



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 02:36 AM GMT

PDB ID : 2HPC
Title : Crystal structure of fragment D from Human Fibrinogen Complexed with Gly-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
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) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

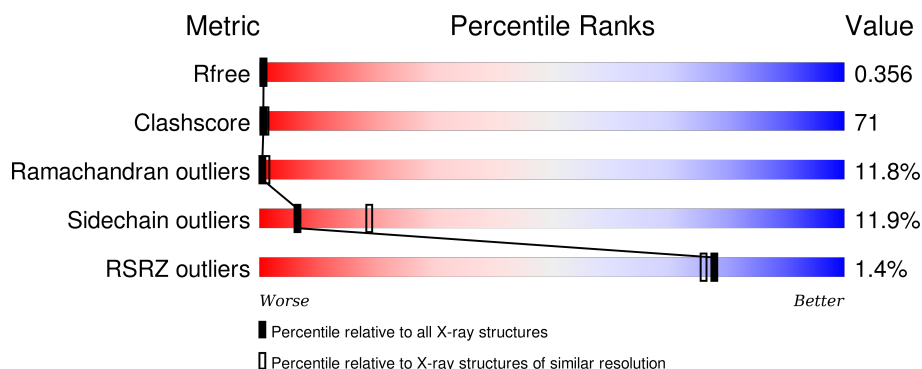
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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}	91344	1451 (2.90-2.90)
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)
RSRZ outliers	91569	1456 (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 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.

Mol	Chain	Length	Quality of chain
1	A	87	<div> <div>2%</div> <div>8% 56% 20% 15%</div> </div>
1	D	87	<div> <div>23% 47% 10% 18%</div> </div>
1	G	87	<div> <div>2%</div> <div>10% 51% 22% 15%</div> </div>
1	J	87	<div> <div>23% 54% 14% 9%</div> </div>
2	B	328	<div> <div>17% 61% 12% 6%</div> </div>

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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
7	CA	I	1	-	-	-	X

2 Entry composition

There are 7 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
1	A	74	Total	C	N	O	S	0	0	0
			608	377	115	113	3			
1	D	71	Total	C	N	O	S	0	0	0
			584	361	112	108	3			
1	G	74	Total	C	N	O	S	0	0	0
			608	377	115	113	3			
1	J	79	Total	C	N	O	S	0	0	0
			652	402	126	121	3			

- Molecule 2 is a protein called Fibrinogen beta chain.

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

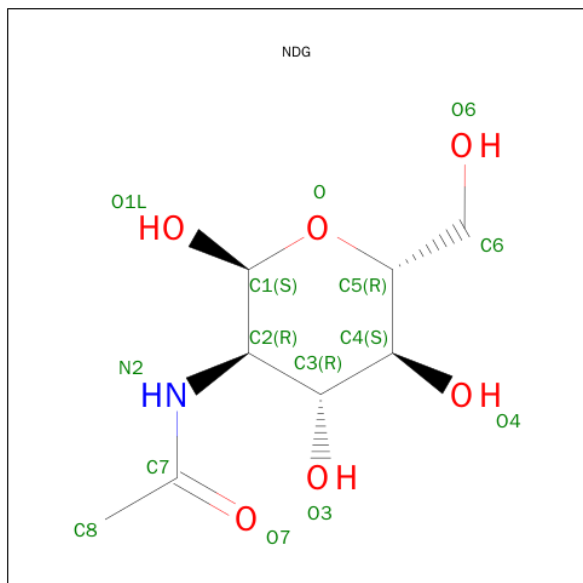
- Molecule 3 is a protein called Fibrinogen, gamma polypeptide.

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

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

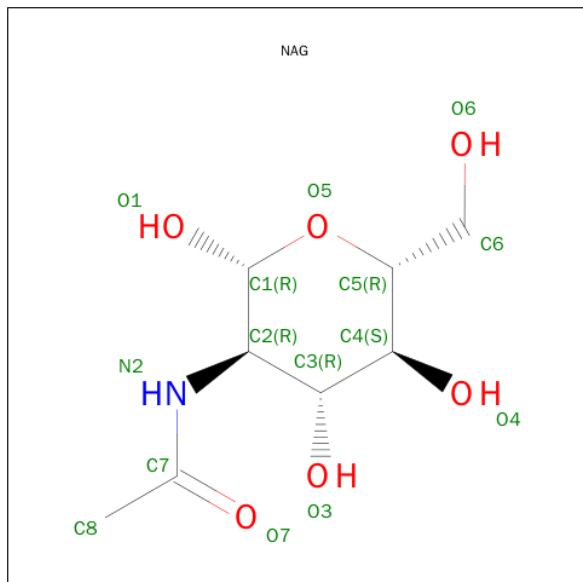
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	M	5	Total	C	N	O	0	0	1
			30	18	8	4			
4	N	5	Total	C	N	O	0	0	1
			30	18	8	4			
4	O	5	Total	C	N	O	0	0	1
			30	18	8	4			
4	P	5	Total	C	N	O	0	0	1
			30	18	8	4			
4	Q	5	Total	C	N	O	0	0	1
			30	18	8	4			
4	R	5	Total	C	N	O	0	0	1
			30	18	8	4			
4	S	5	Total	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 SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NDG) (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		

- Molecule 6 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

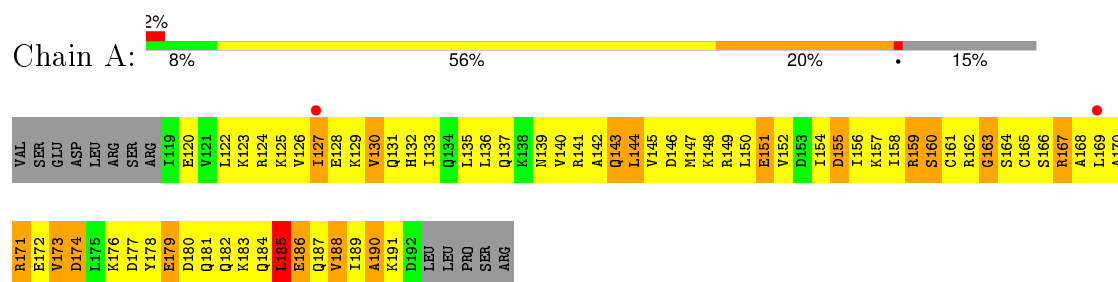
- Molecule 7 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

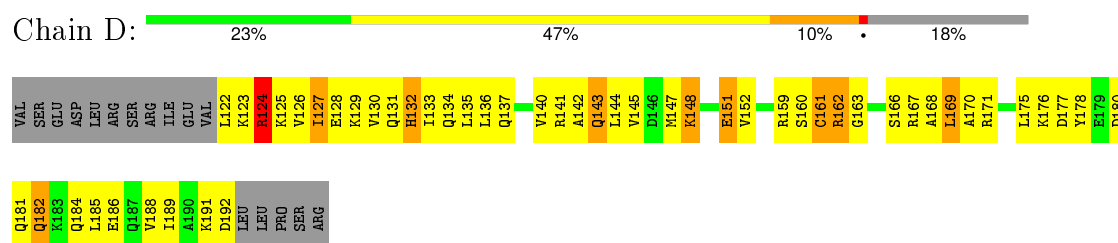
3 Residue-property plots

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.

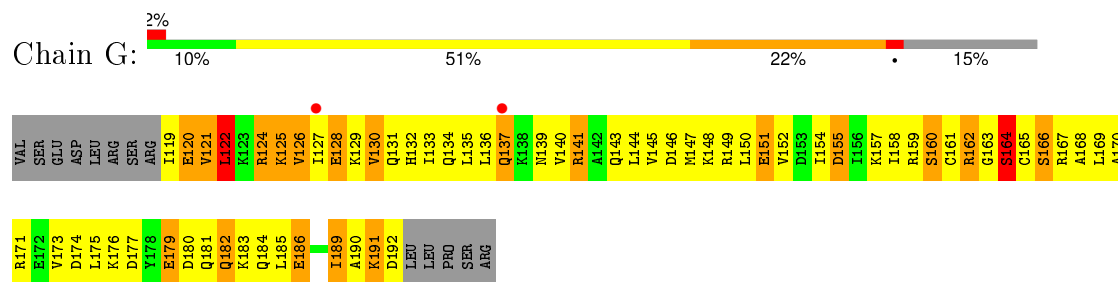
- Molecule 1: Fibrinogen alpha chain



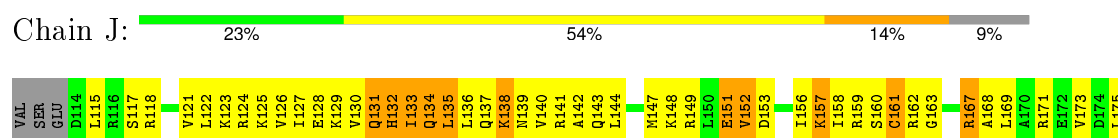
- Molecule 1: Fibrinogen alpha chain

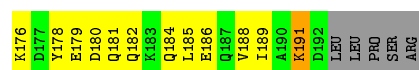


- Molecule 1: Fibrinogen alpha chain

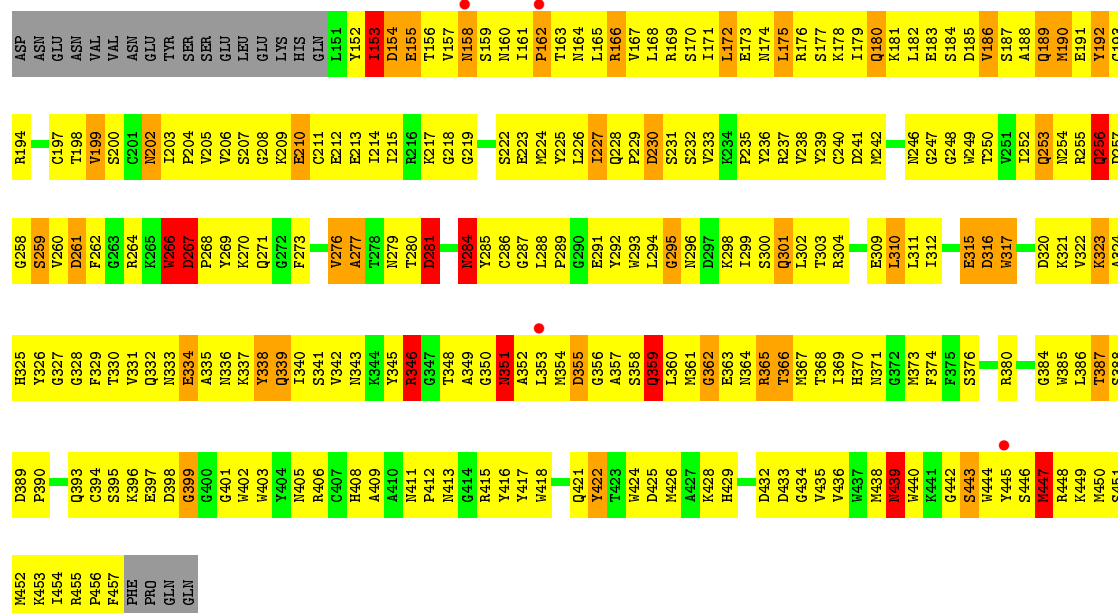


- Molecule 1: Fibrinogen alpha chain

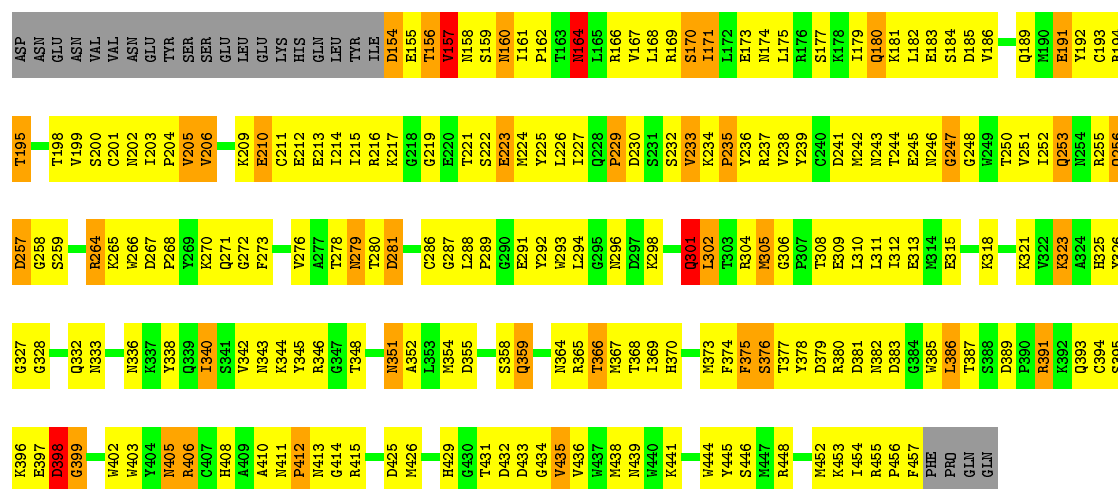




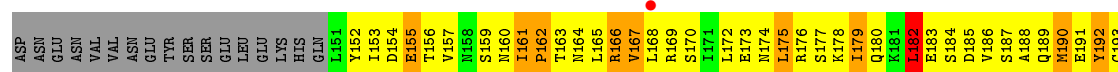
• Molecule 2: Fibrinogen beta chain

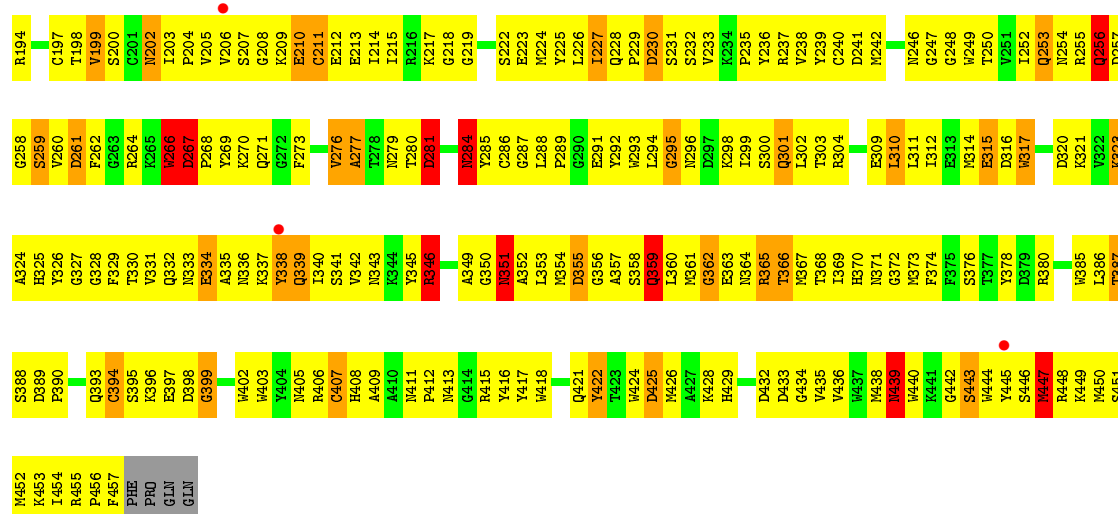


• Molecule 2: Fibrinogen beta chain

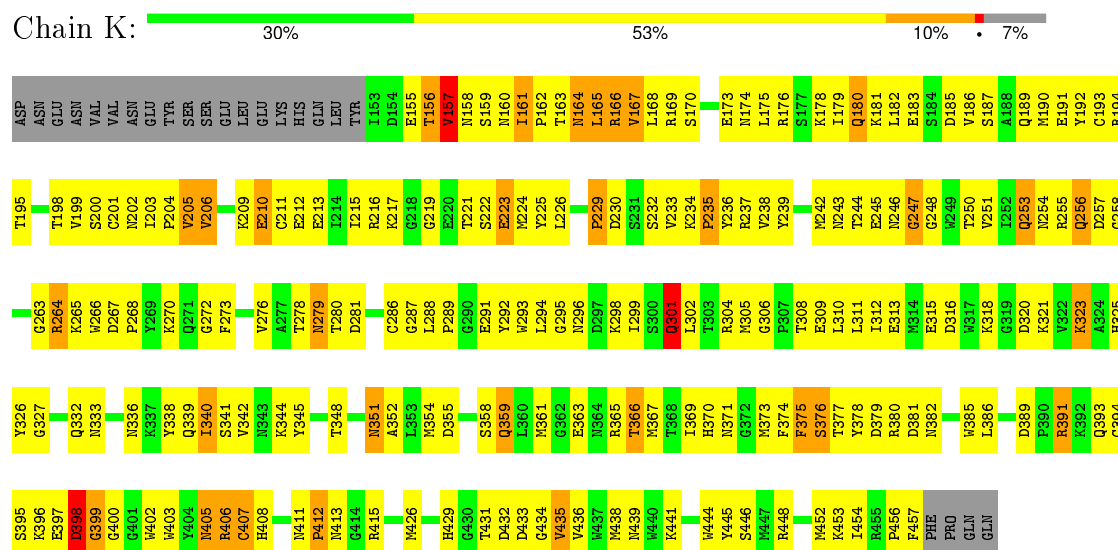


• Molecule 2: Fibrinogen beta chain

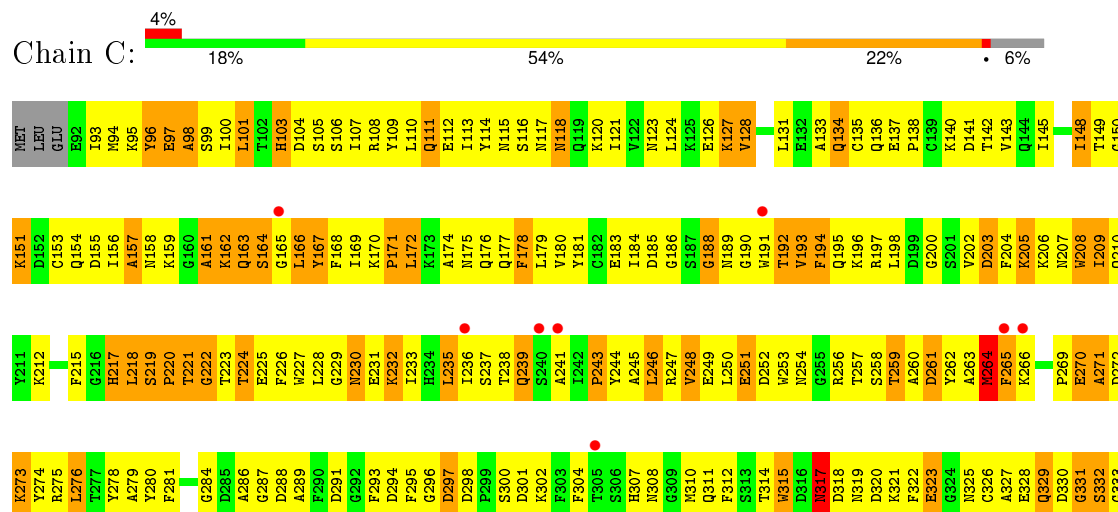


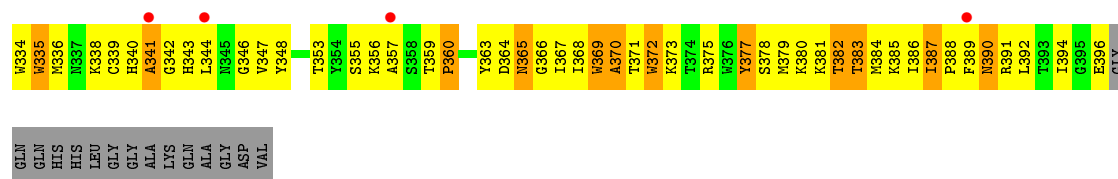


• Molecule 2: Fibrinogen beta chain



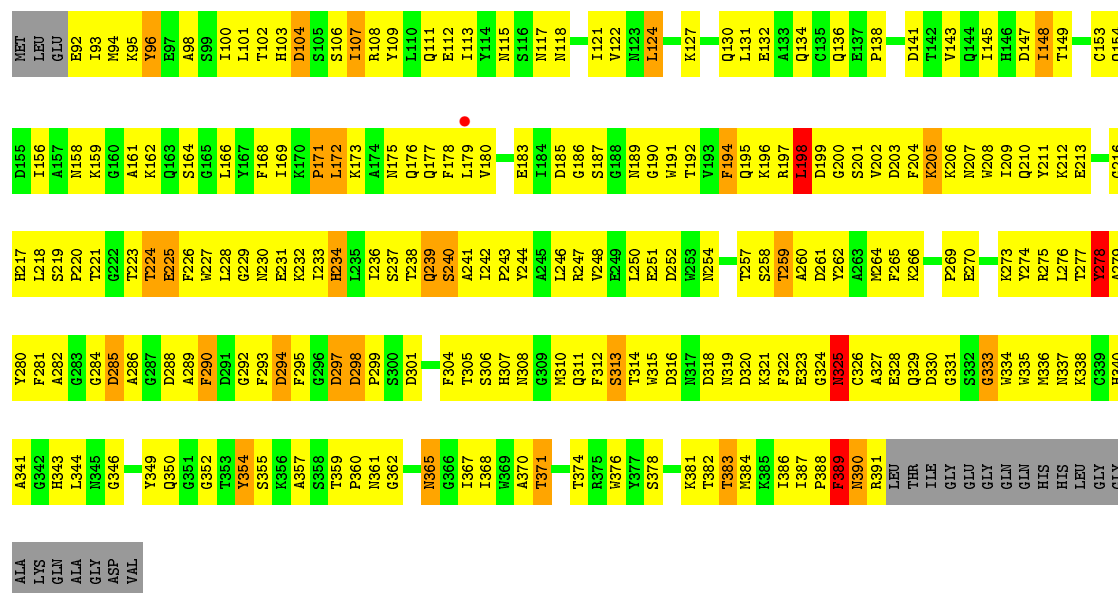
• Molecule 3: Fibrinogen, gamma polypeptide





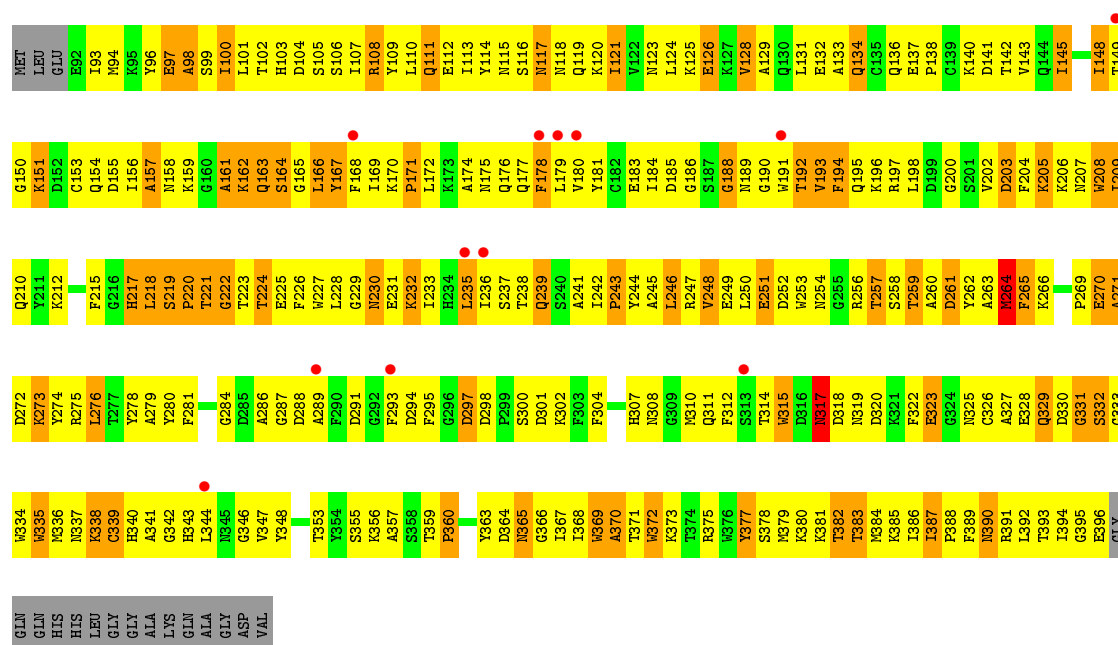
• Molecule 3: Fibrinogen, gamma polypeptide

Chain F: 25% 58% 8% 7%

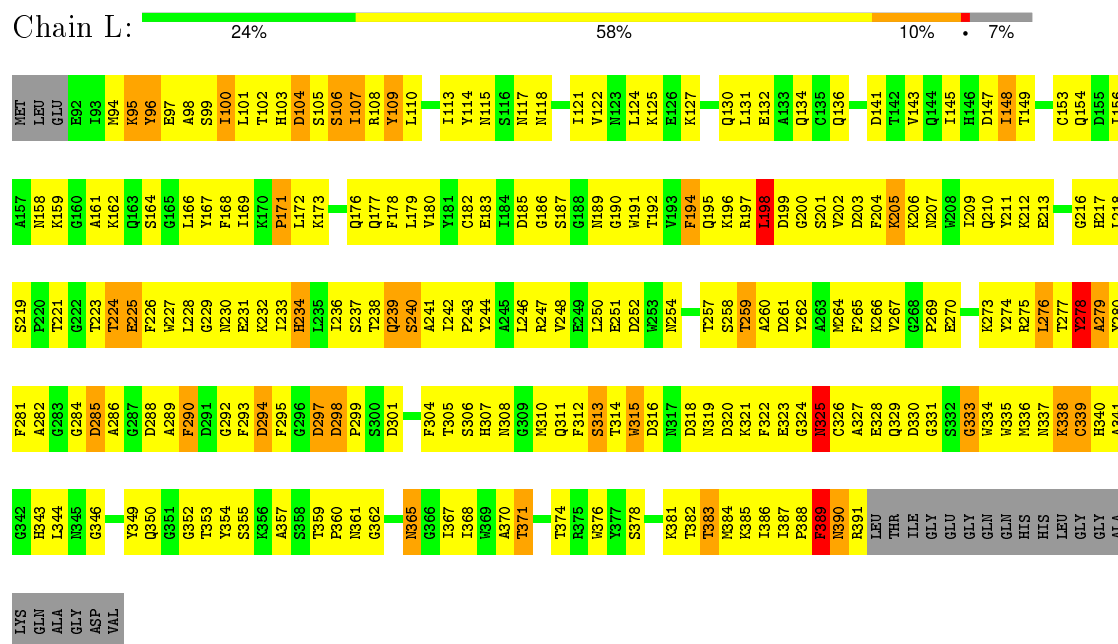


• Molecule 3: Fibrinogen, gamma polypeptide

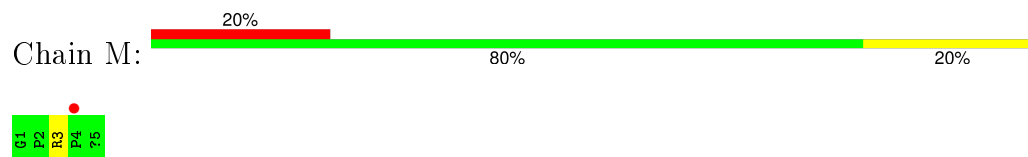
Chain I: 4% 16% 55% 22% 6%



- Molecule 3: Fibrinogen, gamma polypeptide



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



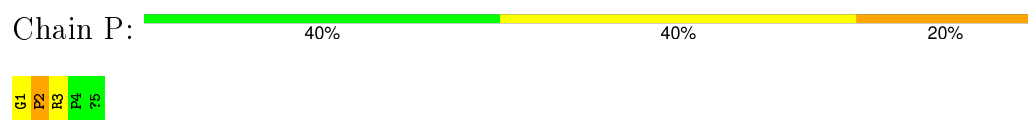
- Molecule 4: Gly-Pro-Arg-Pro-amide peptide ligand



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



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



- 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

Property	Value	Source
Space group	P 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	81.68Å 46.07Å 429.90Å 90.00° 89.99° 90.00°	Depositor
Resolution (Å)	30.00 – 2.90 49.09 – 2.56	Depositor EDS
% Data completeness (in resolution range)	97.9 (30.00-2.90) 86.5 (49.09-2.56)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.12 (at 2.54Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.275 , 0.360 0.275 , 0.356	Depositor DCC
R_{free} test set	3599 reflections (5.32%)	DCC
Wilson B-factor (Å ²)	71.1	Xtriage
Anisotropy	0.182	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 28.0	EDS
Estimated twinning fraction	0.467 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 91090 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	22270	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage'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.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: CA, NAG, NDG, NH2

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	0.38	0/609	0.75	0/811
1	D	0.44	0/585	0.77	0/778
1	G	0.42	0/609	0.78	0/811
1	J	0.42	0/653	0.74	0/869
2	B	0.40	0/2523	0.76	2/3409 (0.1%)
2	E	0.50	0/2494	0.78	1/3369 (0.0%)
2	H	0.41	0/2523	0.76	1/3409 (0.0%)
2	K	0.50	0/2502	0.79	3/3380 (0.1%)
3	C	0.40	0/2512	0.68	0/3396
3	F	0.44	0/2476	0.72	1/3347 (0.0%)
3	I	0.40	0/2512	0.70	1/3396 (0.0%)
3	L	0.43	0/2476	0.73	2/3347 (0.1%)
4	M	0.45	0/30	0.66	0/40
4	N	0.65	0/30	0.72	0/40
4	O	0.51	0/30	0.71	0/40
4	P	0.48	0/30	0.80	0/40
4	Q	0.52	0/30	0.73	0/40
4	R	0.56	0/30	0.66	0/40
4	S	0.49	0/30	0.59	0/40
4	T	0.53	0/30	0.79	0/40
All	All	0.43	0/22714	0.74	11/30642 (0.0%)

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

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	K	406	ARG	C-N-CA	5.83	136.28	121.70
2	K	412	PRO	N-CA-C	-5.72	97.22	112.10
2	E	412	PRO	N-CA-C	-5.71	97.26	112.10
2	K	406	ARG	CA-C-N	-5.70	104.66	117.20
2	H	346	ARG	N-CA-C	-5.53	96.08	111.00

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	142	0
1	D	584	0	623	80	0
1	G	608	0	649	118	0
1	J	652	0	695	97	0
2	B	2462	0	2327	497	0
2	E	2434	0	2295	236	0
2	H	2462	0	2326	430	0
2	K	2442	0	2307	234	0
3	C	2446	0	2294	450	0
3	F	2410	0	2256	293	0
3	I	2446	0	2294	443	0
3	L	2410	0	2256	303	0
4	M	30	0	32	2	0
4	N	30	0	32	7	0
4	O	30	0	32	3	0
4	P	30	0	32	4	0
4	Q	30	0	32	2	0
4	R	30	0	32	8	0
4	S	30	0	32	7	0
4	T	30	0	32	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	14	0	13	1	0
5	E	14	0	13	0	0
6	H	14	0	13	4	0
6	K	14	0	13	3	0
7	B	1	0	0	0	0
7	C	1	0	0	0	0
7	E	2	0	0	0	0
7	F	1	0	0	0	0
7	H	1	0	0	0	0
7	I	1	0	0	0	0
7	K	2	0	0	0	0
7	L	1	0	0	0	0
All	All	22270	0	21279	3110	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 71.

The worst 5 of 3110 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
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
3:C:171:PRO:HB2	3:C:174:ALA:HB2	1.33	1.05

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%)	2	6
1	G	72/87 (83%)	44 (61%)	14 (19%)	14 (19%)	0	0
1	J	77/87 (88%)	55 (71%)	18 (23%)	4 (5%)	2	8
2	B	305/328 (93%)	186 (61%)	76 (25%)	43 (14%)	0	0
2	E	302/328 (92%)	235 (78%)	41 (14%)	26 (9%)	1	2
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	4
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	3
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	3
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 ⓘ

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%)	58 (84%)	11 (16%)	3	9
1	D	66/82 (80%)	57 (86%)	9 (14%)	5	13
1	G	69/82 (84%)	60 (87%)	9 (13%)	5	15
1	J	74/82 (90%)	62 (84%)	12 (16%)	3	9
2	B	265/286 (93%)	235 (89%)	30 (11%)	7	22
2	E	262/286 (92%)	233 (89%)	29 (11%)	8	22
2	H	265/286 (93%)	236 (89%)	29 (11%)	8	23
2	K	263/286 (92%)	234 (89%)	29 (11%)	8	23
3	C	257/269 (96%)	229 (89%)	28 (11%)	8	23
3	F	253/269 (94%)	221 (87%)	32 (13%)	5	16
3	I	257/269 (96%)	228 (89%)	29 (11%)	7	22
3	L	253/269 (94%)	218 (86%)	35 (14%)	4	13
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%)	2095 (88%)	282 (12%)	6	19

5 of 282 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	F	264	MET
2	H	256	GLN
3	L	194	PHE
3	F	294	ASP
1	G	155	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 136 such sidechains are listed below:

Mol	Chain	Res	Type
3	F	254	ASN
2	H	256	GLN
3	L	163	GLN
3	F	311	GLN
1	G	134	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 carbohydrates 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	NDG	B	470	2	14,14,15	0.77	0	15,19,21	0.88	1 (6%)
5	NDG	E	470	2	14,14,15	0.62	0	15,19,21	0.98	1 (6%)
6	NAG	H	470	2	14,14,15	0.68	0	15,19,21	1.05	2 (13%)
6	NAG	K	470	2	14,14,15	0.52	0	15,19,21	0.97	1 (6%)

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	NDG	B	470	2	-	0/6/23/26	0/1/1/1
5	NDG	E	470	2	-	1/6/23/26	0/1/1/1
6	NAG	H	470	2	-	0/6/23/26	0/1/1/1
6	NAG	K	470	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	H	470	NAG	C2-N2-C7	-2.88	119.34	123.04
5	B	470	NDG	C2-N2-C7	-2.45	119.89	123.04
6	K	470	NAG	C2-N2-C7	-2.36	120.00	123.04
5	E	470	NDG	C2-N2-C7	-2.30	120.08	123.04
6	H	470	NAG	C1-O5-C5	2.04	114.83	112.25

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	E	470	NDG	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	NDG	1	0
6	H	470	NAG	4	0
6	K	470	NAG	3	0

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, 95th 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 ²)	Q<0.9
1	A	74/87 (85%)	-0.04	2 (2%) 58 52	62, 83, 105, 111	0
1	D	71/87 (81%)	-0.33	0 100 100	29, 56, 89, 96	0
1	G	74/87 (85%)	-0.16	2 (2%) 58 52	62, 81, 100, 115	0
1	J	79/87 (90%)	-0.33	0 100 100	35, 58, 108, 122	0
2	B	307/328 (93%)	-0.25	4 (1%) 79 78	42, 76, 99, 108	0
2	E	304/328 (92%)	-0.43	0 100 100	27, 51, 79, 99	0
2	H	307/328 (93%)	-0.28	4 (1%) 79 78	42, 76, 99, 107	0
2	K	305/328 (92%)	-0.44	0 100 100	25, 51, 80, 97	0
3	C	305/323 (94%)	-0.07	12 (3%) 43 36	49, 83, 107, 116	0
3	F	300/323 (92%)	-0.34	1 (0%) 94 94	39, 66, 92, 116	0
3	I	305/323 (94%)	-0.12	12 (3%) 43 36	54, 84, 109, 136	0
3	L	300/323 (92%)	-0.36	0 100 100	36, 66, 91, 117	0
4	M	4/5 (80%)	0.59	1 (25%) 1 0	63, 64, 65, 97	0
4	N	4/5 (80%)	0.22	0 100 100	41, 48, 60, 86	0
4	O	4/5 (80%)	0.25	0 100 100	90, 94, 99, 106	0
4	P	4/5 (80%)	-0.19	0 100 100	64, 73, 79, 93	0
4	Q	4/5 (80%)	0.13	0 100 100	63, 64, 65, 94	0
4	R	4/5 (80%)	-0.36	0 100 100	44, 50, 62, 87	0
4	S	4/5 (80%)	0.06	0 100 100	89, 100, 101, 104	0
4	T	4/5 (80%)	-0.34	0 100 100	66, 73, 74, 91	0
All	All	2763/2992 (92%)	-0.27	38 (1%) 78 76	25, 71, 100, 136	0

The worst 5 of 38 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	344	LEU	5.2
3	I	236	ILE	4.0
3	I	344	LEU	4.0
3	C	241	ALA	3.8
1	A	169	LEU	3.8

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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th 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	LLDF	B-factors(Å ²)	Q<0.9
7	CA	I	1	1/1	0.92	0.22	2.40	76,76,76,76	0
7	CA	K	2	1/1	0.96	0.22	0.79	60,60,60,60	0
7	CA	B	2	1/1	0.94	0.19	0.47	90,90,90,90	0
7	CA	H	2	1/1	0.93	0.18	0.12	83,83,83,83	0
7	CA	E	2	1/1	0.91	0.17	0.01	57,57,57,57	0
6	NAG	K	470	14/15	0.92	0.17	-0.19	65,75,82,89	0
7	CA	C	1	1/1	0.94	0.15	-0.22	78,78,78,78	0
7	CA	F	1	1/1	0.93	0.15	-0.23	54,54,54,54	0
7	CA	L	1	1/1	0.97	0.09	-1.37	58,58,58,58	0
7	CA	E	3	1/1	0.85	0.09	-2.16	90,90,90,90	0
7	CA	K	3	1/1	0.86	0.07	-	89,89,89,89	0
5	NDG	B	470	14/15	0.84	0.12	-	60,83,88,91	0
5	NDG	E	470	14/15	0.90	0.19	-	68,77,92,92	0
6	NAG	H	470	14/15	0.78	0.25	-	94,105,117,117	0

6.5 Other polymers [i](#)

There are no such residues in this entry.