



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 06:33 AM UTC

PDB ID : 2HPC / pdb\_00002hpc  
Title : Crystal structure of fragment D from Human Fibrinogen Complexed with Gl  
y-Pro-Arg-Pro-amide.  
Authors : Doolittle, R.F.; Kollman, J.M.; Chen, A.; Pandi, L.  
Deposited on : 2006-07-17  
Resolution : 2.90 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](mailto: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 : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

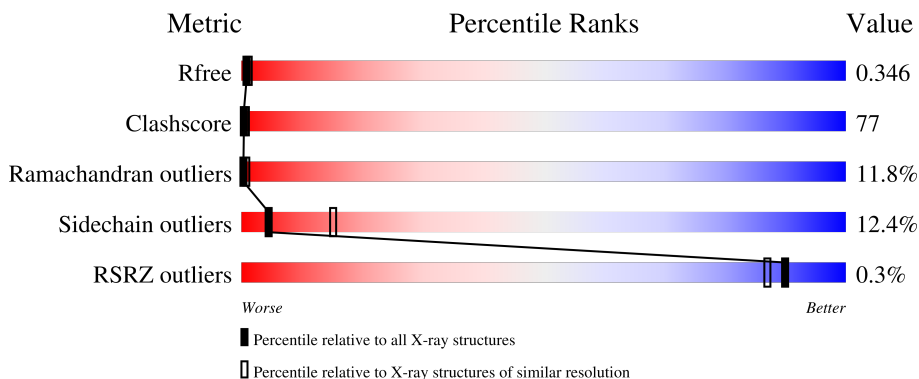
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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))
$R_{free}$	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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  $\geq 3$ , 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	87	
1	D	87	
1	G	87	
1	J	87	
2	B	328	

*Continued on next page...*

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	E	328	
2	H	328	
2	K	328	
3	C	323	
3	F	323	
3	I	323	
3	L	323	
4	M	5	
4	N	5	
4	O	5	
4	P	5	
4	Q	5	
4	R	5	
4	S	5	
4	T	5	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	NAG	B	470	X	-	-	-
5	NAG	E	470	X	-	-	-

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 22270 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 Fibrinogen alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	74	Total 608	C 377	N 115	O 113	S 3	0	0	0
1	D	71	Total 584	C 361	N 112	O 108	S 3	0	0	0
1	G	74	Total 608	C 377	N 115	O 113	S 3	0	0	0
1	J	79	Total 652	C 402	N 126	O 121	S 3	0	0	0

- Molecule 2 is a protein called Fibrinogen beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	307	Total 2462	C 1535	N 433	O 472	S 22	0	0	0
2	E	304	Total 2434	C 1514	N 430	O 468	S 22	0	0	0
2	H	307	Total 2462	C 1535	N 433	O 472	S 22	0	0	0
2	K	305	Total 2442	C 1520	N 431	O 469	S 22	0	0	0

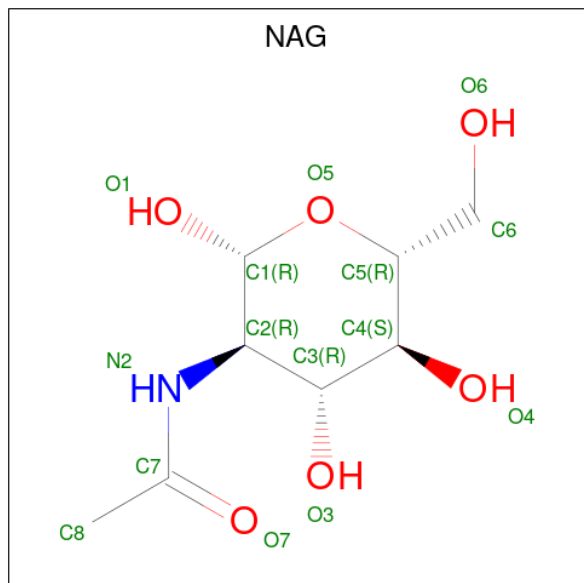
- Molecule 3 is a protein called Fibrinogen, gamma polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	305	Total 2446	C 1552	N 410	O 472	S 12	0	0	0
3	F	300	Total 2410	C 1529	N 405	O 464	S 12	0	0	0
3	I	305	Total 2446	C 1552	N 410	O 472	S 12	0	0	0
3	L	300	Total 2410	C 1529	N 405	O 464	S 12	0	0	0

- Molecule 4 is a protein called Gly-Pro-Arg-Pro-amide peptide ligand.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	M	5	Total	C	N	O	0	0	1
			30	18	8	4			
4	N	5	Total	C	N	O	0	0	1
			30	18	8	4			
4	O	5	Total	C	N	O	0	0	1
			30	18	8	4			
4	P	5	Total	C	N	O	0	0	1
			30	18	8	4			
4	Q	5	Total	C	N	O	0	0	1
			30	18	8	4			
4	R	5	Total	C	N	O	0	0	1
			30	18	8	4			
4	S	5	Total	C	N	O	0	0	1
			30	18	8	4			
4	T	5	Total	C	N	O	0	0	1
			30	18	8	4			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	N	O	0	0
			14	8	1	5		
5	E	1	Total	C	N	O	0	0
			14	8	1	5		

Continued on next page...

*Continued from previous page...*

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	H	1	Total	C	N	O	0	0
			14	8	1	5		
5	K	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 6 is CALCIUM ION (CCD ID: CA) (formula: Ca).

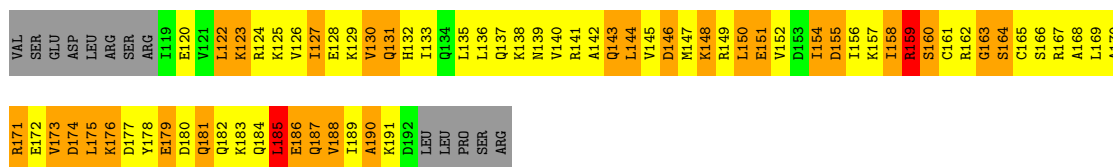
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	Ca	0	0
			1	1		
6	C	1	Total	Ca	0	0
			1	1		
6	E	2	Total	Ca	0	0
			2	2		
6	F	1	Total	Ca	0	0
			1	1		
6	H	1	Total	Ca	0	0
			1	1		
6	I	1	Total	Ca	0	0
			1	1		
6	K	2	Total	Ca	0	0
			2	2		
6	L	1	Total	Ca	0	0
			1	1		

### 3 Residue-property plots


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.

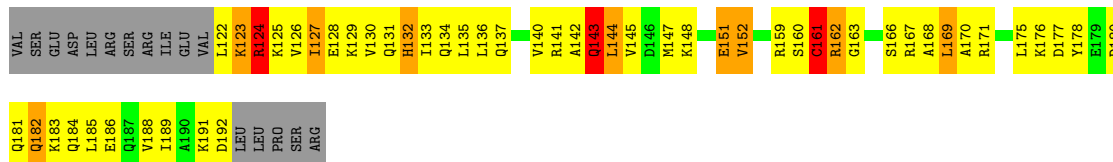
- Molecule 1: Fibrinogen alpha chain

Chain A: 



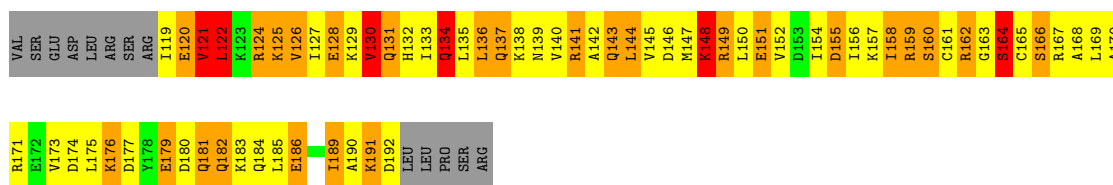
- Molecule 1: Fibrinogen alpha chain

Chain D: 



- Molecule 1: Fibrinogen alpha chain

Chain G: 

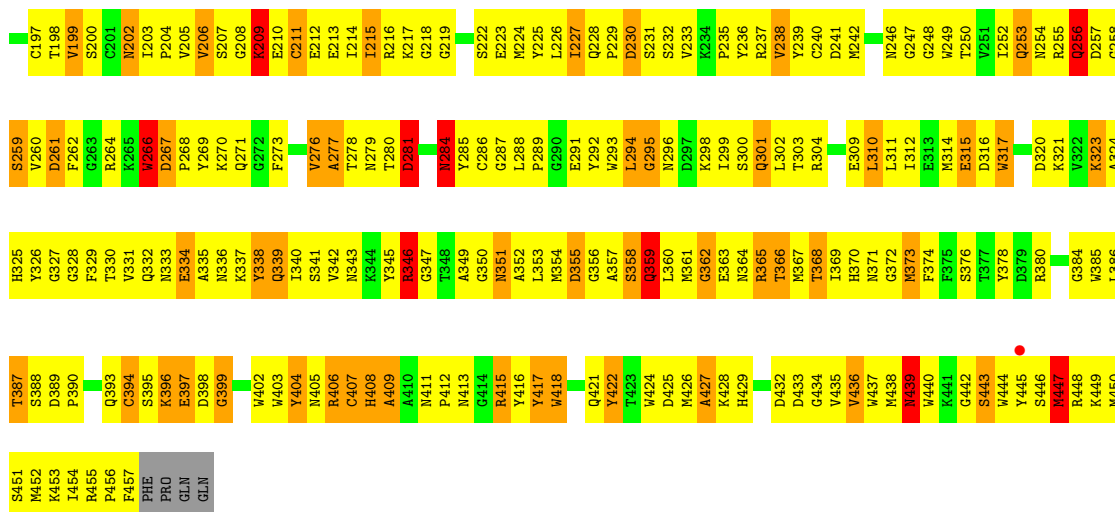


- Molecule 1: Fibrinogen alpha chain

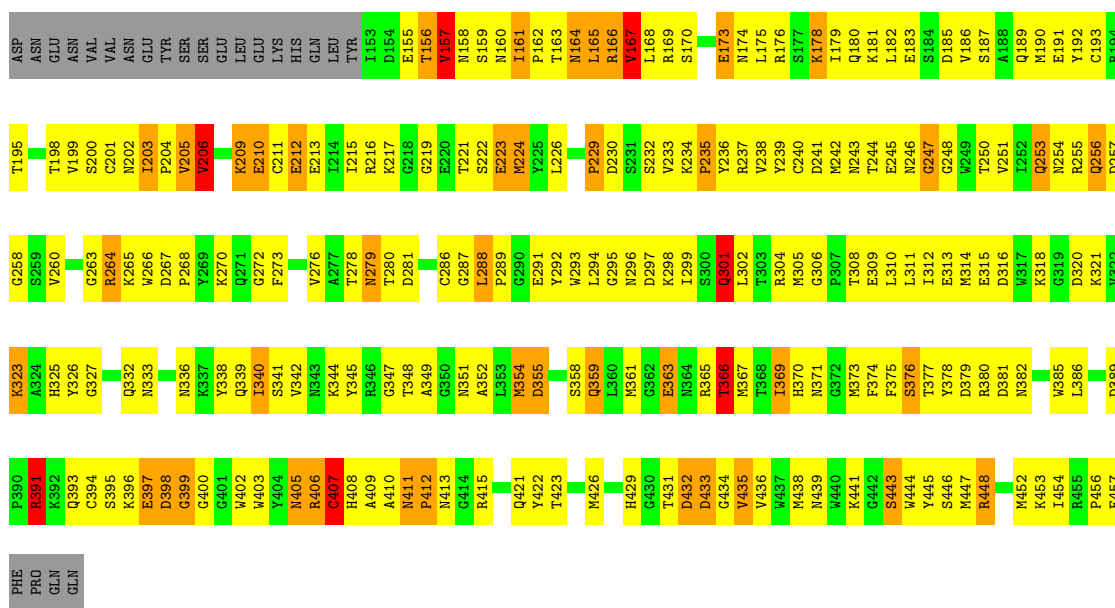
Chain J: 



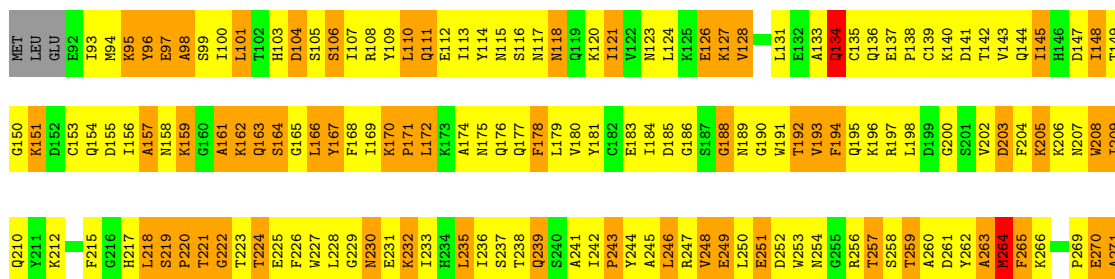
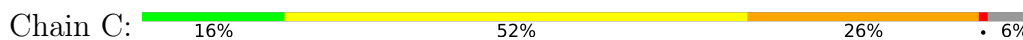


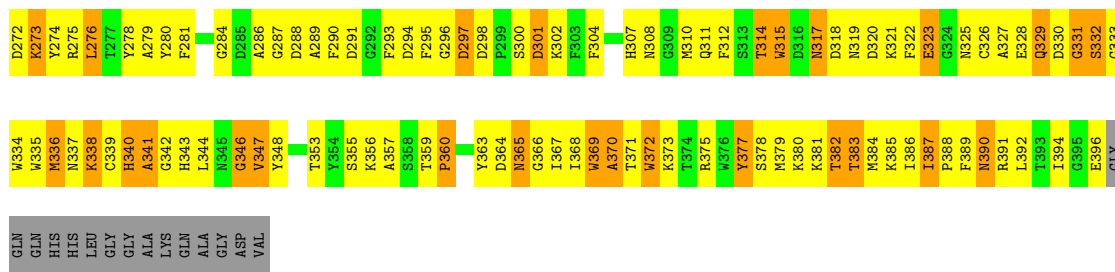


• Molecule 2: Fibrinogen beta chain

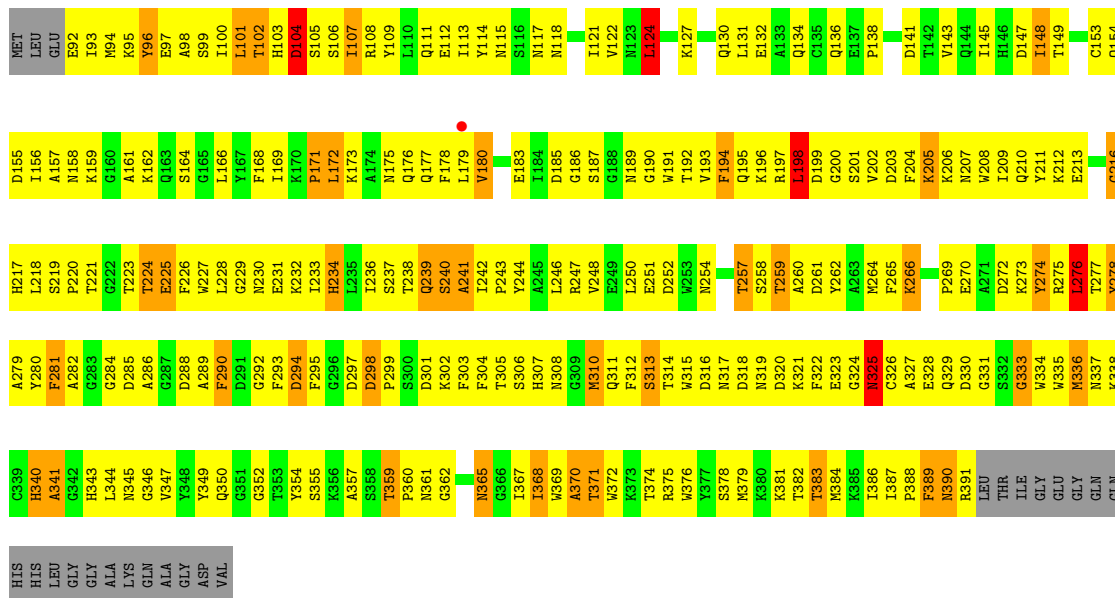
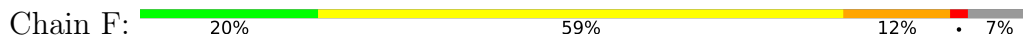


• Molecule 3: Fibrinogen, gamma polypeptide

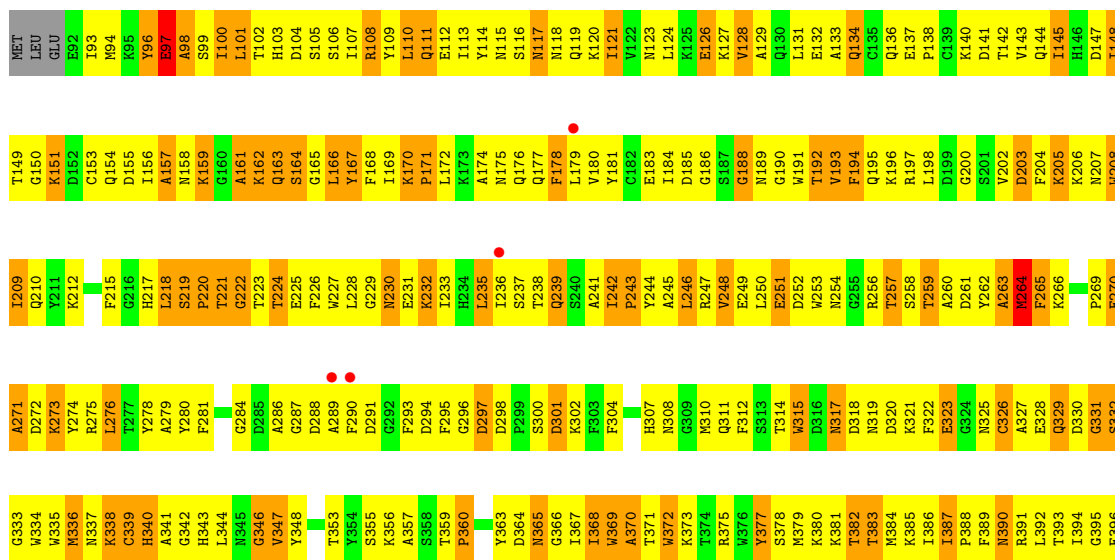
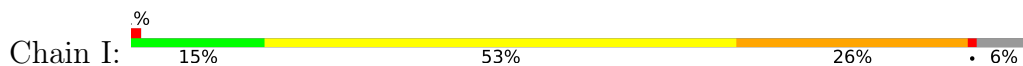




• Molecule 3: Fibrinogen, gamma polypeptide



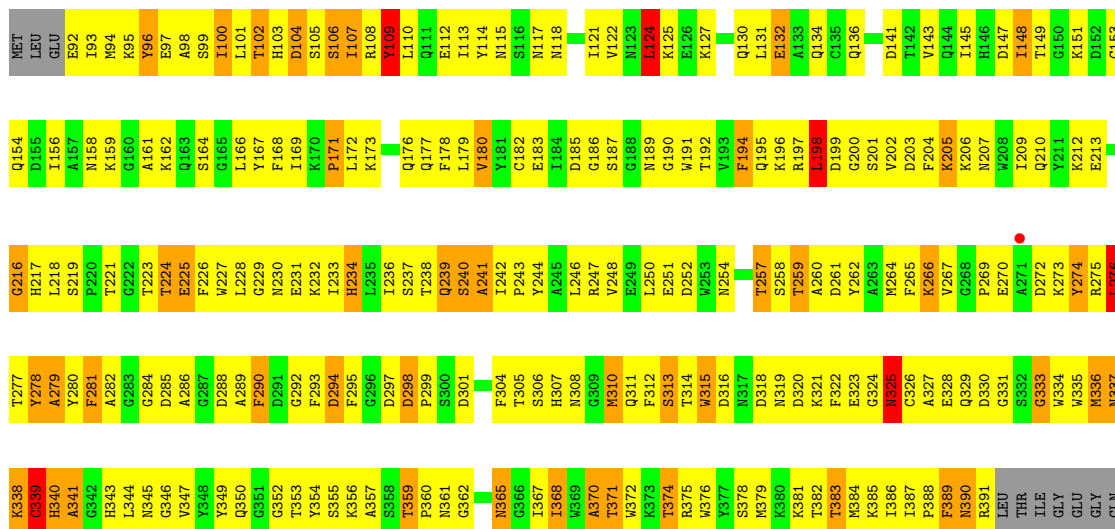
• Molecule 3: Fibrinogen, gamma polypeptide



GLY  
GLN  
GLN  
GLN  
HIS  
HIS  
LEU  
LEU  
GLY  
GLY  
ALA  
ALA  
GLN  
GLN  
ALA  
GLY  
ASP  
VAL

- Molecule 3: Fibrinogen, gamma polypeptide

Chain L: 21% 56% 15% 7%



GLN  
HIS  
HIS  
LEU  
LEU  
GLY  
GLY  
ALA  
LYS  
GLN  
GLY  
ASP  
VAL

- Molecule 4: Gly-Pro-Arg-Pro-amide peptide ligand

Chain M: 80% 20%

G1  
P2  
R3  
P4  
NH25

- Molecule 4: Gly-Pro-Arg-Pro-amide peptide ligand

Chain N: 100%

G1  
P2  
R3  
P4  
NH25

- Molecule 4: Gly-Pro-Arg-Pro-amide peptide ligand

Chain O: 60% 40%

G1  
P2  
R3  
P4  
NH25

- Molecule 4: Gly-Pro-Arg-Pro-amide peptide ligand

Chain P: 40% 40% 20%



- Molecule 4: Gly-Pro-Arg-Pro-amide peptide ligand



- Molecule 4: Gly-Pro-Arg-Pro-amide peptide ligand



- Molecule 4: Gly-Pro-Arg-Pro-amide peptide ligand



- Molecule 4: Gly-Pro-Arg-Pro-amide peptide ligand



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	81.68Å 46.07Å 429.90Å 90.00° 89.99° 90.00°	Depositor
Resolution (Å)	30.00 – 2.90 30.00 – 2.90	Depositor EDS
% Data completeness (in resolution range)	97.9 (30.00-2.90) 99.0 (30.00-2.90)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.12 (at 2.54Å)	Xtrriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.275 , 0.360 0.265 , 0.346	Depositor DCC
$R_{free}$ test set	3644 reflections (4.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	71.1	Xtrriage
Anisotropy	0.182	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.26 , 95.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.467 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	22270	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	70.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.44% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: NH2, NAG, CA

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	0.48	0/609	1.29	13/811 (1.6%)
1	D	0.59	0/585	1.16	5/778 (0.6%)
1	G	0.47	0/609	1.26	12/811 (1.5%)
1	J	0.56	0/653	1.16	7/869 (0.8%)
2	B	0.49	0/2523	1.18	32/3409 (0.9%)
2	E	0.64	1/2494 (0.0%)	1.15	18/3369 (0.5%)
2	H	0.49	0/2523	1.18	30/3409 (0.9%)
2	K	0.65	0/2502	1.16	25/3380 (0.7%)
3	C	0.44	0/2512	1.04	23/3396 (0.7%)
3	F	0.52	0/2476	1.09	28/3347 (0.8%)
3	I	0.44	0/2512	1.06	20/3396 (0.6%)
3	L	0.52	0/2476	1.10	27/3347 (0.8%)
4	M	0.57	0/30	0.94	0/40
4	N	0.74	0/30	0.90	0/40
4	O	0.60	0/30	0.88	0/40
4	P	0.62	0/30	1.11	0/40
4	Q	0.68	0/30	1.36	0/40
4	R	0.66	0/30	0.89	0/40
4	S	0.58	0/30	0.90	0/40
4	T	0.62	0/30	1.12	0/40
All	All	0.53	1/22714 (0.0%)	1.13	240/30642 (0.8%)

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	H	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	373	MET	SD-CE	5.44	1.93	1.79

The worst 5 of 240 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	101	LEU	N-CA-C	-12.58	98.03	113.50
3	L	102	THR	N-CA-C	-12.54	97.69	111.36
1	J	135	LEU	N-CA-C	-12.17	99.10	114.56
2	B	347	GLY	N-CA-C	10.83	122.24	111.95
2	E	409	ALA	N-CA-C	-10.55	101.17	114.56

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	H	378	TYR	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	608	0	649	151	0
1	D	584	0	623	84	0
1	G	608	0	649	126	0
1	J	652	0	695	101	0
2	B	2462	0	2327	531	0
2	E	2434	0	2295	259	0
2	H	2462	0	2326	461	0
2	K	2442	0	2307	254	0
3	C	2446	0	2294	489	0
3	F	2410	0	2256	311	0
3	I	2446	0	2294	474	0
3	L	2410	0	2256	328	0
4	M	30	0	32	2	0
4	N	30	0	32	7	0
4	O	30	0	32	4	0
4	P	30	0	32	4	0
4	Q	30	0	32	2	0

*Continued on next page...*

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	R	30	0	32	8	0
4	S	30	0	32	8	0
4	T	30	0	32	3	0
5	B	14	0	13	1	0
5	E	14	0	13	0	0
5	H	14	0	13	4	0
5	K	14	0	13	3	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
6	E	2	0	0	0	0
6	F	1	0	0	0	0
6	H	1	0	0	0	0
6	I	1	0	0	0	0
6	K	2	0	0	0	0
6	L	1	0	0	0	0
All	All	22270	0	21279	3347	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 77.

The worst 5 of 3347 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)
2:B:165:LEU:H	2:B:166:ARG:NH2	1.45	1.15
3:C:197:ARG:HA	3:C:225:GLU:HG2	1.27	1.14
1:G:147:MET:HE2	2:H:179:ILE:HG12	1.28	1.12
3:I:197:ARG:HA	3:I:225:GLU:HG2	1.30	1.12
3:I:171:PRO:HB2	3:I:174:ALA:HB2	1.33	1.06

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	72/87 (83%)	44 (61%)	15 (21%)	13 (18%)	0	0
1	D	69/87 (79%)	50 (72%)	15 (22%)	4 (6%)	1	4
1	G	72/87 (83%)	44 (61%)	14 (19%)	14 (19%)	0	0
1	J	77/87 (88%)	55 (71%)	18 (23%)	4 (5%)	1	5
2	B	305/328 (93%)	186 (61%)	76 (25%)	43 (14%)	0	0
2	E	302/328 (92%)	235 (78%)	41 (14%)	26 (9%)	0	1
2	H	305/328 (93%)	196 (64%)	64 (21%)	45 (15%)	0	0
2	K	303/328 (92%)	236 (78%)	47 (16%)	20 (7%)	1	3
3	C	303/323 (94%)	167 (55%)	86 (28%)	50 (16%)	0	0
3	F	298/323 (92%)	207 (70%)	69 (23%)	22 (7%)	1	2
3	I	303/323 (94%)	170 (56%)	81 (27%)	52 (17%)	0	0
3	L	298/323 (92%)	207 (70%)	68 (23%)	23 (8%)	1	2
4	M	3/5 (60%)	1 (33%)	2 (67%)	0	100	100
4	N	3/5 (60%)	0	2 (67%)	1 (33%)	0	0
4	O	3/5 (60%)	2 (67%)	1 (33%)	0	100	100
4	P	3/5 (60%)	1 (33%)	1 (33%)	1 (33%)	0	0
4	Q	3/5 (60%)	1 (33%)	1 (33%)	1 (33%)	0	0
4	R	3/5 (60%)	0	2 (67%)	1 (33%)	0	0
4	S	3/5 (60%)	3 (100%)	0	0	100	100
4	T	3/5 (60%)	1 (33%)	1 (33%)	1 (33%)	0	0
All	All	2731/2992 (91%)	1806 (66%)	604 (22%)	321 (12%)	0	1

5 of 321 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	166	SER
1	A	190	ALA
2	B	227	ILE
2	B	230	ASP
2	B	259	SER

### 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	69/82 (84%)	57 (83%)	12 (17%)	2	7
1	D	66/82 (80%)	57 (86%)	9 (14%)	3	12
1	G	69/82 (84%)	54 (78%)	15 (22%)	1	3
1	J	74/82 (90%)	60 (81%)	14 (19%)	1	5
2	B	265/286 (93%)	234 (88%)	31 (12%)	5	17
2	E	262/286 (92%)	229 (87%)	33 (13%)	4	14
2	H	265/286 (93%)	236 (89%)	29 (11%)	6	20
2	K	263/286 (92%)	233 (89%)	30 (11%)	5	18
3	C	257/269 (96%)	229 (89%)	28 (11%)	6	20
3	F	253/269 (94%)	221 (87%)	32 (13%)	4	14
3	I	257/269 (96%)	229 (89%)	28 (11%)	6	20
3	L	253/269 (94%)	219 (87%)	34 (13%)	4	12
4	M	3/3 (100%)	3 (100%)	0	100	100
4	N	3/3 (100%)	3 (100%)	0	100	100
4	O	3/3 (100%)	3 (100%)	0	100	100
4	P	3/3 (100%)	3 (100%)	0	100	100
4	Q	3/3 (100%)	3 (100%)	0	100	100
4	R	3/3 (100%)	3 (100%)	0	100	100
4	S	3/3 (100%)	3 (100%)	0	100	100
4	T	3/3 (100%)	3 (100%)	0	100	100
All	All	2377/2572 (92%)	2082 (88%)	295 (12%)	4	15

5 of 295 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	K	157	VAL
3	L	276	LEU
2	K	209	LYS
2	K	433	ASP
2	E	279	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 143 such sidechains are listed below:

Mol	Chain	Res	Type
2	K	189	GLN
2	K	301	GLN
3	L	158	ASN
2	E	351	ASN
2	E	339	GLN

### 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 oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 10 are monoatomic - leaving 4 for Mogul analysis.

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	$\# Z  > 2$
5	NAG	B	470	2	14,14,15	0.82	0	17,19,21	0.81	1 (5%)
5	NAG	K	470	2	14,14,15	0.51	0	17,19,21	0.97	1 (5%)
5	NAG	H	470	2	14,14,15	0.72	0	17,19,21	0.99	1 (5%)
5	NAG	E	470	2	14,14,15	0.63	0	17,19,21	0.90	1 (5%)

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
5	NAG	B	470	2	1/1/5/7	3/6/23/26	0/1/1/1
5	NAG	K	470	2	-	4/6/23/26	0/1/1/1
5	NAG	H	470	2	-	5/6/23/26	0/1/1/1
5	NAG	E	470	2	1/1/5/7	3/6/23/26	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	H	470	NAG	C2-N2-C7	-2.66	119.34	122.90
5	B	470	NAG	C2-N2-C7	-2.24	119.89	122.90
5	K	470	NAG	C2-N2-C7	-2.16	120.00	122.90
5	E	470	NAG	C2-N2-C7	-2.10	120.08	122.90

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	B	470	NAG	C1
5	E	470	NAG	C1

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	E	470	NAG	C8-C7-N2-C2
5	E	470	NAG	O7-C7-N2-C2
5	H	470	NAG	C1-C2-N2-C7
5	H	470	NAG	C8-C7-N2-C2
5	H	470	NAG	O7-C7-N2-C2

There are no ring outliers.

3 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	470	NAG	1	0
5	K	470	NAG	3	0
5	H	470	NAG	4	0

## 5.7 Other polymers [i](#)

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 [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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	74/87 (85%)	-1.03	0 100 100	62, 83, 105, 111	0
1	D	71/87 (81%)	-1.07	0 100 100	29, 56, 89, 96	0
1	G	74/87 (85%)	-1.01	0 100 100	62, 81, 100, 115	0
1	J	79/87 (90%)	-1.06	0 100 100	35, 58, 108, 122	0
2	B	307/328 (93%)	-0.93	0 100 100	42, 76, 99, 108	0
2	E	304/328 (92%)	-1.07	0 100 100	27, 51, 79, 99	0
2	H	307/328 (93%)	-0.95	1 (0%) 90 87	42, 76, 99, 107	0
2	K	305/328 (92%)	-1.01	0 100 100	25, 51, 80, 97	0
3	C	305/323 (94%)	-0.87	0 100 100	49, 83, 107, 116	0
3	F	300/323 (92%)	-1.02	1 (0%) 90 87	39, 66, 92, 116	0
3	I	305/323 (94%)	-0.86	4 (1%) 75 67	54, 84, 109, 136	0
3	L	300/323 (92%)	-0.99	1 (0%) 90 87	36, 66, 91, 117	0
4	M	4/5 (80%)	-0.68	0 100 100	63, 64, 65, 97	0
4	N	4/5 (80%)	-0.85	0 100 100	41, 48, 60, 86	0
4	O	4/5 (80%)	-0.83	0 100 100	90, 94, 99, 106	0
4	P	4/5 (80%)	-0.84	0 100 100	64, 73, 79, 93	0
4	Q	4/5 (80%)	-1.16	0 100 100	63, 64, 64, 94	0
4	R	4/5 (80%)	-1.06	0 100 100	44, 50, 62, 87	0
4	S	4/5 (80%)	-0.68	0 100 100	89, 100, 101, 104	0
4	T	4/5 (80%)	-0.54	0 100 100	66, 73, 74, 91	0
All	All	2763/2992 (92%)	-0.97	7 (0%) 90 87	25, 71, 100, 136	0

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	I	289	ALA	3.3
3	I	290	PHE	2.7
3	I	179	LEU	2.6
3	L	271	ALA	2.6
2	H	445	TYR	2.5

## 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 oligosaccharides 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
5	NAG	K	470	14/15	0.96	0.06	65,75,82,89	0
5	NAG	H	470	14/15	0.97	0.09	94,105,117,117	0
5	NAG	B	470	14/15	0.97	0.06	60,83,88,91	0
5	NAG	E	470	14/15	0.98	0.06	68,77,92,92	0
6	CA	B	2	1/1	0.98	0.05	90,90,90,90	0
6	CA	K	3	1/1	0.98	0.03	89,89,89,89	0
6	CA	H	2	1/1	0.99	0.03	83,83,83,83	0
6	CA	I	1	1/1	0.99	0.03	76,76,76,76	0
6	CA	K	2	1/1	0.99	0.03	60,60,60,60	0
6	CA	C	1	1/1	0.99	0.02	78,78,78,78	0
6	CA	L	1	1/1	0.99	0.02	58,58,58,58	0
6	CA	F	1	1/1	1.00	0.03	54,54,54,54	0
6	CA	E	2	1/1	1.00	0.02	57,57,57,57	0
6	CA	E	3	1/1	1.00	0.02	90,90,90,90	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.