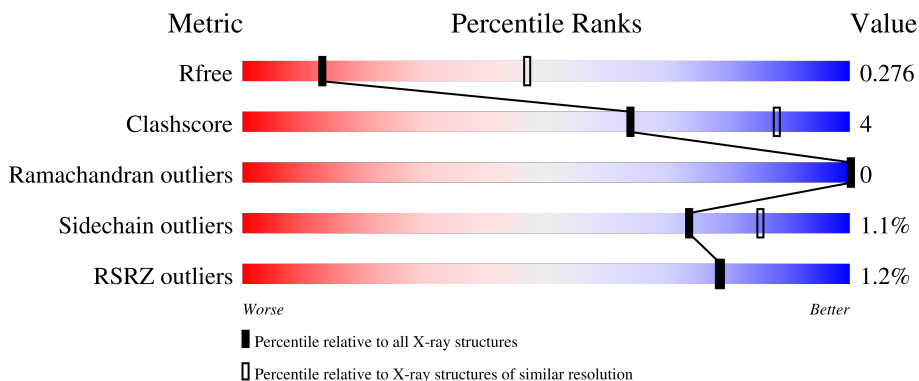
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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.



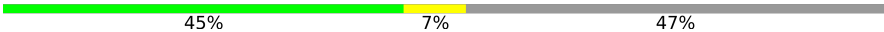
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1149 (3.34-3.26)
Clashscore	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)
RSRZ outliers	127900	1115 (3.34-3.26)

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	98	 67% 9% 23%
1	D	98	 74% 21%
2	B	110	 86% 9% 5%
2	E	110	 86% 9% 5%
3	C	297	 23% 75%

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Mol	Chain	Length	Quality of chain
3	F	297	 45% 7% 47%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4390 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 Serine/threonine-protein kinase receptor R3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	75	Total 546	C 334	N 108	O 94	S 10	0	0	0
1	D	77	Total 587	C 355	N 115	O 107	S 10	0	0	0

- Molecule 2 is a protein called Growth/differentiation factor 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	105	Total 786	C 504	N 127	O 146	S 9	0	1	0
2	E	105	Total 801	C 514	N 129	O 149	S 9	0	1	0

- Molecule 3 is a protein called Growth/differentiation factor 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	73	Total 483	C 310	N 86	O 86	S 1	0	0	0
3	F	156	Total 1150	C 735	N 188	O 223	S 4	0	0	0

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
4	C	1	Total	C	N	O	0	0
			14	8	1	5		
4	F	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	3	Total	O	0	0
			3	3		
5	D	2	Total	O	0	0
			2	2		
5	E	1	Total	O	0	0
			1	1		
5	F	3	Total	O	0	0
			3	3		

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.

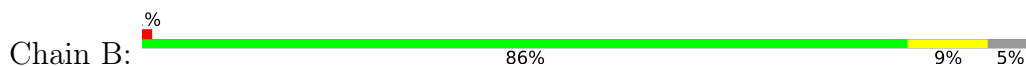
- Molecule 1: Serine/threonine-protein kinase receptor R3



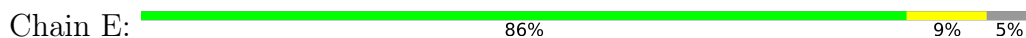
- Molecule 1: Serine/threonine-protein kinase receptor R3



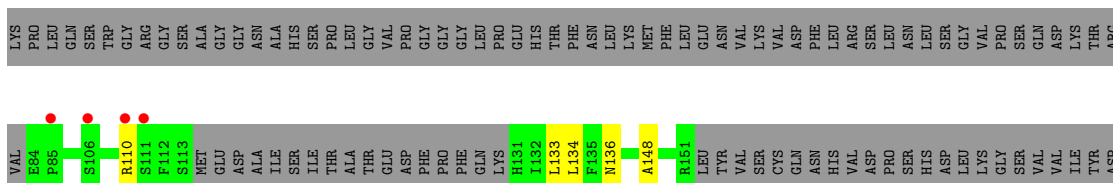
- Molecule 2: Growth/differentiation factor 2



- Molecule 2: Growth/differentiation factor 2



- Molecule 3: Growth/differentiation factor 2



VAL LEU ASP PRO GLY THR ASP ALA TRP ASP SER ALA THR GLU THR LYS THR PHE THR LEU VAL SER GLN ASP ILE GLN ASP GLU V202 S208 V214 VAL ARG SER ASP THR LYS LYS LYS LYS LEU VAL THR VAL GLU SER HIS ARG LYS GLY CYS ASP THR LEU ASP HIS ASP VAL ILE

SER VAL PRO GLY THR SER ARG ASN LEU P252 D260 HIS SER SER GLY THR LEU PHE THR LYS LEU VAL SER ARG GLN MET ILE SER HIS GLU GLN VAL SER LEU LYS LYS LEU SER ASP ASN LYS LYS LEU THR THR ALA THR VAL GLU SER HIS ARG LYS GLY CYS ASP THR ASP THR HIS ASP VAL ILE

ALA ALA GLY SER THR LEU ALA ARG LYS ARG

- Molecule 3: Growth/differentiation factor 2

Chain F:  45% 7% 47%

LYS PRO LEU GLN SER TRP GLY ARG GLY SER ALA ALA GLY ASN ALA HIS SER PRO LEU VAL VAL GLY GLY LEU PRO HIS THR PHE ASN LEU LYS MET PHE LEU GLU ASN VAL VAL VAL ASP PHE LEU ARG LEU ASN LEU SER GLY VAL PRO SER GLN ASP LYS THR ARG

VAL E84 P85 D89 LYS SER T102 T1121 ALA THR GLU ASP F126 F127 F128 M136 H137 A148 L152 S155 C156 H159 VAL ASP PRO S163 H164 V170 D177 G178 THR ASP ALA TRP ASP SER ALA THR T188 T197 E200 S208 S219 THR LYS S222

K223 M224 V230 C237 D241 I242 S243 V244 P245 P246 SER R249 P252 H261 SER SER GLY THR LYS LYS THR ARG LEU LEU ARG MET ILE HIS GLU GLN SER VAL LEU LYS LYS LEU SER THR ALA GLY ASP SER THR ALA GLY GLU SER SER HIS GLU

GLU ASP THR ASP GLY HIS VAL ALA ALA GLY SER THR LEU ALA ARG ARG LYS ARG

4 Data and refinement statistics i

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	72.61Å 72.61Å 438.49Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	62.25 – 3.30 62.25 – 3.30	Depositor EDS
% Data completeness (in resolution range)	100.0 (62.25-3.30) 99.9 (62.25-3.30)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.72 (at 3.33Å)	Xtrriage
Refinement program	PHENIX 1.17_3644	Depositor
R, R_{free}	0.243 , 0.274 0.243 , 0.276	Depositor DCC
R_{free} test set	996 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	90.1	Xtrriage
Anisotropy	0.284	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 67.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.073 for h,-h-k,-l	Xtrriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	4390	wwPDB-VP
Average B, all atoms (Å ²)	89.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.74% 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](#)

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

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	0.22	0/559	0.48	0/762
1	D	0.22	0/602	0.46	0/819
2	B	0.24	0/811	0.41	0/1108
2	E	0.24	0/827	0.42	0/1128
3	C	0.22	0/493	0.42	0/679
3	F	0.23	0/1172	0.45	0/1600
All	All	0.23	0/4464	0.44	0/6096

There are no bond length outliers.

There are no bond angle outliers.

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	A	546	0	486	5	0
1	D	587	0	532	2	0
2	B	786	0	724	9	0
2	E	801	0	749	8	0
3	C	483	0	359	6	0
3	F	1150	0	1006	11	0
4	C	14	0	13	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	F	14	0	13	0	0
5	A	3	0	0	0	0
5	D	2	0	0	0	0
5	E	1	0	0	0	0
5	F	3	0	0	0	0
All	All	4390	0	3882	35	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 4.

The worst 5 of 35 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:F:170:VAL:HG23	3:F:197:ILE:HD11	1.74	0.70
1:D:92:SER:HB2	1:D:95:CYS:HB3	1.75	0.67
3:F:177:ASP:O	3:F:188:THR:N	2.33	0.62
3:C:133:LEU:HD23	3:C:134:LEU:H	1.64	0.61
2:B:413:THR:HG22	3:C:110:ARG:HG2	1.86	0.57

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	73/98 (74%)	71 (97%)	2 (3%)	0	100	100
1	D	75/98 (76%)	73 (97%)	2 (3%)	0	100	100
2	B	104/110 (94%)	101 (97%)	3 (3%)	0	100	100
2	E	104/110 (94%)	101 (97%)	3 (3%)	0	100	100
3	C	65/297 (22%)	60 (92%)	5 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	F	142/297 (48%)	133 (94%)	9 (6%)	0	100	100
All	All	563/1010 (56%)	539 (96%)	24 (4%)	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	56/86 (65%)	55 (98%)	1 (2%)	59	78
1	D	66/86 (77%)	65 (98%)	1 (2%)	65	81
2	B	82/93 (88%)	82 (100%)	0	100	100
2	E	86/93 (92%)	86 (100%)	0	100	100
3	C	32/265 (12%)	32 (100%)	0	100	100
3	F	116/265 (44%)	113 (97%)	3 (3%)	46	71
All	All	438/888 (49%)	433 (99%)	5 (1%)	73	85

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	CYS
1	D	36	CYS
3	F	128	PHE
3	F	156	CYS
3	F	237	CYS

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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
4	NAG	C	501	3	14,14,15	0.37	0	17,19,21	0.56	0
4	NAG	F	501	3	14,14,15	0.35	0	17,19,21	0.46	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
4	NAG	C	501	3	-	2/6/23/26	0/1/1/1
4	NAG	F	501	3	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	501	NAG	O5-C5-C6-O6
4	C	501	NAG	C4-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
4	F	501	NAG	C1-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	501	NAG	1	0

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	75/98 (76%)	0.25	1 (1%) 77 77	73, 84, 109, 118	0
1	D	77/98 (78%)	0.15	0 100 100	68, 80, 89, 102	1 (1%)
2	B	105/110 (95%)	0.34	1 (0%) 82 82	67, 81, 96, 103	0
2	E	105/110 (95%)	0.31	0 100 100	66, 75, 85, 89	0
3	C	73/297 (24%)	0.05	4 (5%) 25 23	110, 126, 137, 139	0
3	F	156/297 (52%)	0.20	1 (0%) 89 90	80, 93, 118, 127	0
All	All	591/1010 (58%)	0.23	7 (1%) 79 78	66, 85, 127, 139	1 (0%)

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	106	SER	2.6
1	A	60	GLY	2.4
3	C	85	PRO	2.3
3	C	111	SER	2.3
3	C	110	ARG	2.2

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 monosaccharides 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
4	NAG	C	501	14/15	0.76	0.22	130,133,134,135	0
4	NAG	F	501	14/15	0.76	0.18	121,122,123,123	0

6.5 Other polymers [i](#)

There are no such residues in this entry.