wwPDB X-ray Structure Validation Summary Report (i)

Feb 17, 2024 – 12:53 PM EST

PDB ID	:	3S51
Title	:	Structure of FANCI
Authors	:	Pavletich, N.P.
Deposited on	:	2011-05-20
Resolution	:	3.30 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
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:

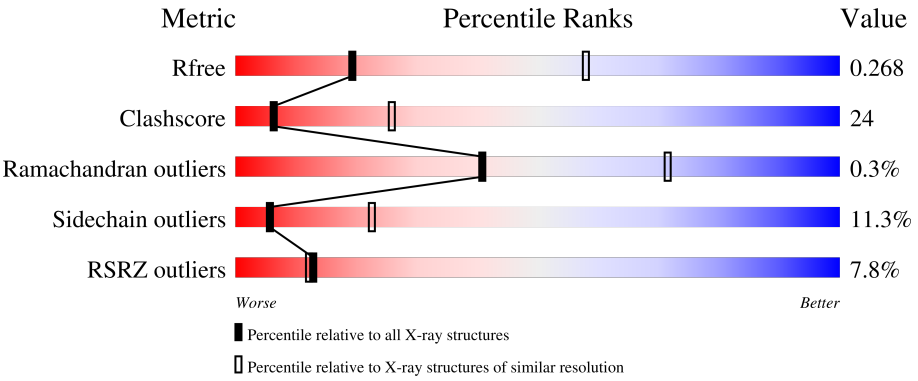
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 3.30 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}	130704	1149 (3.34-3.26)
Clashscore	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)
RSRZ outliers	127900	1115 (3.34-3.26)

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% 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	1308	6% 44% 37% 5% 13%
1	B	1308	8% 41% 36% 5% 18%
1	C	1308	5% 45% 37% 5% 13%
1	D	1308	6% 40% 34% 5% 21%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 34594 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 Fanconi anemia group I protein homolog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1134	Total	C	N	O	S	0	0	0
			8960	5762	1489	1656	53			
1	B	1071	Total	C	N	O	S	0	0	0
			8487	5468	1409	1559	51			
1	C	1134	Total	C	N	O	S	0	0	0
			8960	5762	1489	1656	53			
1	D	1034	Total	C	N	O	S	0	0	0
			8187	5277	1358	1504	48			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1303	HIS	-	expression tag	UNP Q8K368
A	1304	HIS	-	expression tag	UNP Q8K368
A	1305	HIS	-	expression tag	UNP Q8K368
A	1306	HIS	-	expression tag	UNP Q8K368
A	1307	HIS	-	expression tag	UNP Q8K368
A	1308	HIS	-	expression tag	UNP Q8K368
B	1303	HIS	-	expression tag	UNP Q8K368
B	1304	HIS	-	expression tag	UNP Q8K368
B	1305	HIS	-	expression tag	UNP Q8K368
B	1306	HIS	-	expression tag	UNP Q8K368
B	1307	HIS	-	expression tag	UNP Q8K368
B	1308	HIS	-	expression tag	UNP Q8K368
C	1303	HIS	-	expression tag	UNP Q8K368
C	1304	HIS	-	expression tag	UNP Q8K368
C	1305	HIS	-	expression tag	UNP Q8K368
C	1306	HIS	-	expression tag	UNP Q8K368
C	1307	HIS	-	expression tag	UNP Q8K368
C	1308	HIS	-	expression tag	UNP Q8K368
D	1303	HIS	-	expression tag	UNP Q8K368
D	1304	HIS	-	expression tag	UNP Q8K368
D	1305	HIS	-	expression tag	UNP Q8K368

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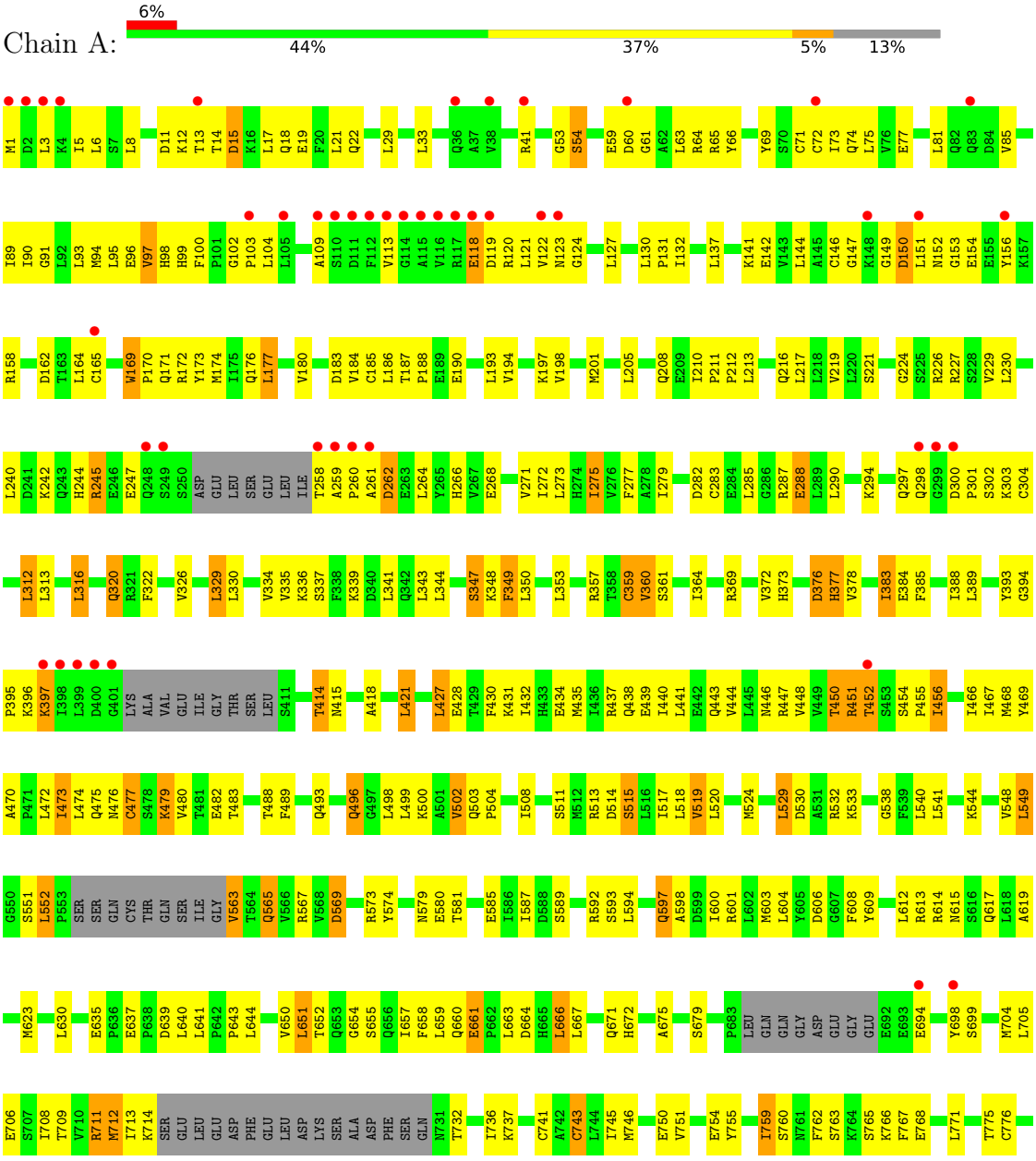
Chain	Residue	Modelled	Actual	Comment	Reference
D	1306	HIS	-	expression tag	UNP Q8K368
D	1307	HIS	-	expression tag	UNP Q8K368
D	1308	HIS	-	expression tag	UNP Q8K368

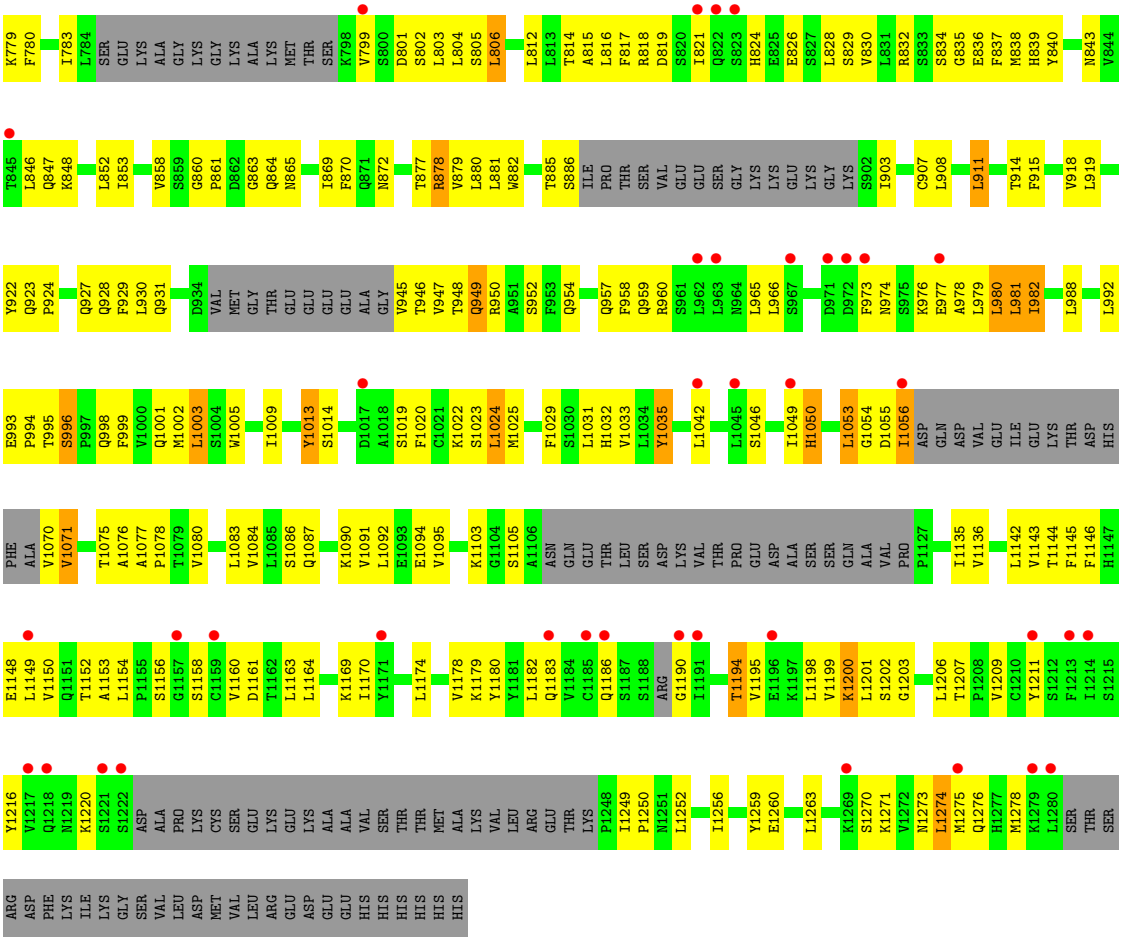
3 Residue-property plots (i)

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 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: Fanconi anemia group I protein homolog

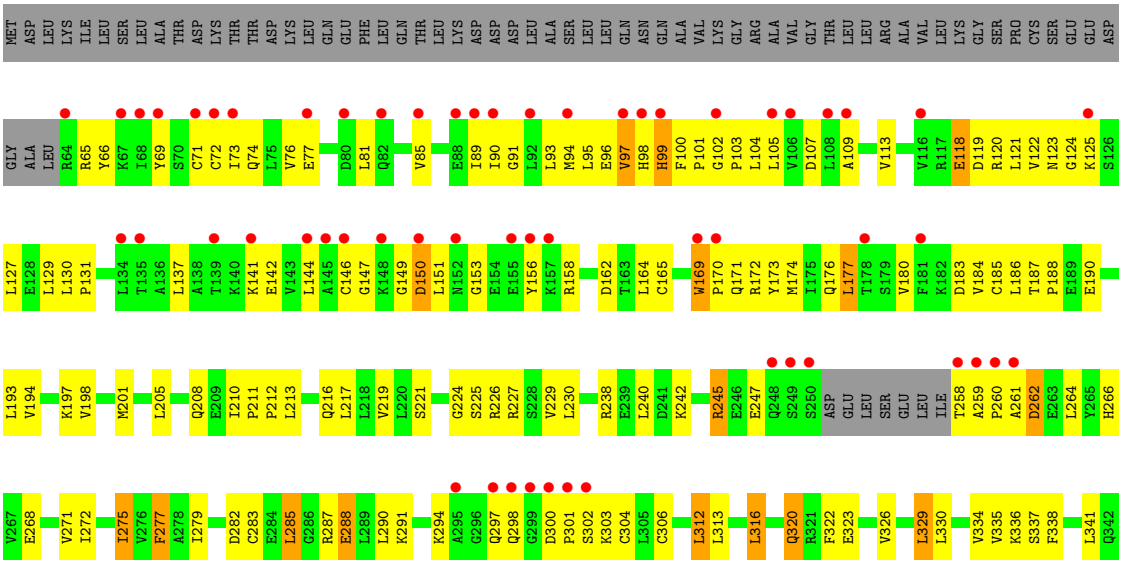
Chain A:

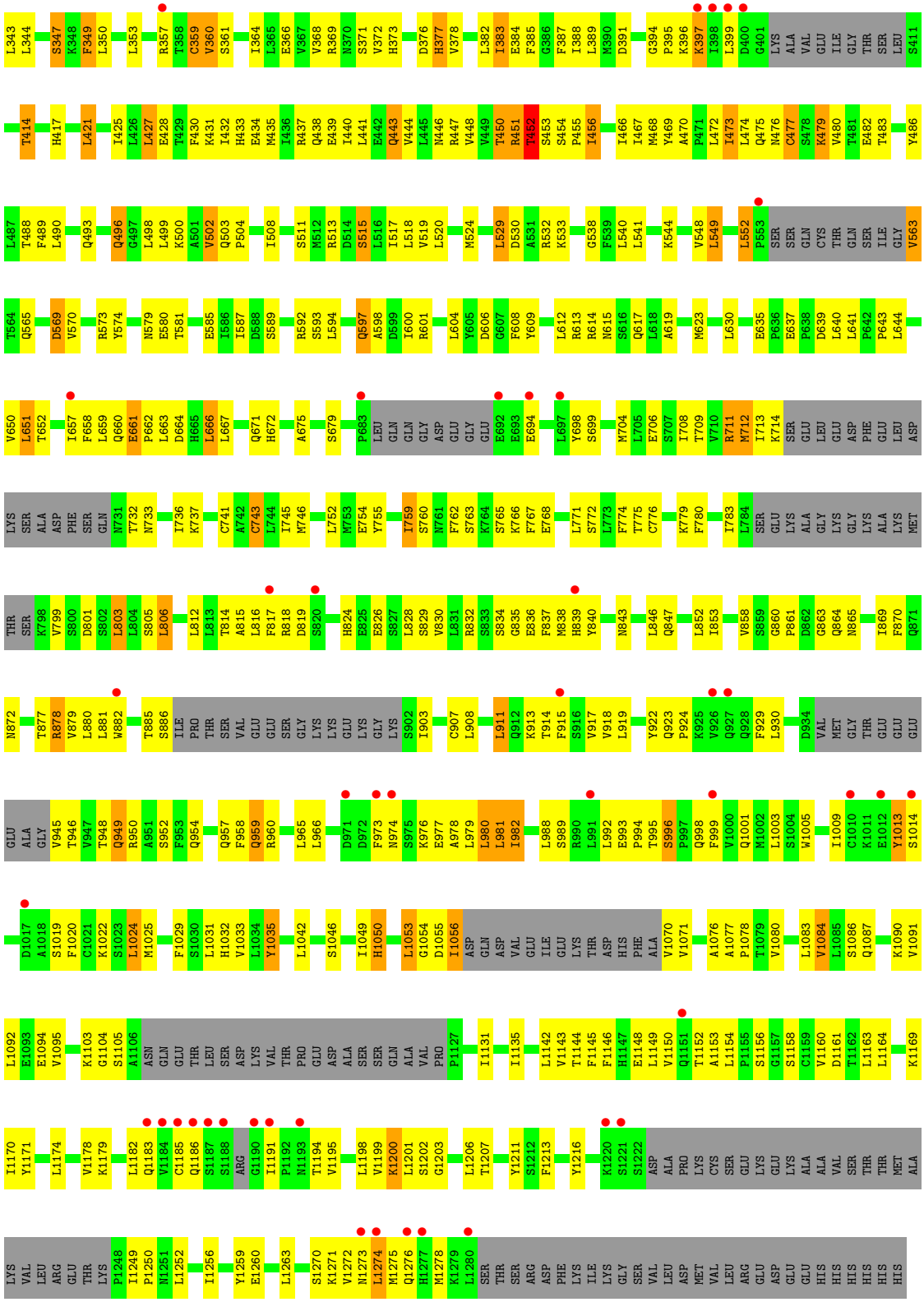




• Molecule 1: Fanconi anemia group I protein homolog

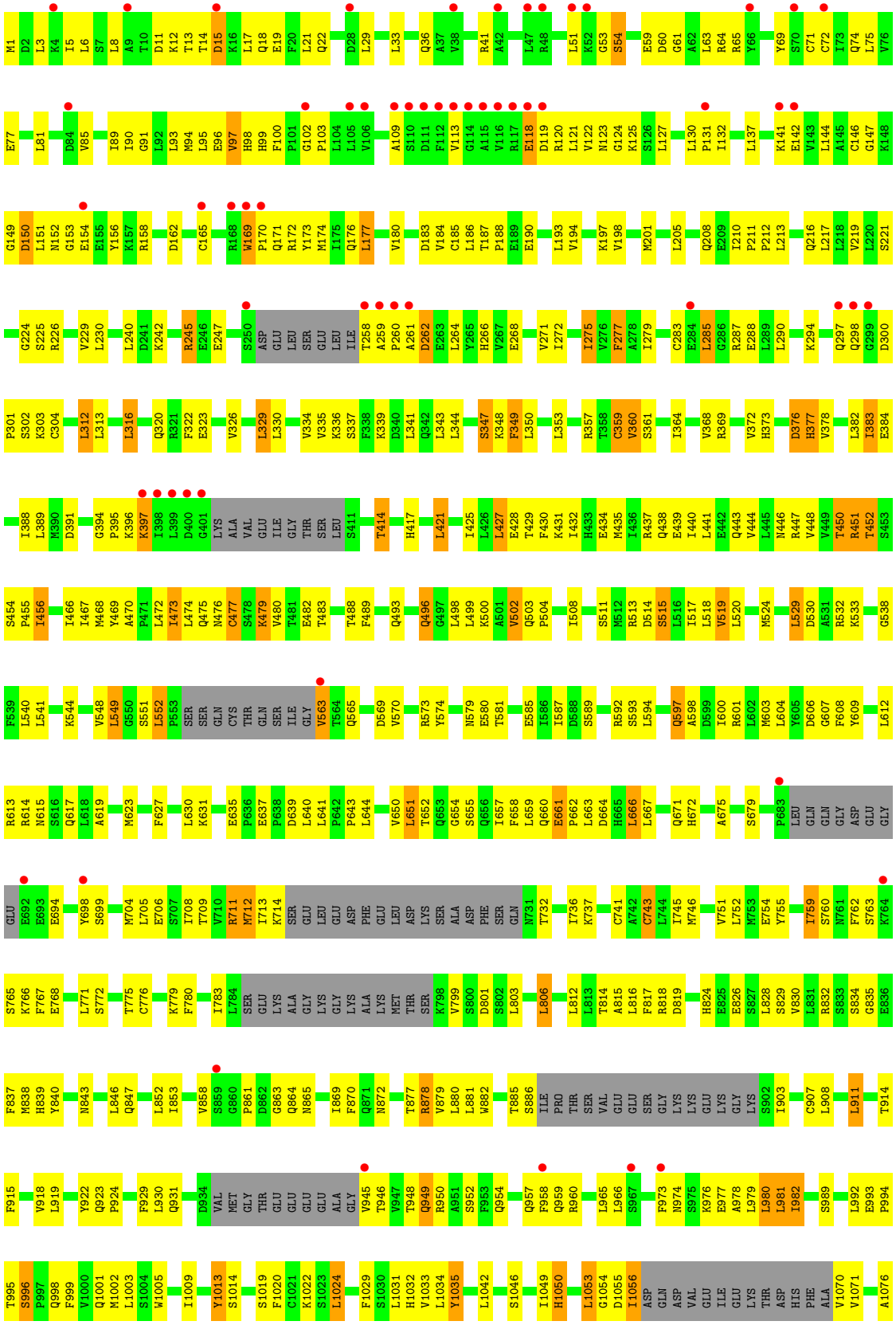
Chain B:

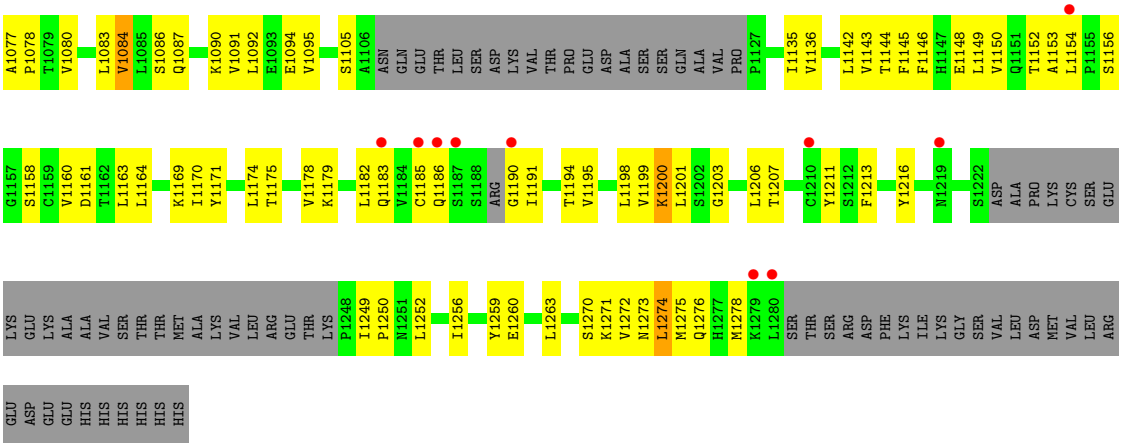




• Molecule 1: Fanconi anemia group I protein homolog

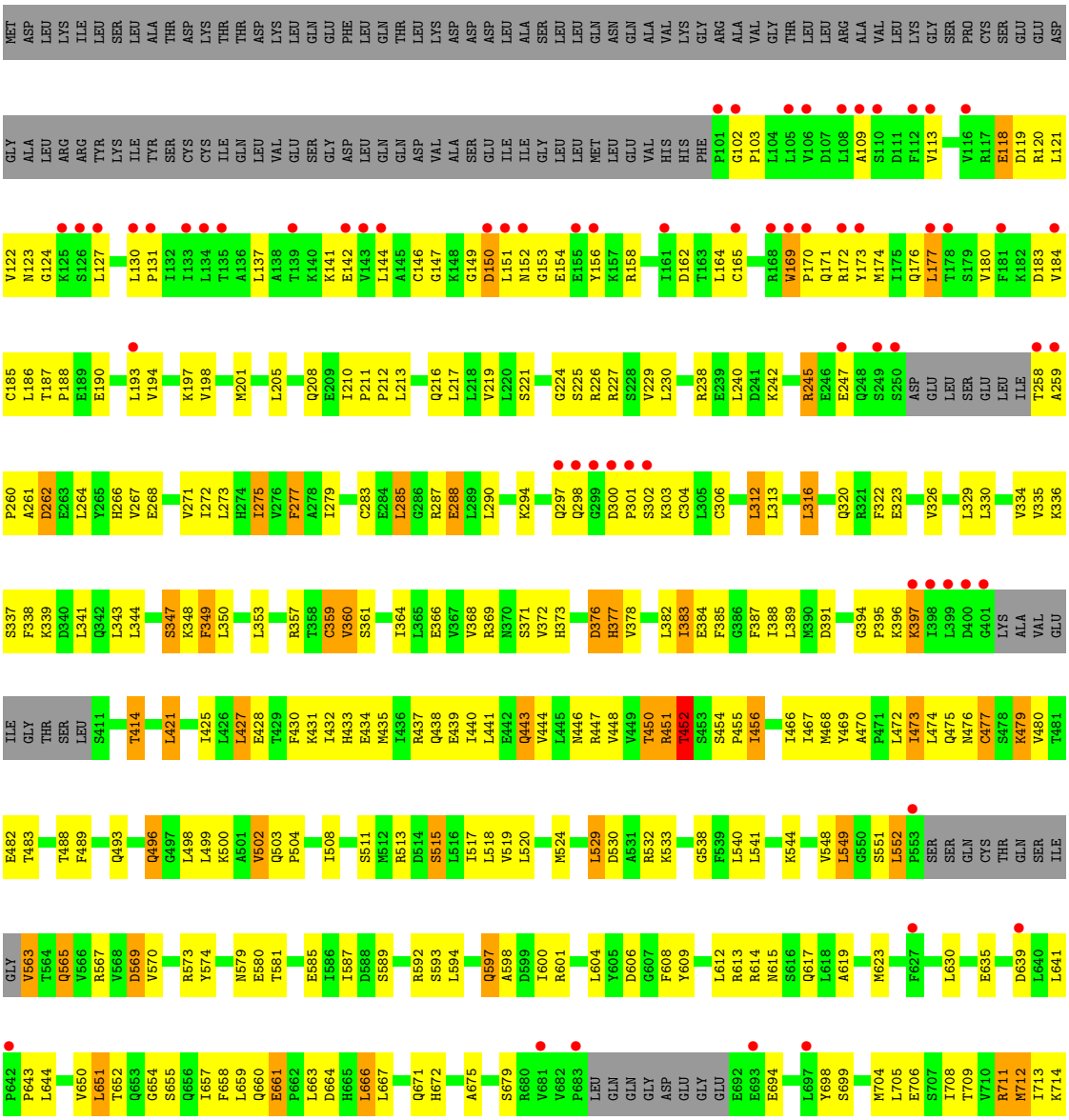
Chain C:

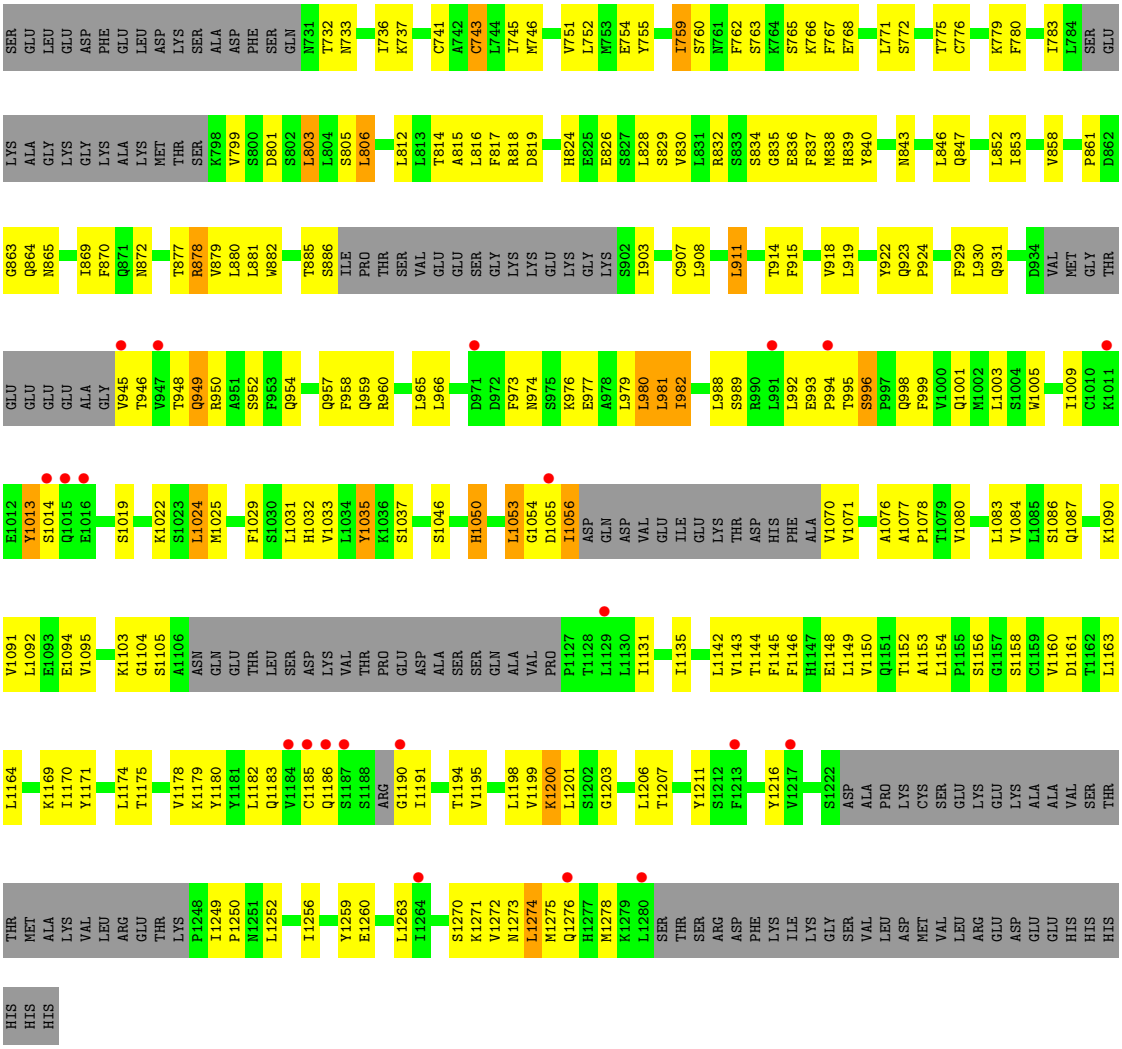

M1 D2 L3 K4 I5 L6 S7 L8 A9 T10 D11 K12 T13 T14 D15 K16 L17 Q18 E19 F20 L21 Q22 D28 L29 L33 Q36 A37 V38 R41 A42 L47 R48 L51 K52 G53 S54 E59 D60 G61 A62 L63 R64 R65 Y66 Y69 S70 C71 C72 I73 Q74 L75 V76
E77 L81 D84 V85 I89 I90 G91 L92 L93 M94 L95 E96 V97 H98 H99 F100 P101 G102 P103 L104 L105 V106 A109 S110 D111 F112 V113 G114 A115 V116 R117 E118 D119 R120 L121 V122 N123 G124 K125 S126 L127 L130 P131 I132 L137 K141 E142 V143 L144 A145 C146 G147 K148
G149 D150 L151 N152 G153 E154 E155 Y156 K157 R158 D162 C165 R168 W169 P170 Q171 R172 Y173 M174 I175 Q176 L177 V180 D183 V184 C185 L186 T187 P188 E189 E190 L193 V194 K197 V198 M201 L205 Q208 E209 I210 P211 P212 L213 Q216 L217 L218 V219 L220 S221
G224 S225 R226 V229 L230 L240 D241 K242 R245 E246 E247 S250 ASP GLU LEU SER GLU LEU ILE T258 A259 P260 A261 D262 E263 L264 Y265 H266 V267 E268 V271 I272 I275 V276 F277 A278 I279 C283 E284 L285 G286 R287 E288 L289 L290 K294 Q297 Q298 G299 D300
P301 S302 K303 C304 L312 L313 L316 Q320 R321 F322 E323 V326 L329 L330 V334 V335 K336 S337 F338 K339 D340 L341 Q342 L343 L344 S347 K348 F349 L350 L353 R357 T358 C359 V360 S361 I364 V368 R369 V372 H373 D376 H377 V378 L382 I383 E384
I388 L389 M390 D391 G394 P395 K396 K397 I398 L399 D400 G401 LYS ALA VAL GLU ILE GLY THR SER LEU S411 T414 H417 L421 I425 L426 L427 E428 T429 F430 K431 I432 H433 E434 M435 I436 R437 Q438 E439 I440 L441 E442 Q443 V444 L445 N446 R447 V448 V449 T450 R451 T452 S453
S454 P455 T456 I466 I467 M468 Y469 A470 P471 L472 I473 L474 Q475 N476 C477 S478 K479 V480 T481 E482 T483 T488 F489 Q493 Q496 C497 L498 L499 K500 A501 V502 Q503 F504 I508 S511 M512 R513 D514 S515 L516 I517 L518 V519 L520 M524 L529 D530 A531 R532 K533 G538
F539 L540 L541 K544 V548 L549 G550 S551 L552 P553 SER SER GLN CYS THR GLN SER ILE GLY V563 T564 Q565 D569 V570 R573 Y574 N579 E580 T581 E585 I586 I587 D588 S589 R592 S593 L594 Q597 A598 D599 I600 R601 L602 M603 L604 Y605 D606 G607 F608 Y609 L612
R613 R614 N615 S616 Q617 L618 A619 M623 F627 L630 K631 E635 P636 E637 P638 D639 L640 L641 P642 P643 L644 V650 L651 T652 Q653 G654 S655 Q656 I657 F658 L659 Q660 E661 P662 L663 D664 H665 L666 L667 Q671 H672 A675 S679 P683 LEU GLN GLN GLY ASP GLU GLY
GLU E692 E693 E694 Y698 S699 M704 L705 E706 S707 I708 T709 V710 R711 M712 I713 K714 SER GLU LEU GLU GLU ASP PHE GLU LEU ASP LYS SER ALA ASP PHE SER GLN N731 T732 I736 K737 C741 A742 C743 L744 I745 M746 V751 L752 M753 E754 Y755 I759 S760 N761 F762 S763 K764
S765 K766 F767 E768 L771 S772 T775 C776 K779 F780 I783 L784 SER GLU LYS ALA GLY LYS GLY LYS ALA LYS MET THR SER K798 V799 S800 D801 S802 L803 L806 L812 L813 T814 A815 L816 F817 R818 D819 H824 E825 E826 S827 L828 S829 V830 L831 R832 S833 S834 G835 E836
F837 M838 H839 Y840 N843 L846 Q847 L852 I853 V858 S859 G860 P861 D862 G863 Q864 N865 I869 F870 Q871 N872 T877 R878 V879 L880 L881 W882 T885 S886 ILE PRO THR SER VAL GLU GLU SER GLY LYS LYS GLU LYS GLY LYS S902 I903 C907 L908 L911 T914
F915 V918 L919 Y922 Q923 P924 F929 L930 Q931 D934 VAL MET GLY THR GLU GLU GLU GLU ALA GLY V945 T946 V947 T948 Q949 R950 A951 S952 F953 Q954 Q957 F958 Q959 R960 L965 L966 S967 F973 N974 S975 K976 E977 A978 L979 L980 L981 I982 S989 L992 E993 P994
T995 S996 P997 Q998 F999 Y1000 Q1001 M1002 L1003 S1004 W1005 I1009 Y1013 S1014 S1019 F1020 C1021 K1022 S1023 L1024 F1029 S1030 L1031 H1032 V1033 L1034 Y1035 L1042 S1046 I1049 H1050 L1053 G1054 D1055 I1056 ASP GLN ASP VAL GLU ILE GLU LYS THR ASP HIS PHE ALA V1070 V1071 A1076



• Molecule 1: Fanconi anemia group I protein homolog

Chain D:




SER GLU LEU GLU ASP PHE GLU LEU ASP LYS SER ALA ASP PHE SER GLN N731 T732 N733 I736 K737 C741 A742 C743 L744 I745 M746 V751 L752 M753 E754 Y755 I759 S760 N761 F762 S763 K764 S765 K766 F767 E768 L771 S772 T775 C776 K779 F780 I783 L784 SER GLU
LYS ALA GLY LYS GLY LYS ALA LYS MET THR SER K798 V799 S800 D801 S802 L803 L804 S805 L806 L812 L813 T814 A815 L816 F817 R818 D819 H824 E825 E826 S827 L828 S829 V830 L831 R832 S833 S834 G835 E836 F837 M838 H839 Y840 N843 L846 Q847 L852 I853 V858 P861 D862
G863 Q864 N865 I869 F870 Q871 N872 T877 R878 V879 L880 L881 W882 T885 S886 ILE PRO THR SER VAL GLU GLU SER GLY LYS LYS GLU LYS GLY LYS S902 I903 C907 L908 L911 T914 F915 V918 L919 Y922 Q923 P924 F929 L930 Q931 D934 VAL MET GLY THR
GLU GLU GLU GLU ALA GLY V945 T946 V947 T948 Q949 R950 A951 S952 F953 Q954 Q957 F958 Q959 R960 L965 L966 D971 D972 F973 N974 S975 K976 E977 A978 L979 L980 L981 I982 L988 S989 R990 L991 L992 E993 P994 T995 S996 P997 Q998 F999 V1000 Q1001 M1002 L1003 S1004 W1005 I1009 C1010 K1011
E1012 Y1013 S1014 Q1015 E1016 S1019 K1022 S1023 L1024 M1025 F1029 S1030 L1031 H1032 V1033 L1034 Y1035 K1036 S1037 S1046 H1050 L1053 G1054 D1055 I1056 ASP GLN ASP VAL GLU ILE GLU LYS THR ASP HIS PHE ALA V1070 V1071 A1076 A1077 P1078 T1079 V1080 L1083 V1084 L1085 S1086 Q1087 K1090
V1091 L1092 E1093 E1094 V1095 K1103 G1104 S1105 A1106 ASN GLN GLU THR LEU SER ASP LYS VAL THR PRO GLU ASP ALA SER SER GLN ALA VAL PRO P1127 T1128 L1129 L1130 I1131 I1135 L1142 V1143 T1144 F1145 F1146 H1147 E1148 L1149 V1150 Q1151 T1152 A1153 L1154 P1155 S1156 G1157 S1158 C1159 V1160 D1161 T1162 L1163
L1164 K1169 I1170 Y1171 L1174 T1175 V1178 K1179 Y1180 Y1181 L1182 Q1183 V1184 C1185 Q1186 S1187 S1188 ARG G1190 I1191 T1194 V1195 L1198 V1199 K1200 L1201 S1202 G1203 L1206 T1207 Y1211 S1212 F1213 Y1216 V1217 S1222 ASP ALA PRO LYS CYS SER GLU LYS GLU LYS ALA ALA VAL SER THR
THR MET ALA LYS VAL LEU ARG GLU THR LYS P1248 I1249 P1250 N1251 L1252 I1256 Y1259 E1260 L1263 I1264 S1270 K1271 V1272 N1273 L1274 M1275 Q1276 H1277 M1278 K1279 L1280 SER THR SER ARG ASP PHE LYS ILE LYS GLY SER VAL LEU ASP MET VAL LEU ARG GLU ASP GLU GLU HIS HIS HIS
HIS HIS HIS

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	114.70Å 136.50Å 149.70Å 115.90° 106.00° 95.00°	Depositor
Resolution (Å)	39.82 – 3.30 39.82 – 3.28	Depositor EDS
% Data completeness (in resolution range)	82.8 (39.82-3.30) 83.1 (39.82-3.28)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.52 (at 3.25Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, R_{free}	0.259 , 0.278 0.245 , 0.268	Depositor DCC
R_{free} test set	2199 reflections (2.00%)	wwPDB-VP
Wilson B-factor (Å^2)	93.7	Xtriage
Anisotropy	0.486	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 117.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	34594	wwPDB-VP
Average B, all atoms (Å^2)	192.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.11% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] 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

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	0.26	2/9099 (0.0%)	0.46	0/12286
1	B	0.29	4/8624 (0.0%)	0.46	0/11646
1	C	0.26	2/9099 (0.0%)	0.46	0/12286
1	D	0.26	2/8319 (0.0%)	0.46	0/11234
All	All	0.27	10/35141 (0.0%)	0.46	0/47452

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
1	B	0	1
1	C	0	1
1	D	0	1
All	All	0	4

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	959	GLN	CD-NE2	-9.98	1.07	1.32
1	B	959	GLN	CD-OE1	-7.80	1.06	1.24
1	C	320	GLN	CD-NE2	-6.76	1.16	1.32
1	D	320	GLN	CD-NE2	-6.59	1.16	1.32
1	A	320	GLN	CD-NE2	-6.15	1.17	1.32

There are no bond angle outliers.

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1053	LEU	Peptide
1	B	1053	LEU	Peptide
1	C	1053	LEU	Peptide
1	D	1053	LEU	Peptide

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	8960	0	9275	454	0
1	B	8487	0	8776	449	0
1	C	8960	0	9275	435	0
1	D	8187	0	8476	411	0
All	All	34594	0	35802	1705	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 24.

The worst 5 of 1705 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:C:799:VAL:O	1:C:847:GLN:NE2	1.87	1.07
1:A:799:VAL:O	1:A:847:GLN:NE2	1.88	1.07
1:B:799:VAL:O	1:B:847:GLN:NE2	1.88	1.06
1:D:799:VAL:O	1:D:847:GLN:NE2	1.88	1.05
1:A:489:PHE:HB3	1:C:450:THR:HG21	1.35	1.04

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	1108/1308 (85%)	1023 (92%)	82 (7%)	3 (0%)	41	71
1	B	1045/1308 (80%)	969 (93%)	72 (7%)	4 (0%)	34	66
1	C	1108/1308 (85%)	1022 (92%)	83 (8%)	3 (0%)	41	71
1	D	1008/1308 (77%)	933 (93%)	71 (7%)	4 (0%)	34	66
All	All	4269/5232 (82%)	3947 (92%)	308 (7%)	14 (0%)	41	71

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	122	VAL
1	A	150	ASP
1	B	122	VAL
1	B	150	ASP
1	C	122	VAL

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	1032/1188 (87%)	917 (89%)	115 (11%)	6	23
1	B	979/1188 (82%)	867 (89%)	112 (11%)	5	22
1	C	1032/1188 (87%)	917 (89%)	115 (11%)	6	23
1	D	945/1188 (80%)	838 (89%)	107 (11%)	6	22
All	All	3988/4752 (84%)	3539 (89%)	449 (11%)	6	22

5 of 449 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	81	LEU
1	D	1142	LEU
1	C	549	LEU

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Continued from previous page...

Mol	Chain	Res	Type
1	D	1050	HIS
1	D	587	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	672	HIS
1	C	377	HIS
1	D	847	GLN
1	D	433	HIS
1	D	672	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 monosaccharides 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

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>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	1134/1308 (86%)	0.25	85 (7%) 14 13	85, 192, 306, 410	0
1	B	1071/1308 (81%)	0.27	101 (9%) 8 9	87, 188, 306, 415	0
1	C	1134/1308 (86%)	0.25	70 (6%) 20 20	81, 191, 306, 410	0
1	D	1034/1308 (79%)	0.28	84 (8%) 12 11	84, 185, 302, 416	0
All	All	4373/5232 (83%)	0.26	340 (7%) 13 12	81, 189, 304, 416	0

The worst 5 of 340 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	109	ALA	12.3
1	D	250	SER	11.1
1	D	135	THR	10.9
1	D	150	ASP	8.9
1	D	299	GLY	8.7

6.2 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.