



# wwPDB X-ray Structure Validation Summary Report i

Feb 28, 2014 – 05:08 AM GMT

PDB ID : 4EAH  
Title : Crystal structure of the formin homology 2 domain of FMNL3 bound to actin  
Authors : Thompson, M.E.; Heimsath, E.G.; Gauvin, T.J.; Higgs, H.N.; Kull, F.J.  
Deposited on : 2012-03-22  
Resolution : 3.40 Å(reported)

This is a wwPDB 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 <http://wwpdb.org/ValidationPDFNotes.html>

---

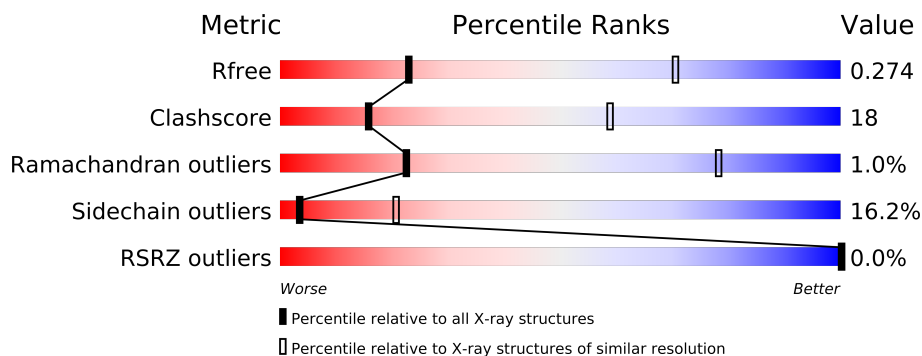
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 3.40 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))
$R_{free}$	66092	1017 (3.52-3.28)
Clashscore	79885	1214 (3.50-3.30)
Ramachandran outliers	78287	1177 (3.50-3.30)
Sidechain outliers	78261	1177 (3.50-3.30)
RSRZ outliers	66119	1017 (3.52-3.28)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	D	377	
1	F	377	
1	G	377	
1	H	377	
2	A	402	
2	B	402	
2	C	402	
2	E	402	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	ACT	E	1001	-	X

Continued on next page...

*Continued from previous page...*

Mol	Type	Chain	Res	Geometry	Electron density
3	ACT	F	401	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 22892 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Actin, alpha skeletal muscle.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	356	Total	C	N	O	S	121	0	0
			2785	1766	468	533	18			
1	H	356	Total	C	N	O	S	123	0	0
			2785	1766	468	533	18			
1	G	356	Total	C	N	O	S	132	0	0
			2785	1766	468	533	18			
1	F	356	Total	C	N	O	S	65	0	0
			2785	1766	468	533	18			

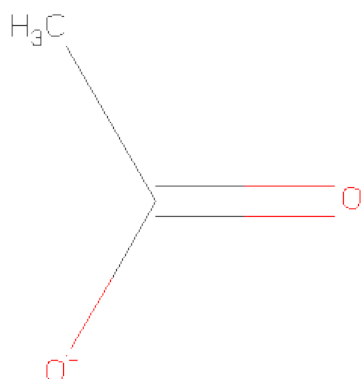
- Molecule 2 is a protein called Formin-like protein 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	357	Total	C	N	O	S	265	0	0
			2895	1848	502	533	12			
2	E	357	Total	C	N	O	S	272	0	0
			2895	1848	502	533	12			
2	C	357	Total	C	N	O	S	252	0	0
			2895	1848	502	533	12			
2	B	357	Total	C	N	O	S	260	0	0
			2895	1848	502	533	12			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	553	GLY	-	EXPRESSION TAG	UNP Q6ZPF4
A	554	SER	-	EXPRESSION TAG	UNP Q6ZPF4
E	553	GLY	-	EXPRESSION TAG	UNP Q6ZPF4
E	554	SER	-	EXPRESSION TAG	UNP Q6ZPF4
C	553	GLY	-	EXPRESSION TAG	UNP Q6ZPF4
C	554	SER	-	EXPRESSION TAG	UNP Q6ZPF4
B	553	GLY	-	EXPRESSION TAG	UNP Q6ZPF4
B	554	SER	-	EXPRESSION TAG	UNP Q6ZPF4

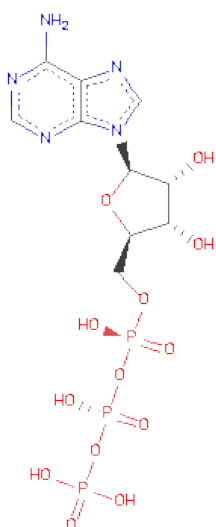
- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula:  $C_2H_3O_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	D	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	E	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	H	1	Total	C	O	0	0
			4	2	2		
3	G	1	Total	C	O	0	0
			4	2	2		
3	F	1	Total	C	O	0	0
			4	2	2		
3	F	1	Total	C	O	0	0
			4	2	2		

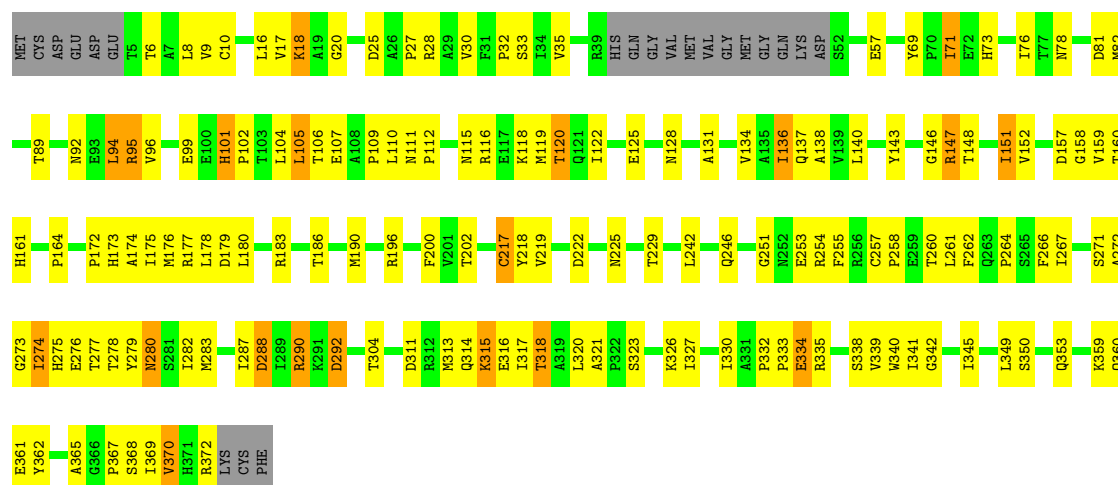
- Molecule 4 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula:

C<sub>10</sub>H<sub>16</sub>N<sub>5</sub>O<sub>13</sub>P<sub>3</sub>).



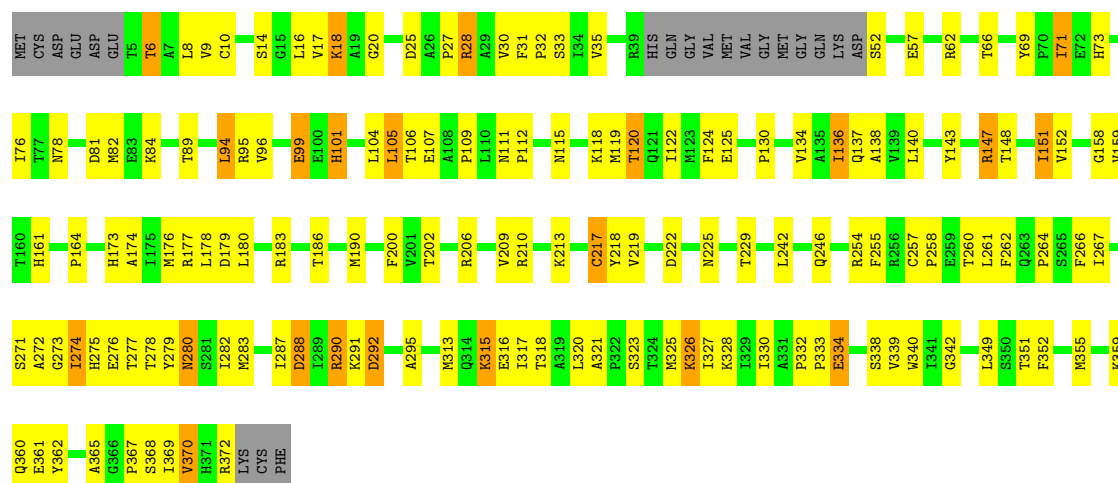
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	D	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
4	H	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
4	G	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
4	F	1	Total	C	N	O	P	0	0
			31	10	5	13	3		





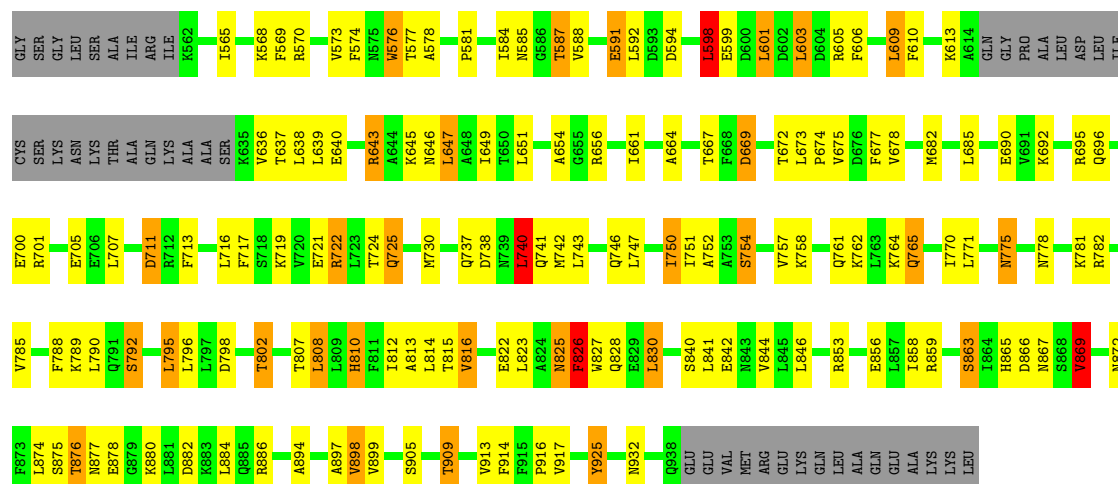
- Molecule 1: Actin, alpha skeletal muscle

Chain F:



- Molecule 2: Formin-like protein 3

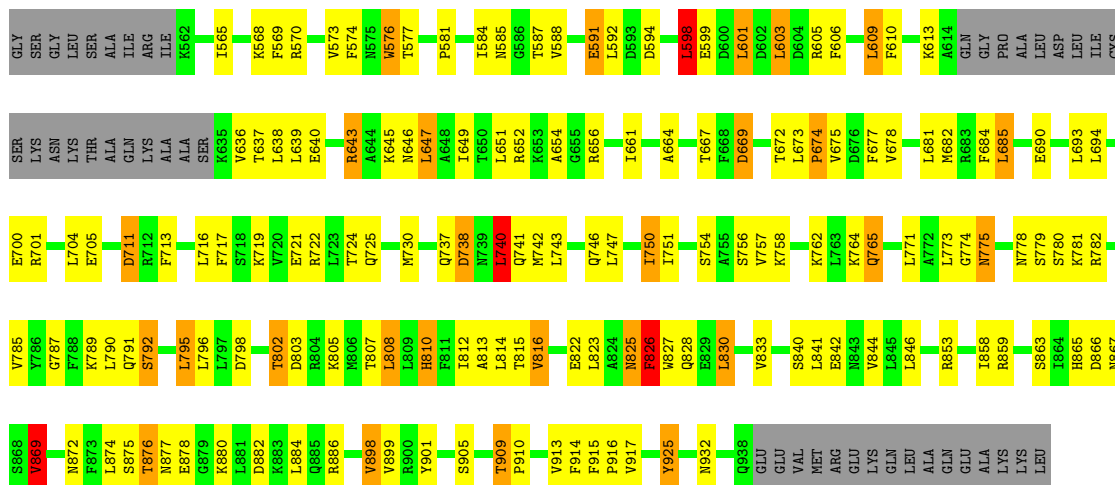
Chain A:





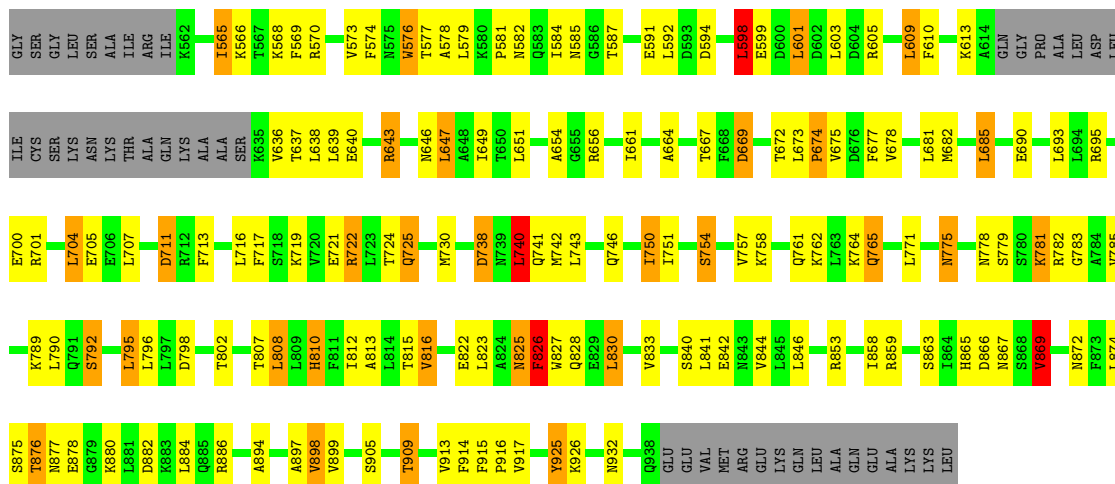
- Molecule 2: Formin-like protein 3

## Chain E:



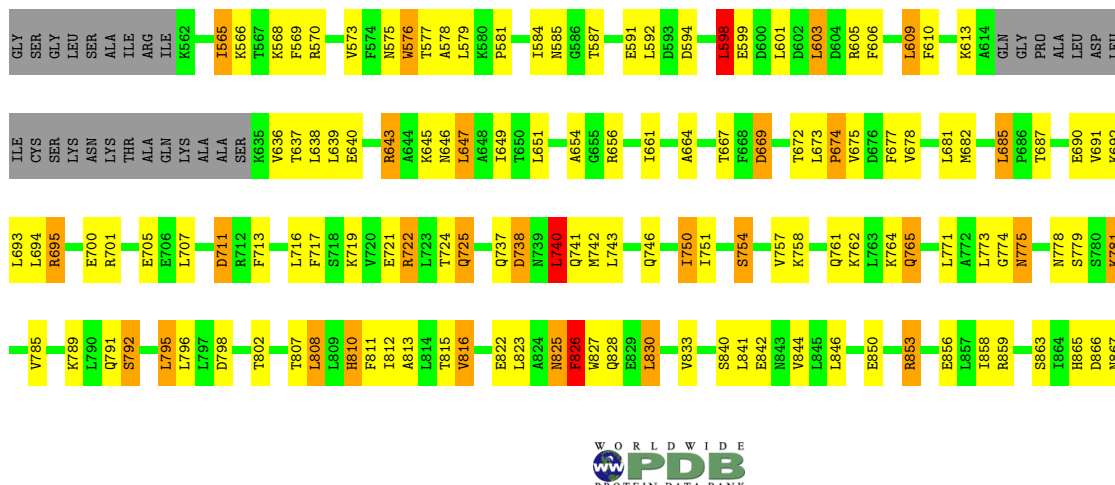
- Molecule 2: Formin-like protein 3

## Chain C:



- Molecule 2: Formin-like protein 3

## Chain B:





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	125.98Å 126.05Å 129.62Å 90.00° 93.17° 90.00°	Depositor
Resolution (Å)	19.82 – 3.40 19.82 – 3.40	Depositor EDS
% Data completeness (in resolution range)	99.8 (19.82-3.40) 99.8 (19.82-3.40)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.92 (at 3.44Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, $R_{free}$	0.230 , 0.277 0.225 , 0.274	Depositor DCC
$R_{free}$ test set	2892 reflections (5.22%)	DCC
Wilson B-factor (Å <sup>2</sup> )	98.3	Xtriage
Anisotropy	0.607	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 65.2	EDS
Estimated twinning fraction	0.037 for l,-k,h	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	0 of 55418 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	22892	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	105.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.14% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ATP, ACT

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	D	0.51	0/2845	0.70	0/3858
1	F	0.48	0/2845	0.69	0/3858
1	G	0.48	0/2845	0.70	0/3858
1	H	0.48	0/2845	0.70	0/3858
2	A	0.48	0/2942	0.70	1/3956 (0.0%)
2	B	0.49	0/2942	0.69	1/3956 (0.0%)
2	C	0.49	0/2942	0.70	1/3956 (0.0%)
2	E	0.49	0/2942	0.70	1/3956 (0.0%)
All	All	0.49	0/23148	0.70	4/31256 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	740	LEU	CA-CB-CG	5.37	127.64	115.30
2	C	740	LEU	CA-CB-CG	5.25	127.37	115.30
2	A	740	LEU	CA-CB-CG	5.15	127.14	115.30
2	B	740	LEU	CA-CB-CG	5.07	126.96	115.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the

chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	2785	0	2758	100	1
1	F	2785	0	2758	97	1
1	G	2785	0	2758	105	0
1	H	2785	0	2758	111	0
2	A	2895	0	2971	101	0
2	B	2895	0	2971	104	0
2	C	2895	0	2971	99	0
2	E	2895	0	2971	105	0
3	A	12	0	9	1	0
3	B	4	0	3	2	0
3	C	8	0	6	2	0
3	D	4	0	3	2	0
3	E	4	0	3	1	0
3	F	8	0	6	1	0
3	G	4	0	3	2	0
3	H	4	0	3	2	0
4	D	31	0	12	5	0
4	F	31	0	12	1	0
4	G	31	0	12	2	0
4	H	31	0	12	2	0
All	All	22892	0	23000	776	1

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 18.

The worst 5 of 776 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:H:147:ARG:HH12	1:H:330:ILE:HG12	1.29	0.94
1:H:261:LEU:HB3	1:H:274:ILE:HD11	1.54	0.90
1:D:261:LEU:HB3	1:D:274:ILE:HD11	1.55	0.89
1:D:147:ARG:HH12	1:D:330:ILE:HG12	1.36	0.88
1:G:261:LEU:HB3	1:G:274:ILE:HD11	1.55	0.88

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	Distance(Å)	Clash(Å)
1:D:199:SER:OG	1:F:62:ARG:O[1_554]	2.11	0.09

## 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	D	352/377 (93%)	326 (93%)	25 (7%)	1 (0%)	50	92
1	F	352/377 (93%)	324 (92%)	27 (8%)	1 (0%)	50	92
1	G	352/377 (93%)	324 (92%)	27 (8%)	1 (0%)	50	92
1	H	352/377 (93%)	325 (92%)	26 (7%)	1 (0%)	50	92
2	A	353/402 (88%)	310 (88%)	37 (10%)	6 (2%)	14	66
2	B	353/402 (88%)	313 (89%)	34 (10%)	6 (2%)	14	66
2	C	353/402 (88%)	313 (89%)	34 (10%)	6 (2%)	14	66
2	E	353/402 (88%)	310 (88%)	38 (11%)	5 (1%)	16	69
All	All	2820/3116 (90%)	2545 (90%)	248 (9%)	27 (1%)	22	78

5 of 27 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	869	VAL
2	E	869	VAL
2	C	869	VAL
2	B	869	VAL
2	A	598	LEU

### 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	D	302/320 (94%)	262 (87%)	40 (13%)	6	31
1	F	302/320 (94%)	260 (86%)	42 (14%)	5	28
1	G	302/320 (94%)	263 (87%)	39 (13%)	6	32

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H	302/320 (94%)	265 (88%)	37 (12%)	7	34
2	A	316/351 (90%)	256 (81%)	60 (19%)	2	11
2	B	316/351 (90%)	255 (81%)	61 (19%)	2	11
2	C	316/351 (90%)	254 (80%)	62 (20%)	2	10
2	E	316/351 (90%)	256 (81%)	60 (19%)	2	11
All	All	2472/2684 (92%)	2071 (84%)	401 (16%)	3	21

5 of 401 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	700	GLU
2	B	577	THR
1	F	101	HIS
2	C	721	GLU
2	C	802	THR

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

Mol	Chain	Res	Type
2	C	746	GLN
1	F	101	HIS
1	H	101	HIS
2	A	746	GLN
2	B	746	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

16 ligands are 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
3	ACT	A	1001	-	1,3,3	0.32	0	0,3,3	0.00	-
3	ACT	A	1002	-	1,3,3	1.59	0	0,3,3	0.00	-
3	ACT	A	1003	-	1,3,3	1.55	0	0,3,3	0.00	-
3	ACT	B	1001	-	1,3,3	1.08	0	0,3,3	0.00	-
3	ACT	C	1001	-	1,3,3	0.66	0	0,3,3	0.00	-
3	ACT	C	1002	-	1,3,3	2.09	1 (100%)	0,3,3	0.00	-
3	ACT	D	401	-	1,3,3	0.60	0	0,3,3	0.00	-
4	ATP	D	402	-	33,33,33	1.24	3 (9%)	52,52,52	1.75	9 (17%)
3	ACT	E	1001	-	1,3,3	1.79	0	0,3,3	0.00	-
3	ACT	F	401	-	1,3,3	1.58	0	0,3,3	0.00	-
3	ACT	F	402	-	1,3,3	1.24	0	0,3,3	0.00	-
4	ATP	F	403	-	33,33,33	1.27	4 (12%)	52,52,52	1.63	6 (11%)
3	ACT	G	401	-	1,3,3	0.48	0	0,3,3	0.00	-
4	ATP	G	402	-	33,33,33	1.13	2 (6%)	52,52,52	1.61	7 (13%)
3	ACT	H	401	-	1,3,3	0.88	0	0,3,3	0.00	-
4	ATP	H	402	-	33,33,33	1.27	3 (9%)	52,52,52	1.49	7 (13%)

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
3	ACT	A	1001	-	-	0/0/0/0	0/0/0/0
3	ACT	A	1002	-	-	0/0/0/0	0/0/0/0
3	ACT	A	1003	-	-	0/0/0/0	0/0/0/0
3	ACT	B	1001	-	-	0/0/0/0	0/0/0/0
3	ACT	C	1001	-	-	0/0/0/0	0/0/0/0
3	ACT	C	1002	-	-	0/0/0/0	0/0/0/0
3	ACT	D	401	-	-	0/0/0/0	0/0/0/0

*Continued on next page...*



*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	ATP	D	402	-	-	0/22/38/38	0/1/3/3
3	ACT	E	1001	-	-	0/0/0/0	0/0/0/0
3	ACT	F	401	-	-	0/0/0/0	0/0/0/0
3	ACT	F	402	-	-	0/0/0/0	0/0/0/0
4	ATP	F	403	-	-	0/22/38/38	0/1/3/3
3	ACT	G	401	-	-	0/0/0/0	0/0/0/0
4	ATP	G	402	-	-	0/22/38/38	0/1/3/3
3	ACT	H	401	-	-	0/0/0/0	0/0/0/0
4	ATP	H	402	-	-	0/22/38/38	0/1/3/3

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	402	ATP	C4-N9	-3.89	1.32	1.37
4	F	403	ATP	C4-N9	-3.76	1.32	1.37
4	H	402	ATP	C5-C4	3.60	1.48	1.40
4	G	402	ATP	C5-C4	3.34	1.48	1.40
4	H	402	ATP	C4-N9	-2.96	1.33	1.37

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	402	ATP	N3-C2-N1	-6.18	123.54	128.71
4	F	403	ATP	N3-C2-N1	-5.29	124.29	128.71
4	H	402	ATP	N3-C4-N9	5.16	134.75	125.43
4	F	403	ATP	N3-C4-N9	5.09	134.63	125.43
4	G	402	ATP	N3-C2-N1	-5.05	124.49	128.71

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

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 ⓘ

### 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<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	D	356/377 (94%)	0.00	0 100 100	58, 95, 163, 191	33 (9%)
1	F	356/377 (94%)	0.02	0 100 100	59, 95, 164, 190	15 (4%)
1	G	356/377 (94%)	-0.09	0 100 100	61, 97, 165, 192	33 (9%)
1	H	356/377 (94%)	-0.02	0 100 100	64, 97, 164, 194	28 (7%)
2	A	357/402 (88%)	-0.12	0 100 100	64, 101, 144, 163	61 (17%)
2	B	357/402 (88%)	-0.15	0 100 100	64, 102, 144, 165	59 (16%)
2	C	357/402 (88%)	-0.10	0 100 100	65, 102, 144, 160	56 (15%)
2	E	357/402 (88%)	-0.16	0 100 100	65, 102, 143, 161	62 (17%)
All	All	2852/3116 (91%)	-0.08	0 100 100	58, 99, 156, 194	347 (12%)

There are no RSRZ outliers to report.

### 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 carbohydrates in this entry.

### 6.4 Ligands ⓘ

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, 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	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	ACT	E	1001	4/4	0.57	6.76	73,103,103,103	0
3	ACT	F	401	4/4	0.49	5.06	88,111,123,124	0
3	ACT	H	401	4/4	0.33	1.42	70,89,100,122	0
3	ACT	F	402	4/4	0.28	1.14	78,80,106,107	0
3	ACT	D	401	4/4	0.27	0.56	62,66,91,110	0
3	ACT	G	401	4/4	0.27	0.42	84,88,105,122	0
4	ATP	H	402	31/31	0.18	-0.23	85,109,122,133	0
4	ATP	D	402	31/31	0.22	-0.25	53,86,104,106	0
3	ACT	A	1001	4/4	0.23	-0.26	72,74,83,89	0
3	ACT	B	1001	4/4	0.19	-0.30	75,94,95,97	0
3	ACT	A	1002	4/4	0.21	-0.39	80,96,99,103	0
3	ACT	C	1001	4/4	0.21	-0.41	75,88,90,100	0
4	ATP	G	402	31/31	0.19	-0.41	73,104,119,122	0
3	ACT	C	1002	4/4	0.21	-0.54	69,89,92,102	0
4	ATP	F	403	31/31	0.19	-0.55	70,91,110,116	0
3	ACT	A	1003	4/4	0.17	-0.80	81,83,97,104	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.