

Full wwPDB X-ray Structure Validation Report (i)

Aug 22, 2023 – 10:02 AM EDT

PDB ID : 2SGP

Title : PRO 18 VARIANT OF TURKEY OVOMUCOID INHIBITOR THIRD DO-

MAIN COMPLEXED WITH STREPTOMYCES GRISEUS PROTEINASE

B AT PH 6.5

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Deposited on : 1999-03-25

Resolution : 1.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

MolProbity : 4.02b-467

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

Xtriage (Phenix) : NOT EXECUTED EDS : NOT EXECUTED

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

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

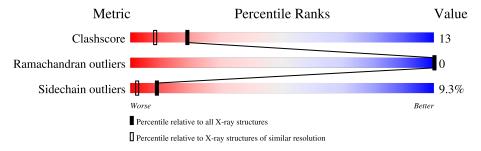
Validation Pipeline (wwPDB-VP) : 2.35

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 1.80 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	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)

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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain						
1	Е	185	69%	27%					
2	I	51	63%	27%	10%				



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 1857 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 PROTEINASE B.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	Ε	185	Total 1309	C 799	N 228	O 276	S 6	0	0	0

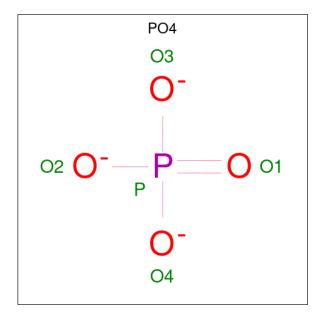
• Molecule 2 is a protein called OVOMUCOID INHIBITOR.

Mol	Chain	Residues		Ato	$\mathbf{m}\mathbf{s}$			ZeroOcc	AltConf	Trace
2	I	51	Total 386	C 237	N 65	O 78	S 6	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	18	PRO	LEU	engineered mutation	UNP P68390

• Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	Е	1	Total 5	O 4	P 1	0	0

• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	Е	115	Total O 115 115	0	0
4	I	42	Total O 42 42	0	0

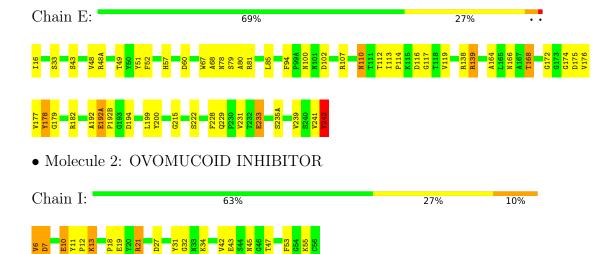


3 Residue-property plots (i)

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. 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. 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.

Note EDS was not executed.

• Molecule 1: PROTEINASE B





4 Data and refinement statistics (i)

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

Property	Value	Source	
Space group	P 1 21 1	Depositor	
Cell constants	45.54Å 54.68Å 45.58Å	Depositor	
a, b, c, α , β , γ	90.00° 119.19° 90.00°	Depositor	
Resolution (Å)	20.00 - 1.80	Depositor	
% Data completeness	92.0 (20.00-1.80)	Depositor	
(in resolution range)	32.0 (20.00 1.00)	Беровног	
R_{merge}	0.08	Depositor	
R_{sym}	(Not available)	Depositor	
Refinement program	TNT	Depositor	
R, R_{free}	0.193 , (Not available)	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	1857	wwPDB-VP	
Average B, all atoms (Å ²)	15.0	wwPDB-VP	



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: PO4

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		nd lengths	Bond angles		
IVIOI		RMSZ	# Z > 5	RMSZ	# Z > 5	
1	Е	1.26	5/1334 (0.4%)	1.50	$10/1818 \; (0.6\%)$	
2	I	1.25	3/395 (0.8%)	1.47	4/534~(0.7%)	
All	All	1.25	8/1729 (0.5%)	1.49	$14/2352 \ (0.6\%)$	

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 maintain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	Е	0	1
2	I	1	0
All	All	1	1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(A)	Ideal(Å)
1	E	242	TYR	C-OXT	-7.88	1.08	1.23
1	Е	233	GLU	CD-OE1	7.84	1.34	1.25
2	I	10	GLU	CD-OE2	7.05	1.33	1.25
2	I	19	GLU	CD-OE2	6.86	1.33	1.25
2	I	43	GLU	CD-OE1	6.75	1.33	1.25
1	Е	242	TYR	CZ-OH	-6.56	1.26	1.37
1	Е	192(A)	GLU	CD-OE1	5.57	1.31	1.25
1	Е	43	SER	CB-OG	5.48	1.49	1.42

All (14) bond angle outliers are listed below:

\mathbf{Mol}	Chain	Res	Type	${f Atoms}$	\mathbf{Z}	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}({}^{o})$
2	I	7	ASP	CB-CG-OD2	-7.63	111.43	118.30

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Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$Ideal(^{o})$
1	Ε	60	ASP	CB-CG-OD2	-6.84	112.15	118.30
2	I	7	ASP	CB-CG-OD1	6.82	124.44	118.30
1	Ε	52	PHE	N-CA-CB	6.67	122.60	110.60
1	Е	192	ALA	N-CA-CB	6.48	119.17	110.10
2	I	27	ASP	CB-CG-OD1	6.30	123.97	118.30
1	Ε	116	ASP	CB-CG-OD2	-6.06	112.84	118.30
1	Ε	178	TYR	N-CA-CB	-6.00	99.80	110.60
1	Ε	139	ARG	NE-CZ-NH1	5.93	123.27	120.30
1	Ε	175	ASP	CB-CG-OD1	-5.76	113.12	118.30
1	Ε	231	VAL	CG1-CB-CG2	5.60	119.86	110.90
1	Е	116	ASP	CB-CG-OD1	5.60	123.34	118.30
1	Е	107	ARG	NE-CZ-NH1	5.51	123.05	120.30
2	I	31	TYR	CB-CG-CD2	-5.47	117.72	121.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	I	6	VAL	CA

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group	
1	Е	242	TYR	Sidechain	

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	Ε	1309	0	1227	34	0
2	I	386	0	354	13	0
3	Е	5	0	0	0	0
4	${ m E}$	115	0	0	4	0
4	I	42	0	0	2	0
All	All	1857	0	1581	43	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 13.



All (43) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

A	A 4 S	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
2:I:21:ARG:HG2	2:I:21:ARG:HH11	1.20	1.06
2:I:11:TYR:HB3	2:I:12:PRO:HA	1.56	0.86
1:E:172:GLY:HA3	2:I:13:LYS:HE2	1.58	0.86
1:E:166:ASN:HD22	1:E:179:GLY:HA2	1.44	0.83
2:I:21:ARG:HG2	2:I:21:ARG:NH1	2.00	0.66
1:E:49:THR:HG22	1:E:51:TYR:CE2	2.32	0.65
1:E:192(B):PRO:HG2	2:I:32:GLY:HA3	1.80	0.63
1:E:67:TRP:CD2	1:E:81:ARG:HG3	2.36	0.60
1:E:113:ILE:HG13	1:E:114:PRO:HD2	1.83	0.60
1:E:174:GLY:HA2	4:E:569:HOH:O	2.02	0.59
1:E:110:ASN:C	1:E:110:ASN:HD22	2.05	0.59
1:E:199:LEU:HD13	1:E:228:PHE:CZ	2.38	0.59
1:E:110:ASN:ND2	1:E:113:ILE:H	2.02	0.58
1:E:215:GLY:HA2	2:I:18:PRO:HD3	1.87	0.57
1:E:168:THR:HG1	1:E:178:TYR:HD1	1.53	0.57
1:E:68:ALA:HB2	1:E:85:LEU:HD21	1.87	0.56
2:I:55:LYS:HD3	4:I:95:HOH:O	2.05	0.56
1:E:199:LEU:HB2	1:E:228:PHE:CD2	2.41	0.55
2:I:6:VAL:N	4:I:90:HOH:O	2.39	0.55
1:E:199:LEU:HD13	1:E:228:PHE:CE2	2.44	0.53
1:E:119:VAL:HG11	1:E:200:TYR:CE1	2.44	0.53
1:E:33:SER:O	1:E:81:ARG:NH2	2.29	0.51
2:I:11:TYR:CB	2:I:12:PRO:HA	2.29	0.51
2:I:12:PRO:HD3	2:I:42:VAL:HG11	1.93	0.49
1:E:176:VAL:HG12	1:E:177:VAL:N	2.29	0.48
1:E:49:THR:CG2	1:E:51:TYR:CE2	2.97	0.48
1:E:192(B):PRO:CG	2:I:32:GLY:HA3	2.45	0.47
1:E:138:ARG:HG2	1:E:139:ARG:N	2.30	0.46
1:E:192(A):GLU:O	1:E:194:ASP:HB2	2.15	0.46
1:E:48:VAL:HG21	1:E:239:VAL:HG21	1.97	0.46
4:E:615:HOH:O	2:I:55:LYS:HD2	2.14	0.46
1:E:164:ALA:HB3	1:E:182:ARG:HB3	1.99	0.45
1:E:78:ASN:ND2	1:E:80:ALA:HB3	2.30	0.45
1:E:166:ASN:ND2	1:E:179:GLY:HA2	2.22	0.44
2:I:11:TYR:HB3	2:I:12:PRO:CA	2.38	0.43
1:E:102:ASP:O	1:E:229:GLN:HG2	2.18	0.42
1:E:228:PHE:CD1	1:E:228:PHE:N	2.87	0.42
1:E:16:ILE:N	4:E:550:HOH:O	2.53	0.42
1:E:100:ASN:OD1	4:E:528:HOH:O	2.22	0.41
1:E:57:HIS:HB3	1:E:94:PHE:CE2	2.56	0.41

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Atom-1	Atom-2	$egin{aligned} & ext{Interatomic} \ & ext{distance} \ & ext{($\mathring{\mathbf{A}}$)} \end{aligned}$	Clash overlap (Å)
1:E:117:GLY:HA3	1:E:242:TYR:C	2.40	0.41
1:E:110:ASN:C	1:E:110:ASN:ND2	2.74	0.40
1:E:110:ASN:ND2	1:E:112:THR:H	2.20	0.40

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	ntiles
1	E	183/185 (99%)	175 (96%)	8 (4%)	0	100	100
2	I	49/51 (96%)	47 (96%)	2 (4%)	0	100	100
All	All	232/236 (98%)	222 (96%)	10 (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	Percen	tiles
1	E	138/138 (100%)	130 (94%)	8 (6%)	20	7
2	I	45/45 (100%)	36 (80%)	9 (20%)	1	0
All	All	183/183 (100%)	166 (91%)	17 (9%)	9	2

All (17) residues with a non-rotameric sidechain are listed below:



Mol	Chain	Res	Type
1	Е	48(A)	ARG
1	Е	79	SER
1	Е	110	ASN
1	Е	168	THR
1	Е	222	SER
1	Е	233	GLU
1	Е	235(A)	SER
1	Е	241	VAL
2	I	6	VAL
2	I	7	ASP
2	I	10	GLU
2	I	13	LYS
2	I	21	ARG
2	I	34	LYS
2	I	45	ASN
2	I	47	THR
2	I	53	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	Е	110	ASN
1	Е	166	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)

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)

1 ligand is 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	l Type Chain Res Link		В	ond leng	gths	Bond angles				
Moi Type		Chain	nes Lilik		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	PO4	Е	500	-	4,4,4	1.96	3 (75%)	6,6,6	0.57	0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(\mathbf{\mathring{A}})$	$\operatorname{Ideal}(ext{\AA})$
3	Е	500	PO4	P-O4	-2.47	1.47	1.54
3	Е	500	PO4	P-O2	-2.04	1.48	1.54
3	Е	500	PO4	P-O3	-2.03	1.48	1.54

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 (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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

