



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 07:58 PM GMT

PDB ID : 1I5K
Title : STRUCTURE AND BINDING DETERMINANTS OF THE RECOMBINANT KRINGLE-2 DOMAIN OF HUMAN PLASMINOGEN TO AN INTERNAL PEPTIDE FROM A GROUP A STREPTOCOCCAL SURFACE PROTEIN
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Deposited on : 2001-02-27
Resolution : 2.70 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

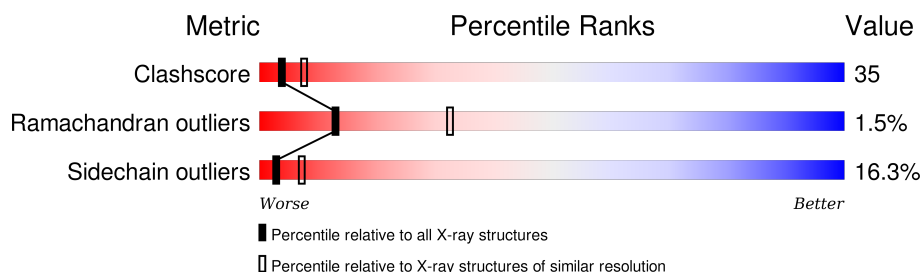
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)

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. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	84	
1	B	84	
2	C	30	
2	D	30	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 1870 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 PLASMINOGEN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	79	Total	C	N	O	S	0	0	0
			646	400	118	120	8			
1	B	80	Total	C	N	O	S	0	0	0
			651	403	119	121	8			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	PHE	-	CLONING ARTIFACT	UNP P00747
A	-2	SER	-	CLONING ARTIFACT	UNP P00747
A	-1	GLU	-	CLONING ARTIFACT	UNP P00747
A	4	GLY	CYS	ENGINEERED	UNP P00747
A	56	ASP	GLU	ENGINEERED	UNP P00747
A	72	TYR	LEU	ENGINEERED	UNP P00747
A	79	ALA	THR	CONFLICT	UNP P00747
A	80	ALA	THR	CONFLICT	UNP P00747
B	97	PHE	-	CLONING ARTIFACT	UNP P00747
B	98	SER	-	CLONING ARTIFACT	UNP P00747
B	99	GLU	-	CLONING ARTIFACT	UNP P00747
B	104	GLY	CYS	ENGINEERED	UNP P00747
B	156	ASP	GLU	ENGINEERED	UNP P00747
B	172	TYR	LEU	ENGINEERED	UNP P00747
B	179	ALA	THR	CONFLICT	UNP P00747
B	180	ALA	THR	CONFLICT	UNP P00747

- Molecule 2 is a protein called M PROTEIN.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	26	Total	C	N	O	0	0	0
			220	133	42	45			
2	D	26	Total	C	N	O	0	0	0
			220	133	42	45			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	330	TYR	ARG	CONFLICT	UNP P49054
D	430	TYR	ARG	CONFLICT	UNP P49054

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	50	Total	O	0	0
			50	50		
3	B	39	Total	O	0	0
			39	39		
3	C	18	Total	O	0	0
			18	18		
3	D	26	Total	O	0	0
			26	26		

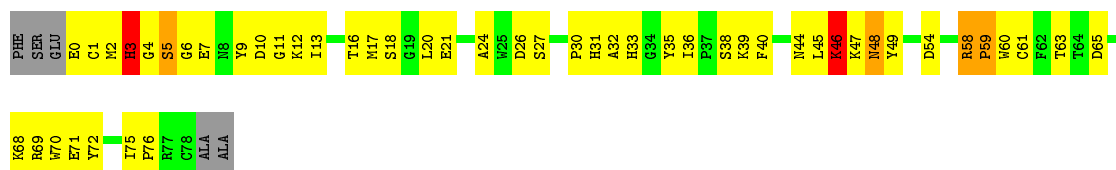
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

Note EDS was not executed.

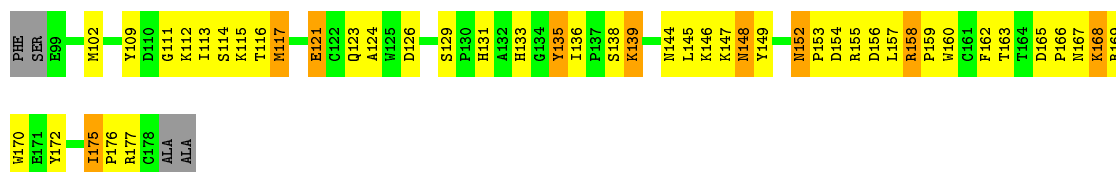
• Molecule 1: PLASMINOGEN

Chain A: 



• Molecule 1: PLASMINOGEN

Chain B: 



• Molecule 2: M PROTEIN

Chain C: 



• Molecule 2: M PROTEIN

Chain D: 



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	91.98 Å 91.98 Å 151.78 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	8.00 – 2.70	Depositor
% Data completeness (in resolution range)	87.2 (8.00-2.70)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.195 , 0.262	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1870	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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	1.16	3/667 (0.4%)	1.15	0/901
1	B	1.07	1/672 (0.1%)	1.11	4/908 (0.4%)
2	C	1.16	0/220	1.11	2/291 (0.7%)
2	D	1.27	1/220 (0.5%)	1.08	0/291
All	All	1.14	5/1779 (0.3%)	1.12	6/2391 (0.3%)

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	1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	424	GLU	CG-CD	6.05	1.61	1.51
1	A	46	LYS	CD-CE	5.41	1.64	1.51
1	A	7	GLU	CB-CG	5.38	1.62	1.52
1	B	135	TYR	CE1-CZ	5.25	1.45	1.38
1	A	7	GLU	CG-CD	5.06	1.59	1.51

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	155	ARG	NE-CZ-NH1	-6.41	117.10	120.30
2	C	317	ARG	NE-CZ-NH2	5.66	123.13	120.30
1	B	123	GLN	N-CA-C	-5.59	95.90	111.00
2	C	310	LEU	CA-CB-CG	-5.54	102.56	115.30
1	B	177	ARG	N-CA-C	-5.48	96.21	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	3	HIS	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	646	0	596	59	0
1	B	651	0	595	46	0
2	C	220	0	221	10	0
2	D	220	0	221	19	0
3	A	50	0	0	1	0
3	B	39	0	0	0	0
3	C	18	0	0	0	1
3	D	26	0	0	1	0
All	All	1870	0	1633	118	1

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 35.

The worst 5 of 118 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)
1:A:36:ILE:HG23	2:D:402:GLU:OE1	1.42	1.18
1:A:63:THR:HG22	1:A:65:ASP:H	1.16	1.10
2:D:426:LEU:O	2:D:427:LYS:HB2	1.62	0.96
1:A:63:THR:HG22	1:A:65:ASP:N	1.80	0.96
1:B:157:LEU:O	1:B:158:ARG:HD3	1.64	0.96

All (1) 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	Interatomic distance (Å)	Clash overlap (Å)
3:C:554:HOH:O	3:C:554:HOH:O[12_555]	1.81	0.39

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	77/84 (92%)	70 (91%)	5 (6%)	2 (3%)	7	16
1	B	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
2	C	24/30 (80%)	22 (92%)	2 (8%)	0	100	100
2	D	24/30 (80%)	21 (88%)	2 (8%)	1 (4%)	3	7
All	All	203/228 (89%)	187 (92%)	13 (6%)	3 (2%)	13	32

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	47	LYS
2	D	424	GLU
1	A	3	HIS

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	72/75 (96%)	61 (85%)	11 (15%)	3	8
1	B	72/75 (96%)	57 (79%)	15 (21%)	1	4
2	C	23/27 (85%)	19 (83%)	4 (17%)	2	6
2	D	23/27 (85%)	22 (96%)	1 (4%)	35	66
All	All	190/204 (93%)	159 (84%)	31 (16%)	3	7

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	129	SER
1	B	145	LEU
2	C	309	GLU
1	B	138	SER
1	B	148	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	108	ASN
2	D	411	GLN
1	B	148	ASN
1	A	48	ASN
1	B	133	HIS

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 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 ⓘ

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.