



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 09:54 AM GMT

PDB ID : 3JSK
Title : Thiazole synthase from *Neurospora crassa*
Authors : Kang, Y.N.; Bale, S.; Ealick, S.E.
Deposited on : 2009-09-10
Resolution : 2.70 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 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

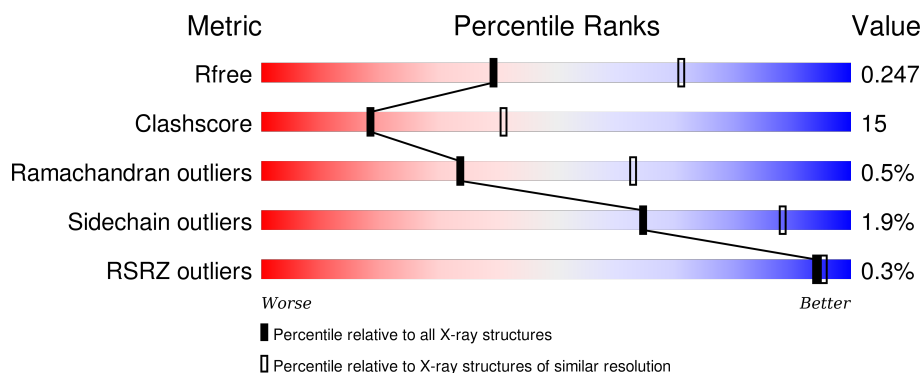
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 2.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.











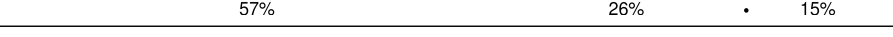
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	344	
1	B	344	
1	C	344	
1	D	344	
1	E	344	

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Mol	Chain	Length	Quality of chain
1	F	344	
1	G	344	
1	H	344	
1	I	344	
1	J	344	
1	K	344	
1	L	344	
1	M	344	
1	N	344	
1	O	344	
1	P	344	

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
1	DHA	B	232	-	X	-	-
1	DHA	D	232	-	X	-	-
1	DHA	E	232	-	X	-	-
1	DHA	F	232	-	X	-	-
1	DHA	H	232	-	X	-	-
1	DHA	K	232	-	X	-	-
1	DHA	O	232	-	X	-	-
1	DHA	P	232	-	X	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 36053 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.

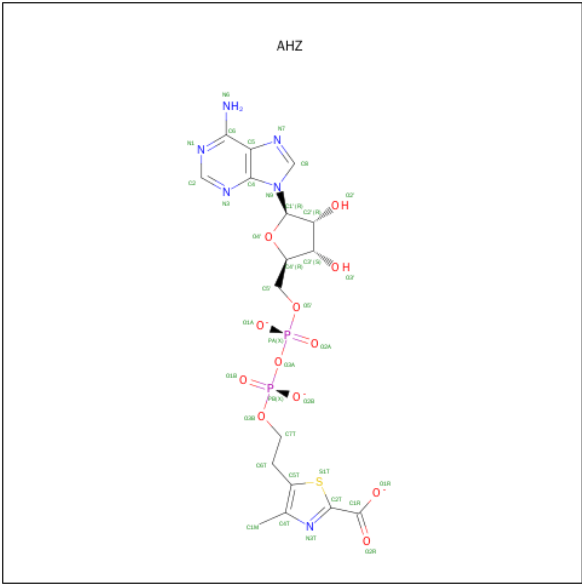
- Molecule 1 is a protein called CyPBP37 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	292	Total	C	N	O	S	0	0	0
			2193	1377	386	416	14			
1	B	291	Total	C	N	O	S	0	0	0
			2188	1374	385	415	14			
1	C	292	Total	C	N	O	S	0	0	0
			2193	1377	386	416	14			
1	D	292	Total	C	N	O	S	0	0	0
			2193	1377	386	416	14			
1	E	291	Total	C	N	O	S	0	0	0
			2188	1374	385	415	14			
1	F	292	Total	C	N	O	S	0	0	0
			2193	1377	386	416	14			
1	G	291	Total	C	N	O	S	0	0	0
			2188	1374	385	415	14			
1	H	291	Total	C	N	O	S	0	0	0
			2188	1374	385	415	14			
1	I	291	Total	C	N	O	S	0	0	0
			2188	1374	385	415	14			
1	J	291	Total	C	N	O	S	0	0	0
			2188	1374	385	415	14			
1	K	291	Total	C	N	O	S	0	0	0
			2188	1374	385	415	14			
1	L	291	Total	C	N	O	S	0	0	0
			2188	1374	385	415	14			
1	M	291	Total	C	N	O	S	0	0	0
			2188	1374	385	415	14			
1	N	292	Total	C	N	O	S	0	0	0
			2193	1377	386	416	14			
1	O	292	Total	C	N	O	S	0	0	0
			2193	1377	386	416	14			
1	P	291	Total	C	N	O	S	0	0	0
			2188	1374	385	415	14			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	232	DHA	CYS	ENGINEERED	UNP Q9HGR2
B	232	DHA	CYS	ENGINEERED	UNP Q9HGR2
C	232	DHA	CYS	ENGINEERED	UNP Q9HGR2
D	232	DHA	CYS	ENGINEERED	UNP Q9HGR2
E	232	DHA	CYS	ENGINEERED	UNP Q9HGR2
F	232	DHA	CYS	ENGINEERED	UNP Q9HGR2
G	232	DHA	CYS	ENGINEERED	UNP Q9HGR2
H	232	DHA	CYS	ENGINEERED	UNP Q9HGR2
I	232	DHA	CYS	ENGINEERED	UNP Q9HGR2
J	232	DHA	CYS	ENGINEERED	UNP Q9HGR2
K	232	DHA	CYS	ENGINEERED	UNP Q9HGR2
L	232	DHA	CYS	ENGINEERED	UNP Q9HGR2
M	232	DHA	CYS	ENGINEERED	UNP Q9HGR2
N	232	DHA	CYS	ENGINEERED	UNP Q9HGR2
O	232	DHA	CYS	ENGINEERED	UNP Q9HGR2
P	232	DHA	CYS	ENGINEERED	UNP Q9HGR2

- Molecule 2 is ADENOSINE DIPHOSPHATE 5-(BETA-ETHYL)-4-METHYL-THIAZOLE-2-CARBOXYLIC ACID (three-letter code: AHZ) (formula: C₁₇H₁₉N₆O₁₂P₂S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	S	0	0
			38	17	6	12	2	1		
2	B	1	Total	C	N	O	P	S	0	0
			38	17	6	12	2	1		

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	C	1	Total	C	N	O	P	S	0	0
			38	17	6	12	2	1		
2	D	1	Total	C	N	O	P	S	0	0
			38	17	6	12	2	1		
2	E	1	Total	C	N	O	P	S	0	0
			38	17	6	12	2	1		
2	F	1	Total	C	N	O	P	S	0	0
			38	17	6	12	2	1		
2	G	1	Total	C	N	O	P	S	0	0
			38	17	6	12	2	1		
2	H	1	Total	C	N	O	P	S	0	0
			38	17	6	12	2	1		
2	I	1	Total	C	N	O	P	S	0	0
			38	17	6	12	2	1		
2	J	1	Total	C	N	O	P	S	0	0
			38	17	6	12	2	1		
2	K	1	Total	C	N	O	P	S	0	0
			38	17	6	12	2	1		
2	L	1	Total	C	N	O	P	S	0	0
			38	17	6	12	2	1		
2	M	1	Total	C	N	O	P	S	0	0
			38	17	6	12	2	1		
2	N	1	Total	C	N	O	P	S	0	0
			38	17	6	12	2	1		
2	O	1	Total	C	N	O	P	S	0	0
			38	17	6	12	2	1		
2	P	1	Total	C	N	O	P	S	0	0
			38	17	6	12	2	1		

- Molecule 3 is FE (II) ION (three-letter code: FE2) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	G	1	Total	Fe	0	0
			1	1		
3	J	1	Total	Fe	0	0
			1	1		
3	D	1	Total	Fe	0	0
			1	1		
3	K	2	Total	Fe	0	0
			2	2		
3	E	1	Total	Fe	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	H	1	Total 1	Fe 1	0	0
3	B	1	Total 1	Fe 1	0	0
3	I	1	Total 1	Fe 1	0	0
3	C	1	Total 1	Fe 1	0	0
3	A	1	Total 1	Fe 1	0	0
3	N	1	Total 1	Fe 1	0	0
3	L	1	Total 1	Fe 1	0	0
3	F	1	Total 1	Fe 1	0	0
3	M	2	Total 2	Fe 2	0	0

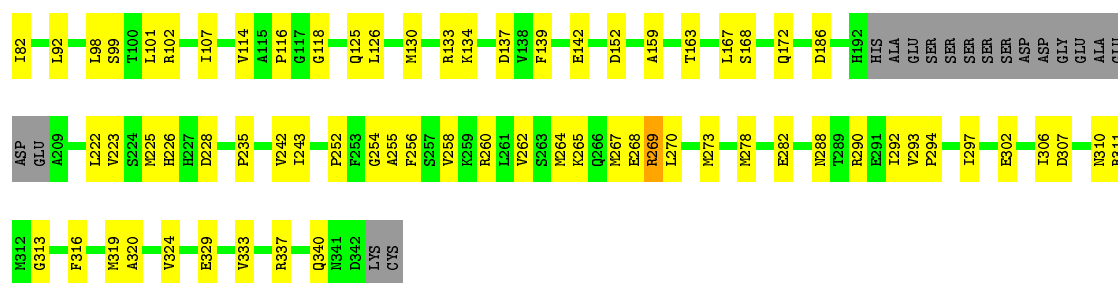
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	30	Total 30	O 30	0	0
4	B	16	Total 16	O 16	0	0
4	C	32	Total 32	O 32	0	0
4	D	21	Total 21	O 21	0	0
4	E	29	Total 29	O 29	0	0
4	F	24	Total 24	O 24	0	0
4	G	21	Total 21	O 21	0	0
4	H	23	Total 23	O 23	0	0
4	I	44	Total 44	O 44	0	0
4	J	20	Total 20	O 20	0	0

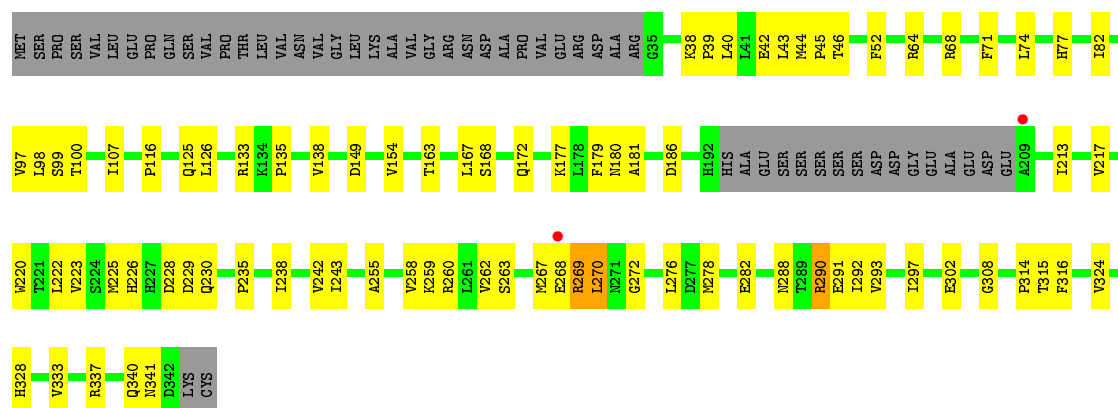
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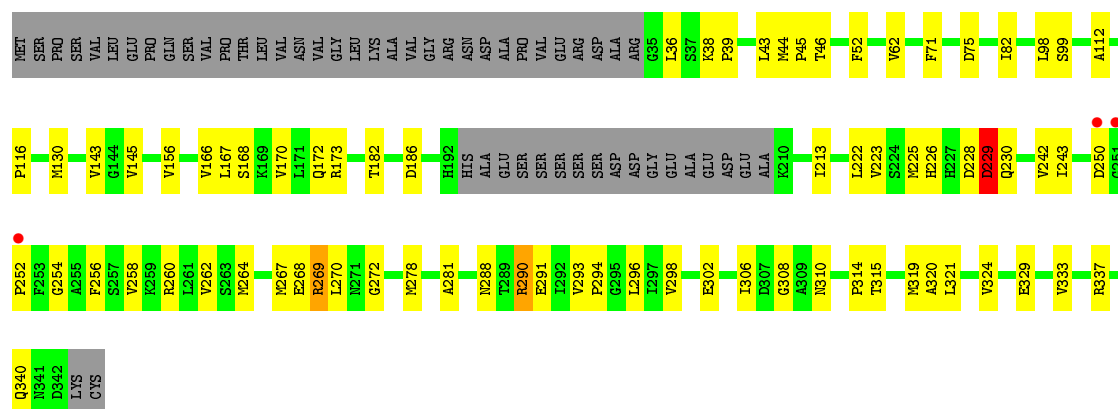
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	K	25	Total 25	O 25	0	0
4	L	21	Total 21	O 21	0	0
4	M	19	Total 19	O 19	0	0
4	N	17	Total 17	O 17	0	0
4	O	25	Total 25	O 25	0	0
4	P	24	Total 24	O 24	0	0



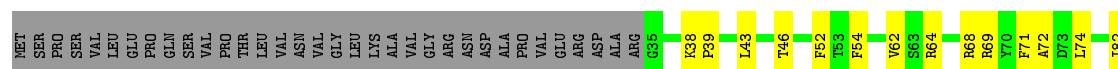
• Molecule 1: CyPBP37 protein

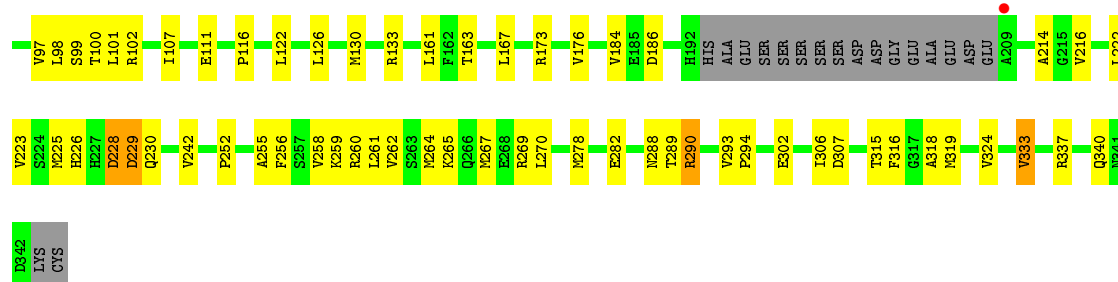


• Molecule 1: CyPBP37 protein



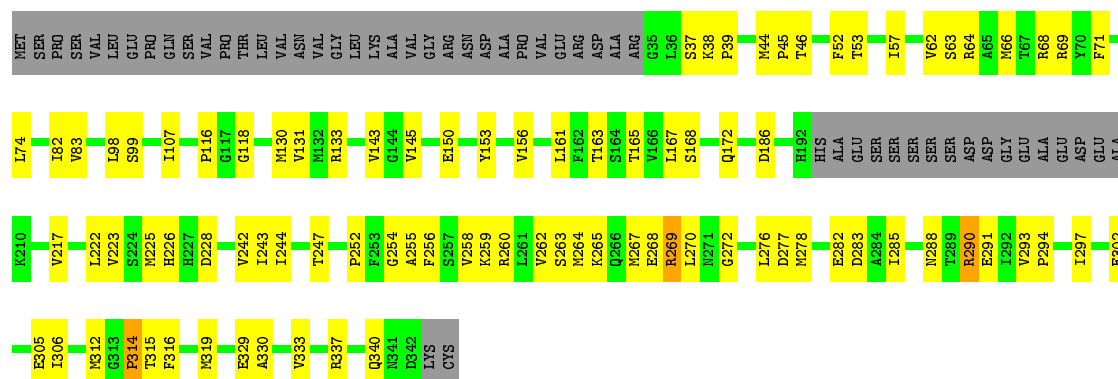
• Molecule 1: CyPBP37 protein





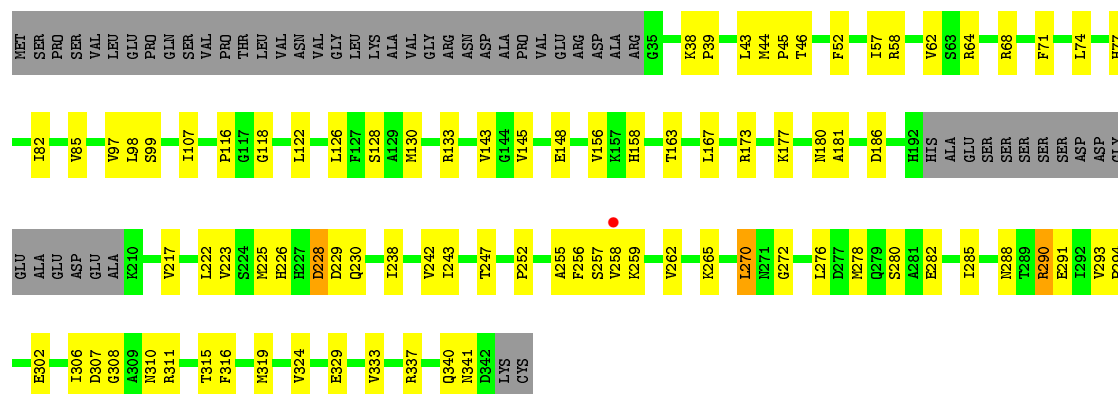
- Molecule 1: CyPBP37 protein

Chain G: 58% 25% 15%



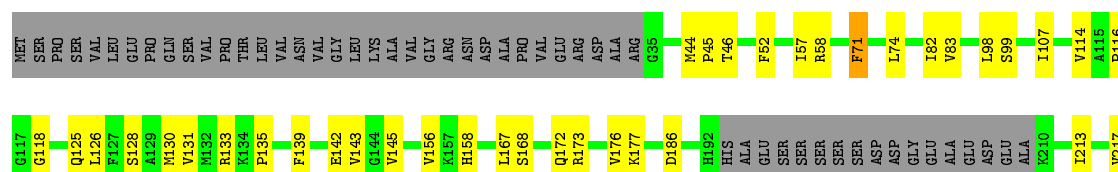
- Molecule 1: CyPBP37 protein

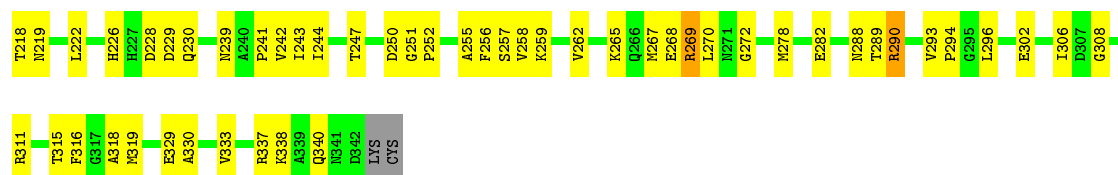
Chain H: 59% 24% 15%



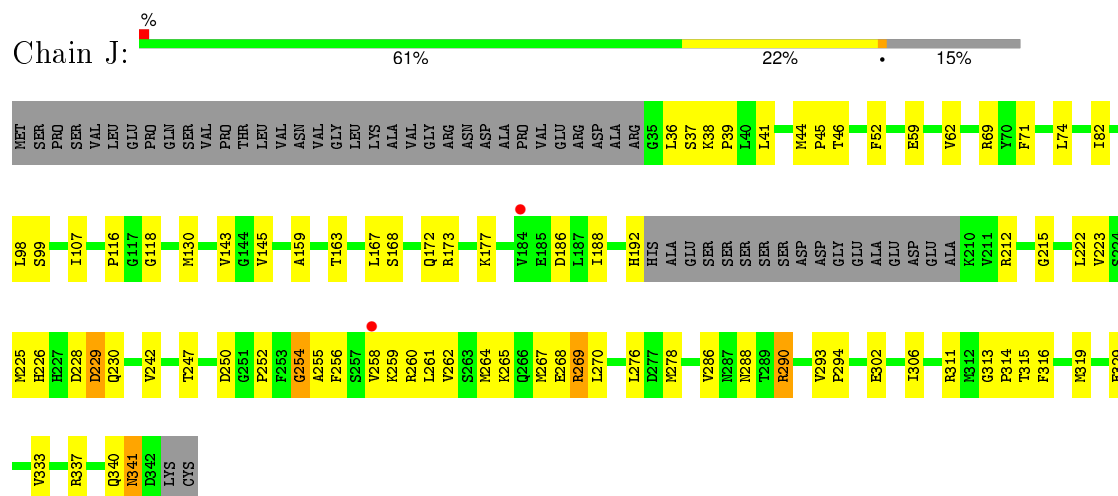
- Molecule 1: CyPBP37 protein

Chain I: 59% 25% 15%

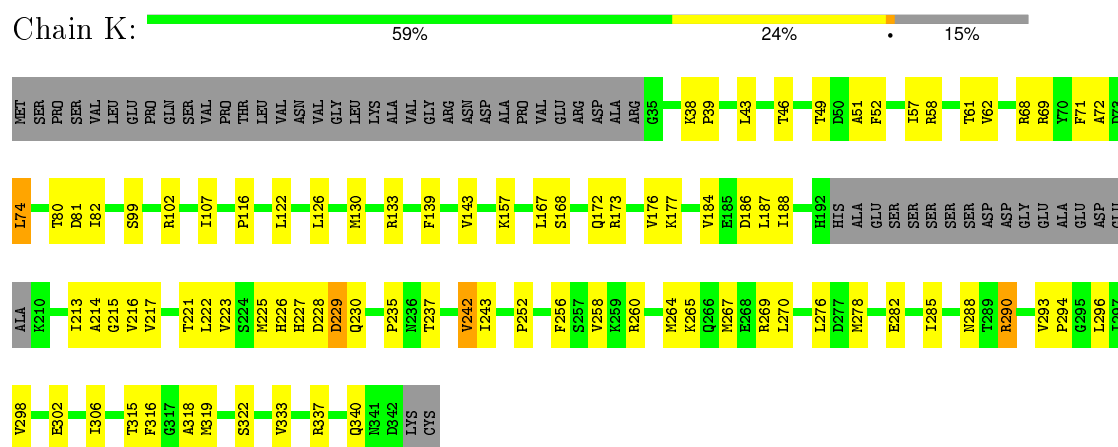




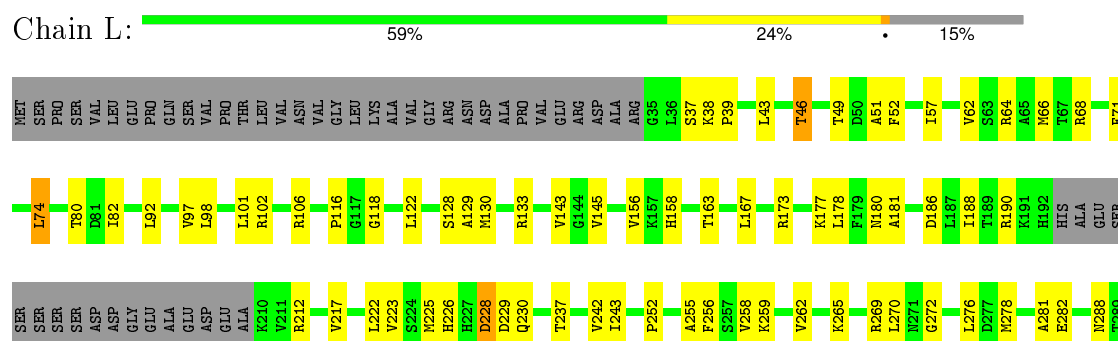
• Molecule 1: CyPBP37 protein



• Molecule 1: CyPBP37 protein



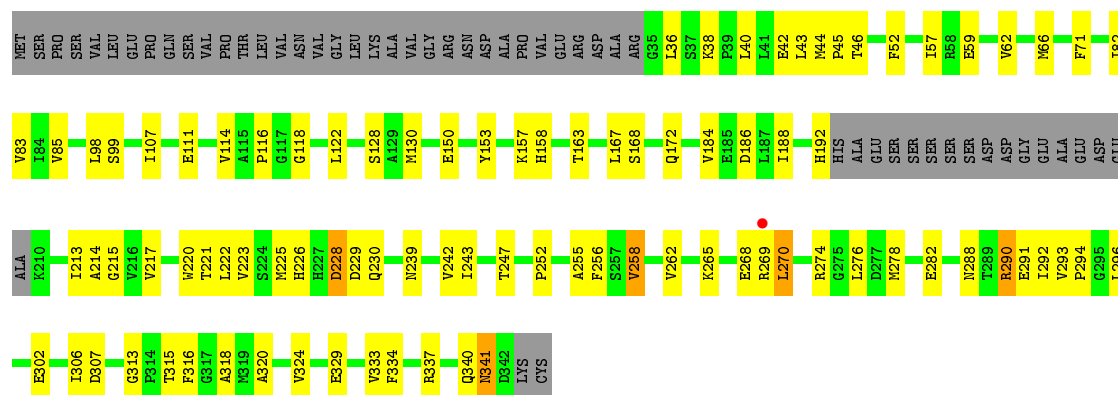
• Molecule 1: CyPBP37 protein





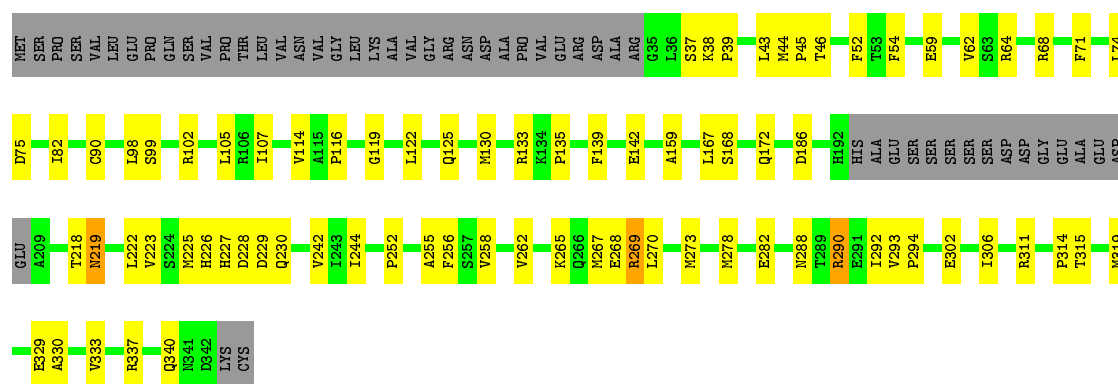
• Molecule 1: CyPBP37 protein

Chain M: 58% 25% 15%



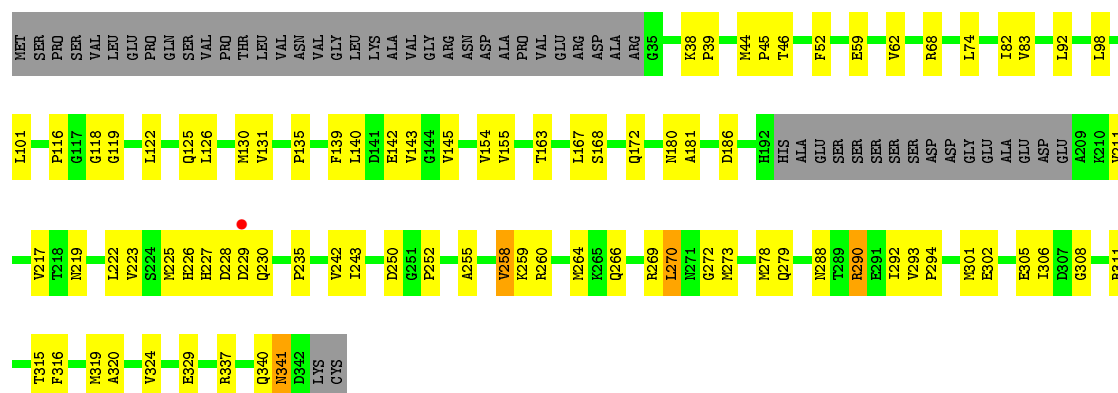
• Molecule 1: CyPBP37 protein

Chain N: 62% 22% 15%

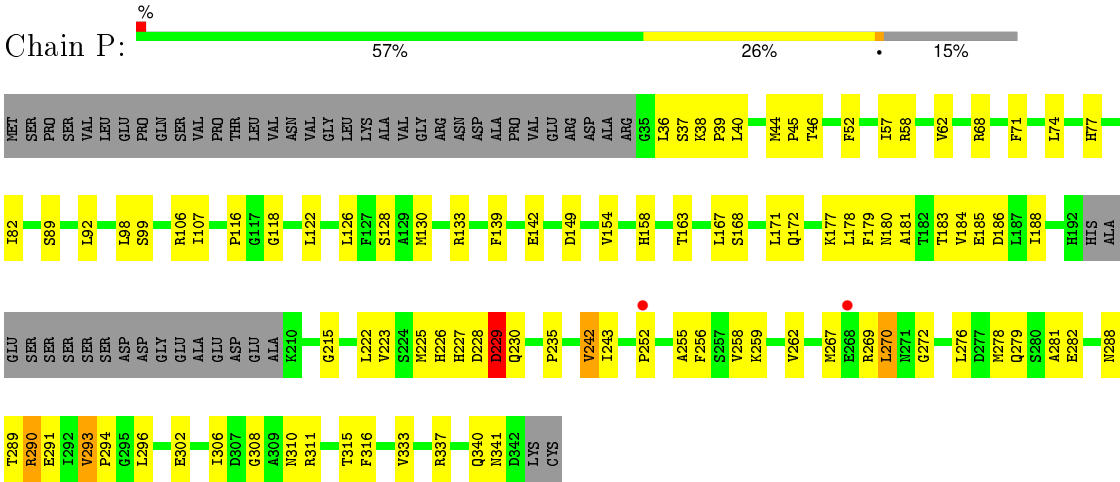


• Molecule 1: CyPBP37 protein

Chain O: 60% 24% 15%



● Molecule 1: CyPBP37 protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	158.24Å 125.91Å 158.21Å 90.00° 90.22° 90.00°	Depositor
Resolution (Å)	49.98 – 2.70 49.98 – 2.70	Depositor EDS
% Data completeness (in resolution range)	92.2 (49.98-2.70) 92.0 (49.98-2.70)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.02 (at 2.69Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.202 , 0.246 0.203 , 0.247	Depositor DCC
R_{free} test set	15651 reflections (9.96%)	DCC
Wilson B-factor (Å ²)	34.2	Xtriage
Anisotropy	0.280	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 14.2	EDS
Estimated twinning fraction	0.024 for -l,k,h 0.417 for -h,-k,l 0.024 for l,-k,h	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 165605 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	36053	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.60% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: AHZ, FE2, DHA

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	0.37	0/2223	0.65	0/3011
1	B	0.36	0/2218	0.63	0/3004
1	C	0.37	0/2223	0.64	1/3011 (0.0%)
1	D	0.37	0/2223	0.62	0/3011
1	E	0.37	0/2218	0.64	1/3004 (0.0%)
1	F	0.36	0/2223	0.65	0/3011
1	G	0.36	0/2218	0.64	0/3004
1	H	0.36	0/2218	0.63	0/3004
1	I	0.37	0/2218	0.63	0/3004
1	J	0.37	0/2218	0.63	1/3004 (0.0%)
1	K	0.37	0/2218	0.64	0/3004
1	L	0.36	0/2218	0.62	0/3004
1	M	0.36	0/2218	0.65	0/3004
1	N	0.36	0/2223	0.64	0/3011
1	O	0.37	0/2223	0.63	0/3011
1	P	0.36	0/2218	0.62	0/3004
All	All	0.37	0/35518	0.63	3/48106 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	254	GLY	N-CA-C	5.22	126.15	113.10
1	E	254	GLY	N-CA-C	5.17	126.03	113.10
1	J	254	GLY	N-CA-C	5.08	125.81	113.10

There are no chirality outliers.

There are no planarity outliers.

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	2193	0	2207	83	0
1	B	2188	0	2202	81	0
1	C	2193	0	2207	85	0
1	D	2193	0	2207	77	0
1	E	2188	0	2202	65	0
1	F	2193	0	2207	75	0
1	G	2188	0	2202	80	0
1	H	2188	0	2202	83	0
1	I	2188	0	2202	76	0
1	J	2188	0	2202	75	0
1	K	2188	0	2202	87	0
1	L	2188	0	2202	86	0
1	M	2188	0	2202	90	0
1	N	2193	0	2207	72	0
1	O	2193	0	2207	78	0
1	P	2188	0	2202	91	0
2	A	38	0	19	3	0
2	B	38	0	19	2	0
2	C	38	0	19	3	0
2	D	38	0	19	0	0
2	E	38	0	19	1	0
2	F	38	0	19	2	0
2	G	38	0	19	3	0
2	H	38	0	19	3	0
2	I	38	0	19	4	0
2	J	38	0	19	2	0
2	K	38	0	19	0	0
2	L	38	0	19	3	0
2	M	38	0	19	3	0
2	N	38	0	19	0	0
2	O	38	0	19	3	0
2	P	38	0	19	2	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
3	I	1	0	0	0	0
3	J	1	0	0	0	0
3	K	2	0	0	0	0
3	L	1	0	0	0	0
3	M	2	0	0	0	0
3	N	1	0	0	0	0
4	A	30	0	0	4	0
4	B	16	0	0	1	0
4	C	32	0	0	2	0
4	D	21	0	0	0	0
4	E	29	0	0	0	0
4	F	24	0	0	1	0
4	G	21	0	0	0	0
4	H	23	0	0	0	0
4	I	44	0	0	0	0
4	J	20	0	0	3	0
4	K	25	0	0	3	0
4	L	21	0	0	1	0
4	M	19	0	0	1	0
4	N	17	0	0	2	0
4	O	25	0	0	0	0
4	P	24	0	0	0	0
All	All	36053	0	35566	1102	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 15.

The worst 5 of 1102 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:H:258:VAL:HG12	1:H:270:LEU:HD11	1.31	1.10
1:I:258:VAL:HG13	1:I:270:LEU:HD11	1.42	1.01
1:H:46:THR:HG22	1:H:52:PHE:HB2	1.44	1.00
1:C:258:VAL:HG12	1:C:270:LEU:HD11	1.45	0.98
1:A:337:ARG:HH11	1:A:340:GLN:HE22	1.12	0.96

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	287/344 (83%)	270 (94%)	16 (6%)	1 (0%)	46	75
1	B	286/344 (83%)	268 (94%)	18 (6%)	0	100	100
1	C	287/344 (83%)	266 (93%)	20 (7%)	1 (0%)	46	75
1	D	287/344 (83%)	266 (93%)	20 (7%)	1 (0%)	46	75
1	E	286/344 (83%)	266 (93%)	17 (6%)	3 (1%)	19	45
1	F	287/344 (83%)	268 (93%)	18 (6%)	1 (0%)	46	75
1	G	286/344 (83%)	266 (93%)	17 (6%)	3 (1%)	19	45
1	H	286/344 (83%)	266 (93%)	20 (7%)	0	100	100
1	I	286/344 (83%)	268 (94%)	17 (6%)	1 (0%)	46	75
1	J	286/344 (83%)	269 (94%)	15 (5%)	2 (1%)	26	55
1	K	286/344 (83%)	264 (92%)	20 (7%)	2 (1%)	26	55
1	L	286/344 (83%)	266 (93%)	19 (7%)	1 (0%)	46	75
1	M	286/344 (83%)	267 (93%)	17 (6%)	2 (1%)	26	55
1	N	287/344 (83%)	264 (92%)	20 (7%)	3 (1%)	19	45
1	O	287/344 (83%)	269 (94%)	17 (6%)	1 (0%)	46	75
1	P	286/344 (83%)	268 (94%)	17 (6%)	1 (0%)	46	75
All	All	4582/5504 (83%)	4271 (93%)	288 (6%)	23 (0%)	34	63

5 of 23 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	269	ARG
1	E	250	ASP
1	E	229	ASP
1	F	229	ASP
1	G	269	ARG

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	235/280 (84%)	230 (98%)	5 (2%)	61	87
1	B	235/280 (84%)	231 (98%)	4 (2%)	68	90
1	C	235/280 (84%)	234 (100%)	1 (0%)	93	98
1	D	235/280 (84%)	230 (98%)	5 (2%)	61	87
1	E	235/280 (84%)	233 (99%)	2 (1%)	84	95
1	F	235/280 (84%)	230 (98%)	5 (2%)	61	87
1	G	235/280 (84%)	232 (99%)	3 (1%)	76	92
1	H	235/280 (84%)	231 (98%)	4 (2%)	68	90
1	I	235/280 (84%)	231 (98%)	4 (2%)	68	90
1	J	235/280 (84%)	229 (97%)	6 (3%)	54	83
1	K	235/280 (84%)	232 (99%)	3 (1%)	76	92
1	L	235/280 (84%)	230 (98%)	5 (2%)	61	87
1	M	235/280 (84%)	229 (97%)	6 (3%)	54	83
1	N	235/280 (84%)	232 (99%)	3 (1%)	76	92
1	O	235/280 (84%)	229 (97%)	6 (3%)	54	83
1	P	235/280 (84%)	227 (97%)	8 (3%)	44	75
All	All	3760/4480 (84%)	3690 (98%)	70 (2%)	65	88

5 of 70 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	135	PRO
1	K	74	LEU
1	P	229	ASP
1	I	290	ARG
1	J	229	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	340	GLN
1	J	340	GLN
1	O	341	ASN
1	H	341	ASN
1	I	310	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

16 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	DHA	A	232	1	4,4,5	1.65	1 (25%)	3,4,6	3.27	2 (66%)
1	DHA	B	232	1	4,4,5	1.77	2 (50%)	3,4,6	3.37	2 (66%)
1	DHA	C	232	1	4,4,5	1.72	1 (25%)	3,4,6	3.43	2 (66%)
1	DHA	D	232	1	4,4,5	1.91	2 (50%)	3,4,6	3.47	2 (66%)
1	DHA	E	232	1	4,4,5	1.96	2 (50%)	3,4,6	3.48	2 (66%)
1	DHA	F	232	1	4,4,5	1.95	2 (50%)	3,4,6	3.39	2 (66%)
1	DHA	G	232	1	4,4,5	1.63	1 (25%)	3,4,6	3.41	2 (66%)
1	DHA	H	232	1	4,4,5	1.70	2 (50%)	3,4,6	3.21	2 (66%)
1	DHA	I	232	1	4,4,5	1.80	1 (25%)	3,4,6	3.32	2 (66%)
1	DHA	J	232	1	4,4,5	1.69	1 (25%)	3,4,6	3.43	2 (66%)
1	DHA	K	232	1	4,4,5	1.74	2 (50%)	3,4,6	3.31	2 (66%)
1	DHA	L	232	1	4,4,5	1.62	1 (25%)	3,4,6	3.28	2 (66%)
1	DHA	M	232	1	4,4,5	1.78	1 (25%)	3,4,6	3.37	2 (66%)
1	DHA	N	232	1	4,4,5	1.73	1 (25%)	3,4,6	3.33	2 (66%)
1	DHA	O	232	1	4,4,5	1.58	2 (50%)	3,4,6	3.34	2 (66%)
1	DHA	P	232	1	4,4,5	1.90	2 (50%)	3,4,6	3.55	2 (66%)

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
1	DHA	A	232	1	-	0/0/2/4	0/0/0/0
1	DHA	B	232	1	-	0/0/2/4	0/0/0/0
1	DHA	C	232	1	-	0/0/2/4	0/0/0/0
1	DHA	D	232	1	-	0/0/2/4	0/0/0/0
1	DHA	E	232	1	-	0/0/2/4	0/0/0/0
1	DHA	F	232	1	-	0/0/2/4	0/0/0/0
1	DHA	G	232	1	-	0/0/2/4	0/0/0/0
1	DHA	H	232	1	-	0/0/2/4	0/0/0/0
1	DHA	I	232	1	-	0/0/2/4	0/0/0/0
1	DHA	J	232	1	-	0/0/2/4	0/0/0/0
1	DHA	K	232	1	-	0/0/2/4	0/0/0/0
1	DHA	L	232	1	-	0/0/2/4	0/0/0/0
1	DHA	M	232	1	-	0/0/2/4	0/0/0/0
1	DHA	N	232	1	-	0/0/2/4	0/0/0/0
1	DHA	O	232	1	-	0/0/2/4	0/0/0/0
1	DHA	P	232	1	-	0/0/2/4	0/0/0/0

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	232	DHA	O-C	2.12	1.27	1.22
1	H	232	DHA	C-CA	2.15	1.48	1.45
1	P	232	DHA	O-C	2.18	1.27	1.22
1	O	232	DHA	C-CA	2.19	1.48	1.45
1	O	232	DHA	O-C	2.19	1.27	1.22

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	P	232	DHA	O-C-CA	-4.90	115.89	125.35
1	D	232	DHA	O-C-CA	-4.75	116.17	125.35
1	E	232	DHA	O-C-CA	-4.71	116.27	125.35
1	B	232	DHA	O-C-CA	-4.61	116.45	125.35
1	J	232	DHA	O-C-CA	-4.61	116.46	125.35

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 32 ligands modelled in this entry, 16 are monoatomic - leaving 16 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	$\# Z > 2$
2	AHZ	A	500	3	29,41,41	1.48	3 (10%)	31,62,62	2.30	6 (19%)
2	AHZ	B	500	3	29,41,41	1.34	3 (10%)	31,62,62	2.27	6 (19%)
2	AHZ	C	500	3	29,41,41	1.30	5 (17%)	31,62,62	2.27	6 (19%)
2	AHZ	D	500	3	29,41,41	1.43	3 (10%)	31,62,62	2.26	5 (16%)
2	AHZ	E	500	3	29,41,41	1.34	4 (13%)	31,62,62	2.33	6 (19%)
2	AHZ	F	500	3	29,41,41	1.25	4 (13%)	31,62,62	2.27	7 (22%)
2	AHZ	G	500	3	29,41,41	1.39	5 (17%)	31,62,62	2.30	6 (19%)
2	AHZ	H	500	3	29,41,41	1.46	5 (17%)	31,62,62	2.33	5 (16%)
2	AHZ	I	500	3	29,41,41	1.36	5 (17%)	31,62,62	2.35	5 (16%)
2	AHZ	J	500	3	29,41,41	1.40	4 (13%)	31,62,62	2.38	5 (16%)
2	AHZ	K	500	3	29,41,41	1.32	4 (13%)	31,62,62	2.34	6 (19%)
2	AHZ	L	500	3	29,41,41	1.40	4 (13%)	31,62,62	2.38	5 (16%)
2	AHZ	M	500	3	29,41,41	1.31	3 (10%)	31,62,62	2.27	6 (19%)
2	AHZ	N	500	3	29,41,41	1.36	4 (13%)	31,62,62	2.28	7 (22%)
2	AHZ	O	500	3	29,41,41	1.39	4 (13%)	31,62,62	2.36	6 (19%)
2	AHZ	P	500	3	29,41,41	1.44	4 (13%)	31,62,62	2.27	8 (25%)

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
2	AHZ	A	500	3	-	0/18/43/43	0/4/4/4
2	AHZ	B	500	3	-	0/18/43/43	0/4/4/4
2	AHZ	C	500	3	-	0/18/43/43	0/4/4/4
2	AHZ	D	500	3	-	0/18/43/43	0/4/4/4
2	AHZ	E	500	3	-	0/18/43/43	0/4/4/4
2	AHZ	F	500	3	-	0/18/43/43	0/4/4/4
2	AHZ	G	500	3	-	0/18/43/43	0/4/4/4
2	AHZ	H	500	3	-	0/18/43/43	0/4/4/4
2	AHZ	I	500	3	-	0/18/43/43	0/4/4/4
2	AHZ	J	500	3	-	0/18/43/43	0/4/4/4
2	AHZ	K	500	3	-	0/18/43/43	0/4/4/4
2	AHZ	L	500	3	-	0/18/43/43	0/4/4/4
2	AHZ	M	500	3	-	0/18/43/43	0/4/4/4
2	AHZ	N	500	3	-	0/18/43/43	0/4/4/4
2	AHZ	O	500	3	-	0/18/43/43	0/4/4/4
2	AHZ	P	500	3	-	0/18/43/43	0/4/4/4

The worst 5 of 64 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	500	AHZ	C2T-S1T	-4.48	1.67	1.73
2	O	500	AHZ	C2T-S1T	-3.72	1.68	1.73
2	K	500	AHZ	C2T-S1T	-3.53	1.68	1.73
2	B	500	AHZ	C2T-S1T	-3.52	1.68	1.73
2	H	500	AHZ	C2T-S1T	-3.45	1.68	1.73

The worst 5 of 95 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	500	AHZ	N3-C2-N1	-10.97	120.49	128.89
2	I	500	AHZ	N3-C2-N1	-10.83	120.60	128.89
2	G	500	AHZ	N3-C2-N1	-10.81	120.62	128.89
2	O	500	AHZ	N3-C2-N1	-10.73	120.68	128.89
2	J	500	AHZ	N3-C2-N1	-10.72	120.69	128.89

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

13 monomers are involved in 34 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	500	AHZ	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	500	AHZ	2	0
2	C	500	AHZ	3	0
2	E	500	AHZ	1	0
2	F	500	AHZ	2	0
2	G	500	AHZ	3	0
2	H	500	AHZ	3	0
2	I	500	AHZ	4	0
2	J	500	AHZ	2	0
2	L	500	AHZ	3	0
2	M	500	AHZ	3	0
2	O	500	AHZ	3	0
2	P	500	AHZ	2	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	291/344 (84%)	-0.03	1 (0%) 94 95	24, 33, 52, 69	0
1	B	290/344 (84%)	-0.03	1 (0%) 94 95	26, 34, 52, 68	0
1	C	291/344 (84%)	-0.02	0 100 100	25, 33, 52, 69	0
1	D	291/344 (84%)	-0.03	2 (0%) 89 90	26, 33, 53, 68	0
1	E	290/344 (84%)	-0.02	3 (1%) 84 85	26, 33, 52, 68	0
1	F	291/344 (84%)	-0.05	1 (0%) 94 95	26, 33, 52, 68	0
1	G	290/344 (84%)	-0.02	0 100 100	26, 33, 52, 69	0
1	H	290/344 (84%)	-0.03	1 (0%) 94 95	26, 33, 53, 68	0
1	I	290/344 (84%)	-0.12	0 100 100	25, 32, 51, 68	0
1	J	290/344 (84%)	0.01	2 (0%) 89 90	25, 33, 52, 68	0
1	K	290/344 (84%)	-0.07	0 100 100	25, 33, 52, 68	0
1	L	290/344 (84%)	-0.08	0 100 100	26, 33, 53, 68	0
1	M	290/344 (84%)	-0.03	1 (0%) 94 95	25, 33, 52, 68	0
1	N	291/344 (84%)	-0.04	0 100 100	25, 33, 51, 69	0
1	O	291/344 (84%)	-0.09	1 (0%) 94 95	25, 32, 52, 69	0
1	P	290/344 (84%)	-0.04	2 (0%) 89 90	26, 33, 52, 68	0
All	All	4646/5504 (84%)	-0.04	15 (0%) 94 95	24, 33, 53, 69	0

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	209	ALA	4.4
1	A	268	GLU	3.3
1	F	209	ALA	3.0
1	H	258	VAL	2.9
1	J	258	VAL	2.7

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	DHA	H	232	5/6	0.97	0.22	-	47,47,47,49	0
1	DHA	J	232	5/6	0.96	0.19	-	48,48,49,50	0
1	DHA	D	232	5/6	0.95	0.24	-	48,48,49,50	0
1	DHA	F	232	5/6	0.92	0.15	-	47,48,48,49	0
1	DHA	B	232	5/6	0.96	0.18	-	47,47,48,48	0
1	DHA	M	232	5/6	0.94	0.23	-	48,48,49,49	0
1	DHA	O	232	5/6	0.98	0.19	-	48,48,49,49	0
1	DHA	I	232	5/6	0.97	0.17	-	46,47,48,49	0
1	DHA	K	232	5/6	0.97	0.13	-	46,47,47,49	0
1	DHA	E	232	5/6	0.93	0.26	-	47,48,49,49	0
1	DHA	P	232	5/6	0.95	0.22	-	47,48,48,49	0
1	DHA	G	232	5/6	0.96	0.16	-	46,47,48,50	0
1	DHA	A	232	5/6	0.97	0.14	-	45,46,47,48	0
1	DHA	L	232	5/6	0.97	0.20	-	46,48,49,50	0
1	DHA	C	232	5/6	0.97	0.20	-	46,47,48,48	0
1	DHA	N	232	5/6	0.97	0.17	-	46,46,47,48	0

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
2	AHZ	P	500	38/38	0.96	0.18	0.57	30,42,55,57	0
2	AHZ	H	500	38/38	0.95	0.18	0.51	33,37,59,61	0
2	AHZ	D	500	38/38	0.97	0.18	0.43	33,42,56,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	AHZ	L	500	38/38	0.95	0.16	0.39	34,40,63,64	0
2	AHZ	G	500	38/38	0.97	0.17	0.28	23,33,51,51	0
2	AHZ	B	500	38/38	0.94	0.17	0.28	39,48,56,58	0
2	AHZ	M	500	38/38	0.95	0.17	0.26	35,47,61,62	0
2	AHZ	I	500	38/38	0.97	0.16	0.21	22,29,47,49	0
2	AHZ	K	500	38/38	0.97	0.17	0.11	33,36,48,50	0
2	AHZ	F	500	38/38	0.97	0.16	-0.03	26,32,48,50	0
2	AHZ	E	500	38/38	0.96	0.17	-0.16	34,39,57,59	0
2	AHZ	A	500	38/38	0.98	0.16	-0.20	27,31,36,37	0
2	AHZ	J	500	38/38	0.96	0.16	-0.33	33,38,55,57	0
2	AHZ	O	500	38/38	0.97	0.15	-0.36	26,33,40,41	0
2	AHZ	N	500	38/38	0.97	0.15	-0.49	26,32,47,49	0
2	AHZ	C	500	38/38	0.97	0.15	-0.52	23,34,50,51	0
3	FE2	C	345	1/1	0.60	0.13	-	100,100,100,100	0
3	FE2	A	345	1/1	0.75	0.13	-	100,100,100,100	0
3	FE2	L	345	1/1	0.75	0.12	-	100,100,100,100	0
3	FE2	N	345	1/1	0.62	0.15	-	100,100,100,100	0
3	FE2	E	345	1/1	0.85	0.07	-	100,100,100,100	0
3	FE2	I	345	1/1	0.80	0.08	-	100,100,100,100	0
3	FE2	M	345	1/1	0.95	0.12	-	91,91,91,91	0
3	FE2	K	345	1/1	0.59	0.14	-	99,99,99,99	0
3	FE2	B	345	1/1	0.84	0.15	-	93,93,93,93	0
3	FE2	D	345	1/1	0.83	0.07	-	97,97,97,97	0
3	FE2	G	345	1/1	0.71	0.14	-	87,87,87,87	0
3	FE2	F	345	1/1	0.88	0.10	-	88,88,88,88	0
3	FE2	H	345	1/1	0.78	0.10	-	100,100,100,100	0
3	FE2	K	346	1/1	0.87	0.11	-	100,100,100,100	0
3	FE2	M	346	1/1	0.57	0.13	-	100,100,100,100	0
3	FE2	J	345	1/1	0.70	0.15	-	100,100,100,100	0

6.5 Other polymers ⓘ

There are no such residues in this entry.