



wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 10:34 AM GMT

PDB ID : 1SMR
Title : The 3-d structure of mouse submaxillary renin complexed with a decapeptide inhibitor ch-66 based on the 4-16 fragment of rat angiotensinogen
Authors : Dealwis, C.G.; Blundell, T.L.
Deposited on : 1992-03-11
Resolution : 2.00 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

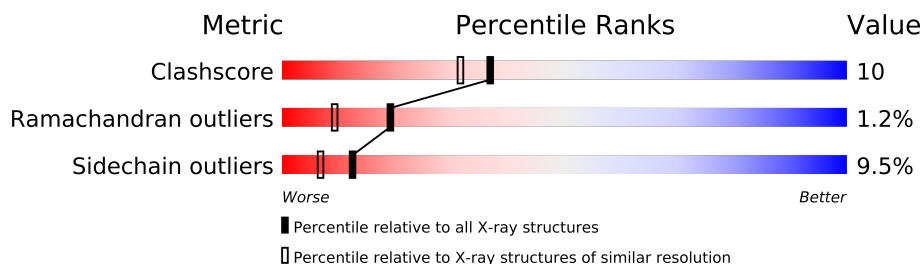
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 21963
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.00 Å.





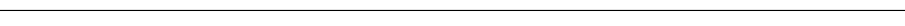


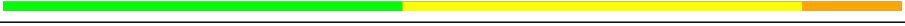
Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	79885	6188 (2.00-2.00)
Ramachandran outliers	78287	6102 (2.00-2.00)
Sidechain outliers	78261	6100 (2.00-2.00)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	335	
1	C	335	
1	E	335	
1	G	335	
2	B	9	
2	D	9	
2	F	9	
2	H	9	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10560 atoms, of which 0 are hydrogen and 0 are deuterium.

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 RENIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	331	Total	C	N	O	S	0	0	0
			2511	1609	409	481	12			
1	C	331	Total	C	N	O	S	0	0	0
			2511	1609	409	481	12			
1	E	331	Total	C	N	O	S	0	0	0
			2511	1609	409	481	12			
1	G	331	Total	C	N	O	S	0	0	0
			2511	1609	409	481	12			

There are 8 discrepancies between the modelled and reference sequences:

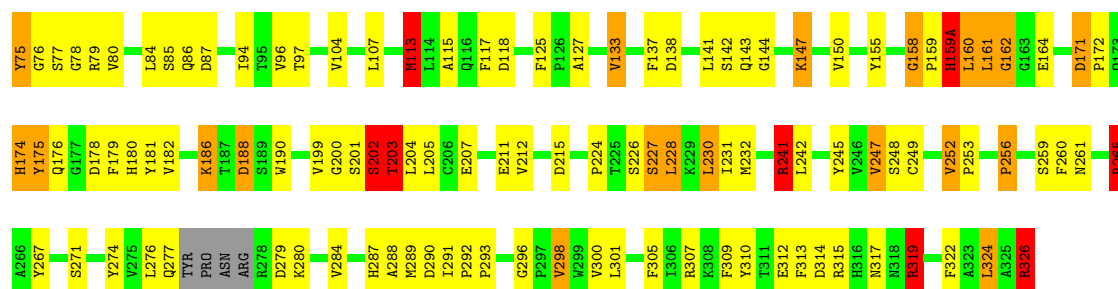
Chain	Residue	Modelled	Actual	Comment	Reference
A	106	GLN	GLU	CONFLICT	UNP P00796
A	173	GLN	GLU	CONFLICT	UNP P00796
C	106	GLN	GLU	CONFLICT	UNP P00796
C	173	GLN	GLU	CONFLICT	UNP P00796
E	106	GLN	GLU	CONFLICT	UNP P00796
E	173	GLN	GLU	CONFLICT	UNP P00796
G	106	GLN	GLU	CONFLICT	UNP P00796
G	173	GLN	GLU	CONFLICT	UNP P00796

- Molecule 2 is a protein called INHIBITOR CH-66.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	9	Total	C	N	O	0	0	0
			90	65	12	13			
2	D	9	Total	C	N	O	0	0	0
			90	65	12	13			
2	F	9	Total	C	N	O	0	0	0
			90	65	12	13			
2	H	9	Total	C	N	O	0	0	0
			90	65	12	13			

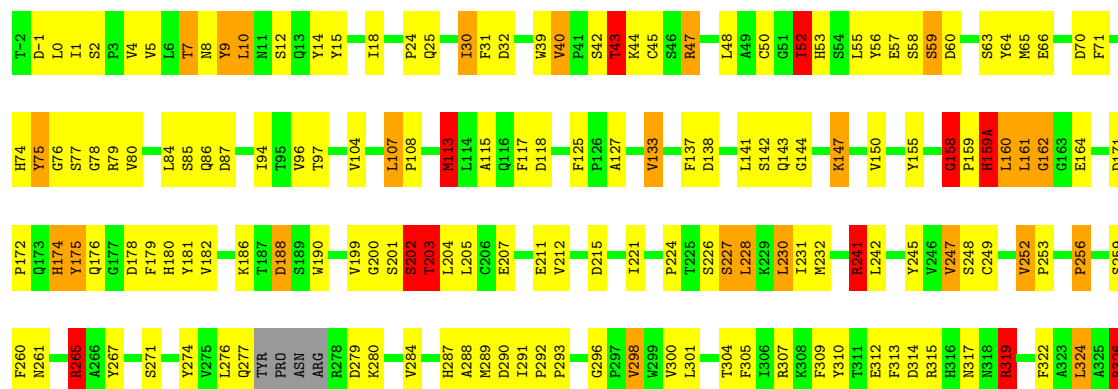
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	148	Total 148	O 148	0	0
3	B	5	Total 5	O 5	0	0
3	C	3	Total 3	O 3	0	0



• Molecule 1: RENIN

Chain G:



• Molecule 2: INHIBITOR CH-66

Chain B:



• Molecule 2: INHIBITOR CH-66

Chain D:



• Molecule 2: INHIBITOR CH-66

Chain F:



• Molecule 2: INHIBITOR CH-66

Chain H:



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	78.34Å 117.76Å 85.88Å 90.00° 101.18° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.00	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	RESTRAIN	Depositor
R, R_{free}	0.180 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	10560	wwPDB-VP
Average B, all atoms (Å ²)	0.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	1.49	18/2572 (0.7%)	2.47	178/3500 (5.1%)
1	C	1.49	18/2572 (0.7%)	2.47	179/3500 (5.1%)
1	E	1.49	18/2572 (0.7%)	2.47	178/3500 (5.1%)
1	G	1.49	18/2572 (0.7%)	2.47	179/3500 (5.1%)
2	B	1.45	0/72	2.62	6/96 (6.2%)
2	D	1.45	0/72	2.62	6/96 (6.2%)
2	F	1.45	0/72	2.62	6/96 (6.2%)
2	H	1.45	0/72	2.62	6/96 (6.2%)
All	All	1.49	72/10576 (0.7%)	2.47	738/14384 (5.1%)

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	3
1	C	0	3
1	E	0	3
1	G	0	3
2	B	0	2
2	D	0	2
2	F	0	2
2	H	0	2
All	All	0	20

The worst 5 of 72 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	42	SER	CB-OG	-19.90	1.16	1.42
1	G	42	SER	CB-OG	-19.87	1.16	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	42	SER	CB-OG	-19.85	1.16	1.42
1	C	42	SER	CB-OG	-19.83	1.16	1.42
1	G	43	THR	CB-OG1	-9.08	1.25	1.43

The worst 5 of 738 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	160	LEU	O-C-N	15.66	147.76	122.70
1	A	160	LEU	O-C-N	15.65	147.74	122.70
1	C	160	LEU	O-C-N	15.65	147.74	122.70
1	G	160	LEU	O-C-N	15.65	147.74	122.70
1	G	307	ARG	NE-CZ-NH1	-14.70	112.95	120.30

There are no chirality outliers.

5 of 20 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	241	ARG	Sidechain
1	A	265	ARG	Sidechain
1	A	319	ARG	Sidechain
2	B	6	LPL	Mainchain,Peptide
1	C	241	ARG	Sidechain

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2511	0	2442	53	16
1	C	2511	0	2442	51	19
1	E	2511	0	2442	53	17
1	G	2511	0	2442	53	19
2	B	90	0	86	2	0
2	D	90	0	86	2	0
2	F	90	0	86	2	0
2	H	90	0	86	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	148	0	0	3	1
3	B	5	0	0	0	0
3	C	3	0	0	1	0
All	All	10560	0	10112	210	36

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 10.

The worst 5 of 210 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:199:VAL:HB	1:C:203:THR:HG23	1.44	1.00
1:E:199:VAL:HB	1:E:203:THR:HG23	1.44	1.00
1:G:199:VAL:HB	1:G:203:THR:HG23	1.44	0.99
1:A:199:VAL:HB	1:A:203:THR:HG23	1.44	0.97
1:A:199:VAL:HB	1:A:203:THR:CG2	2.00	0.92

The worst 5 of 36 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	Distance(Å)	Clash(Å)
1:C:113:MET:CE	1:E:113:MET:CE[1_444]	0.33	1.87
1:E:326:ARG:NE	1:G:326:ARG:NH1[1_565]	0.52	1.68
1:A:326:ARG:NE	1:C:326:ARG:NH1[1_565]	0.63	1.57
1:A:326:ARG:CZ	1:C:326:ARG:CZ[1_565]	0.67	1.53
1:A:113:MET:CE	1:G:113:MET:CE[1_464]	0.69	1.51

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	327/335 (98%)	315 (96%)	8 (2%)	4 (1%)	19	9
1	C	327/335 (98%)	315 (96%)	8 (2%)	4 (1%)	19	9
1	E	327/335 (98%)	315 (96%)	8 (2%)	4 (1%)	19	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	327/335 (98%)	315 (96%)	8 (2%)	4 (1%)	19	9
2	B	6/9 (67%)	6 (100%)	0	0	100	100
2	D	6/9 (67%)	6 (100%)	0	0	100	100
2	F	6/9 (67%)	6 (100%)	0	0	100	100
2	H	6/9 (67%)	6 (100%)	0	0	100	100
All	All	1332/1376 (97%)	1284 (96%)	32 (2%)	16 (1%)	19	9

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	159(A)	HIS
1	A	203	THR
1	A	280	LYS
1	C	159(A)	HIS
1	C	203	THR

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	277/287 (96%)	250 (90%)	27 (10%)	12	6
1	C	277/287 (96%)	250 (90%)	27 (10%)	12	6
1	E	277/287 (96%)	250 (90%)	27 (10%)	12	6
1	G	277/287 (96%)	250 (90%)	27 (10%)	12	6
2	B	7/7 (100%)	7 (100%)	0	100	100
2	D	7/7 (100%)	7 (100%)	0	100	100
2	F	7/7 (100%)	7 (100%)	0	100	100
2	H	7/7 (100%)	7 (100%)	0	100	100
All	All	1136/1176 (97%)	1028 (90%)	108 (10%)	12	7

5 of 108 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	247	VAL
1	E	113	MET
1	G	228	LEU
1	C	265	ARG
1	E	2	SER

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

Mol	Chain	Res	Type
1	C	233	GLN
1	E	53	HIS
1	G	53	HIS
1	C	174	HIS
1	G	86	GLN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

8 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	PIV	B	1	2	5,5,6	8.81	2 (40%)	6,7,9	0.66	0
2	LPL	B	6	2	15,15,16	4.39	3 (20%)	17,19,21	11.26	4 (23%)
2	PIV	D	1	2	5,5,6	8.82	2 (40%)	6,7,9	0.66	0
2	LPL	D	6	2	15,15,16	4.38	3 (20%)	17,19,21	11.27	3 (17%)
2	PIV	F	1	2	5,5,6	8.84	2 (40%)	6,7,9	0.66	0
2	LPL	F	6	2	15,15,16	4.39	3 (20%)	17,19,21	11.27	3 (17%)
2	PIV	H	1	2	5,5,6	8.76	2 (40%)	6,7,9	0.66	0
2	LPL	H	6	2	15,15,16	4.37	3 (20%)	17,19,21	11.26	4 (23%)

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	PIV	B	1	2	-	0/0/3/6	0/0/0/0
2	LPL	B	6	2	-	0/16/18/20	0/0/0/0
2	PIV	D	1	2	-	0/0/3/6	0/0/0/0
2	LPL	D	6	2	-	0/16/18/20	0/0/0/0
2	PIV	F	1	2	-	0/0/3/6	0/0/0/0
2	LPL	F	6	2	-	0/16/18/20	0/0/0/0
2	PIV	H	1	2	-	0/0/3/6	0/0/0/0
2	LPL	H	6	2	-	0/16/18/20	0/0/0/0

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	1	PIV	O1-C	19.59	1.24	1.11
2	D	1	PIV	O1-C	19.53	1.24	1.11
2	B	1	PIV	O1-C	19.49	1.24	1.11
2	H	1	PIV	O1-C	19.40	1.24	1.11
2	B	6	LPL	O-C	16.42	1.22	1.11

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	6	LPL	O-C-CA1	-46.17	125.14	176.50
2	F	6	LPL	O-C-CA1	-46.14	125.18	176.50
2	H	6	LPL	O-C-CA1	-46.12	125.20	176.50
2	B	6	LPL	O-C-CA1	-46.12	125.20	176.50
2	D	6	LPL	CB-CA-CH	2.33	116.62	111.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.