

wwPDB X-ray Structure Validation Summary Report (i)

May 14, 2020 – 10:44 am BST

PDB ID 6APR

> STRUCTURES OF COMPLEXES OF RHIZOPUSPEPSIN WITH PEP-Title

> > STATIN AND OTHER STATINE-CONTAINING INHIBITORS

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Deposited on : 1989-08-03

2.50 Å(reported) Resolution

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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity 4.02b-467

> 1.8.5 (274361), CSD as541be (2020) Mogul

Xtriage (Phenix) 1.13 EDS 2.11

Percentile statistics 20191225.v01 (using entries in the PDB archive December 25th 2019)

> Refmac 5.8.0158

7.0.044 (Gargrove) CCP4 Engh & Huber (2001)

Ideal geometry (proteins) Ideal geometry (DNA, RNA) Parkinson et al. (1996)

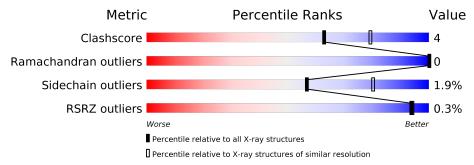
Validation Pipeline (wwPDB-VP) 2.11

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 2.50 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{resolution range}(ext{Å}))$
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 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 <=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	Е	325		84%		15%	-
2	I	6	17%	50%	33%		



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2686 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 RHIZOPUSPEPSIN.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	Е	325	Total 2417	C 1524	N 399	O 488	S 6	0	4	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Е	15	ILE	VAL	CONFLICT	UNP P06026
Е	54	GLY	ARG	CONFLICT	UNP P06026
Е	61	ASN	LYS	CONFLICT	UNP P06026
Е	116	SER	ASN	CONFLICT	UNP P06026
Е	162	LYS	SER	CONFLICT	UNP P06026
Е	230	ILE	VAL	CONFLICT	UNP P06026
Е	256	ALA	ARG	CONFLICT	UNP P06026
Е	281	PHE	TYR	CONFLICT	UNP P06026
Е	294	TRP	PHE	CONFLICT	UNP P06026
Е	295	GLY	ASP	CONFLICT	UNP P06026

• Molecule 2 is a protein called PEPSTATIN.

Mol	Chain	Residues	${f Atoms}$				ZeroOcc	AltConf	Trace
2	I	6	Total 47	C 34	N 5	O 8	0	0	0

• Molecule 3 is water.

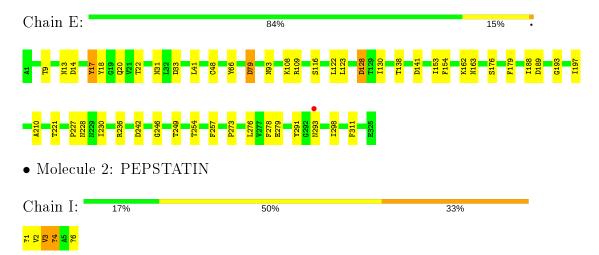
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	E	220	Total O 220 220	0	0
3	I	2	Total O 2 2	0	0



3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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: RHIZOPUSPEPSIN





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	60.33Å 60.66Å 107.00Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 - 2.50	Depositor
Resolution (A)	8.00 - 2.49	EDS
% Data completeness	(Not available) (8.00-2.50)	Depositor
(in resolution range)	84.8 (8.00-2.49)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$	-	Xtriage
Refinement program	PROLSQ	Depositor
D D	0.149 , (Not available)	Depositor
R, R_{free}	0.134 , (Not available)	DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	17.3	Xtriage
Anisotropy	0.431	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.33, 67.2	EDS
L-test for twinning ¹	$< L >=0.40, < L^2>=0.22$	Xtriage
Estimated twinning fraction	0.065 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2686	wwPDB-VP
Average B, all atoms (Å ²)	13.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.59% of the height of the origin peak. No significant pseudotranslation is detected.

Theoretical values of <|L|>, $<L^2>$ 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: STA, IVA

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	Boı	nd lengths	Bond angles		
MIOI	Chain	RMSZ $ $ $\# Z > 5$		RMSZ	# Z > 5	
1	E	0.83	$2/2488 \; (0.1\%)$	1.54	$19/3381 \ (0.6\%)$	
2	I	0.81	0/17	2.44	0/21	
All	All	0.83	2/2505~(0.1%)	1.55	19/3402 (0.6%)	

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	I	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(\operatorname{\AA})$
1	E	13	ASN	CG-OD1	5.17	1.35	1.24
1	Е	228	ASN	CG-OD1	5.09	1.35	1.24

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	\mathbf{Res}	Type	${f Atoms}$	\mathbf{Z}	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^o)$
1	Е	141	ASP	CB-CG-OD2	13.46	130.41	118.30
1	E	109	ARG	NE-CZ-NH2	-9.91	115.34	120.30
1	Е	33	ASP	CB-CG-OD2	7.91	125.42	118.30
1	E	109	ARG	NE-CZ-NH1	7.23	123.92	120.30
1	Е	141	ASP	CB-CG-OD1	-7.17	111.85	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:



Mol	Chain	Res	Type	Group
2	I	4	STA	Mainchain,Peptide

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	Е	2417	0	2331	21	0
2	I	47	0	60	4	0
3	E	220	0	0	0	0
3	I	2	0	0	0	0
All	All	2686	0	2391	21	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 21 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{array}{l} ext{Interatomic} \ ext{distance} \ (ext{Å}) \end{array}$	$egin{array}{c} ext{Clash} \ ext{overlap } (ext{Å}) \end{array}$
1:E:79:ASP:HB3	2:I:3:VAL:HG13	1.81	0.61
1:E:122:LEU:HD21	2:I:4:STA:HD12	1.83	0.61
1:E:188:ILE:HD13	1:E:197:ILE:HG22	1.85	0.58
1:E:162:LYS:NZ	1:E:163:ASN:HD21	2.07	0.53
1:E:273:PRO:HA	1:E:276:LEU:HD12	1.91	0.52

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	Perce	$\mathbf{entiles}$
1	E	$327/325 \ (101\%)$	322 (98%)	5 (2%)	0	100	100
2	I	3/6 (50%)	2 (67%)	1 (33%)	0	100	100
All	All	330/331 (100%)	324 (98%)	6 (2%)	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	E	$259/255 \; (102\%)$	255 (98%)	4 (2%)	65 85		
2	I	2/2~(100%)	0	2 (100%)	0 0		
All	All	$261/257 \; (102\%)$	255 (98%)	6 (2%)	57 76		

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	Ε	116[B]	SER
2	I	3	VAL
1	Ε	293	ASN
1	E	116[A]	SER
2	I	2	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	${f Res}$	Type
1	Е	20	GLN
1	E	119	ASN
1	E	163	ASN
1	Ε	243	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.



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

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	Tuno	Chain	ain Res Link Bond lengths		Bond angles					
MIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	STA	I	4	2	10,10,11	0.87	0	9,12,14	2.07	3 (33%)
2	STA	I	6	2	10,10,11	1.46	2 (20%)	9,12,14	2.69	3 (33%)

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	${f Torsions}$	Rings
2	STA	I	4	2	-	2/11/11/12	_
2	STA	I	6	2	-	5/11/11/12	-

All (2) bond length outliers are listed below:

\mathbf{Mol}	Chain	${f Res}$	\mathbf{Type}	Atoms	\mathbf{Z}	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(ext{ iny A})$
2	I	6	STA	CH-CA	3.51	1.56	1.53
2	I	6	STA	CB-CA	-2.42	1.49	1.53

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^o)$
2	I	6	STA	CG-CB-CA	5.53	127.70	115.82
2	I	4	STA	CM-CH-CA	4.26	119.64	112.94
2	I	6	STA	OH-CH-CM	3.48	116.53	109.08
2	I	6	STA	CM-CH-CA	3.41	118.30	112.94
2	I	4	STA	O-C-CM	-3.20	116.09	125.43

There are no chirality outliers.

5 of 7 torsion outliers are listed below:



Mol	Chain	Res	Type	Atoms
2	I	4	STA	N-CA-CB-CG
2	I	4	STA	O-C-CM-CH
2	I	6	STA	CA-CH-CM-C
2	I	6	STA	O-C-CM-CH
2	I	6	STA	CA-CB-CG-CD2

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	I	4	STA	1	0
2	I	6	STA	1	0

5.5 Carbohydrates (i)

There are no carbohydrates 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, 95^{th} 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 $>$	$\#\mathrm{RSRZ}{>}2$	$OWAB(\AA^2)$	Q < 0.9
1	E	$325/325 \; (100\%)$	-1.06	1 (0%) 94 94	2, 11, 22, 35	0
2	I	3/6 (50%)	-0.83	0 100 100	13, 13, 16, 19	0
All	All	328/331 (99%)	-1.06	1 (0%) 94 94	2, 12, 22, 35	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	293	ASN	3.8

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, 95^{th} 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
2	STA	I	6	11/12	0.84	0.19	23,25,30,32	0
2	STA	I	4	11/12	0.98	0.09	10,12,15,15	0

6.3 Carbohydrates (i)

There are no carbohydrates 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.

