



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 09:02 AM UTC

PDB ID : 6AI0 / pdb_00006ai0
Title : Structure of the 328-692 fragment of FlhA (orthorhombic form)
Authors : Ogawa, Y.; Kinoshita, M.; Minamino, T.; Imada, K.
Deposited on : 2018-08-21
Resolution : 2.40 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

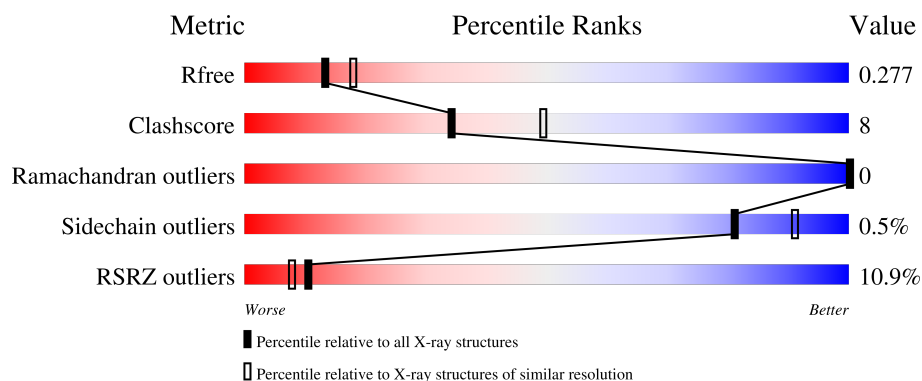
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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 $\leq 5\%$. 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	369	8% 73% 17% 10%
1	B	369	12% 73% 17% 9%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5357 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 Flagellar biosynthesis protein FlhA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	333	Total	C	N	O	S	0	0	0
			2576	1631	460	476	9			
1	B	335	Total	C	N	O	S	0	0	0
			2594	1642	464	479	9			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	324	GLY	-	expression tag	UNP P40729
A	325	PRO	-	expression tag	UNP P40729
A	326	LEU	-	expression tag	UNP P40729
A	327	GLY	-	expression tag	UNP P40729
B	324	GLY	-	expression tag	UNP P40729
B	325	PRO	-	expression tag	UNP P40729
B	326	LEU	-	expression tag	UNP P40729
B	327	GLY	-	expression tag	UNP P40729

- Molecule 2 is (4R)-2-METHYLPENTANE-2,4-DIOL (CCD ID: MRD) (formula: C₆H₁₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			8	6	2		
2	B	1	Total	C	O	0	0
			8	6	2		

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Ca	0	0
			2	2		
3	B	1	Total	Ca	0	0
			1	1		

- Molecule 4 is water.

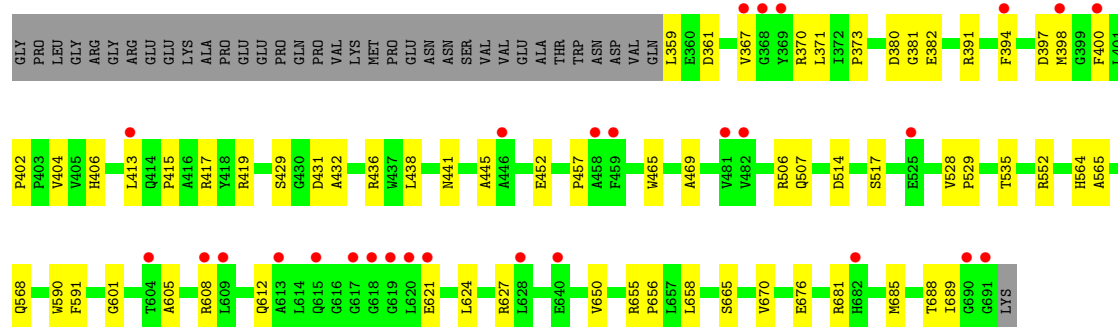
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	82	Total	O	0	0
			82	82		
4	B	86	Total	O	0	0
			86	86		

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.

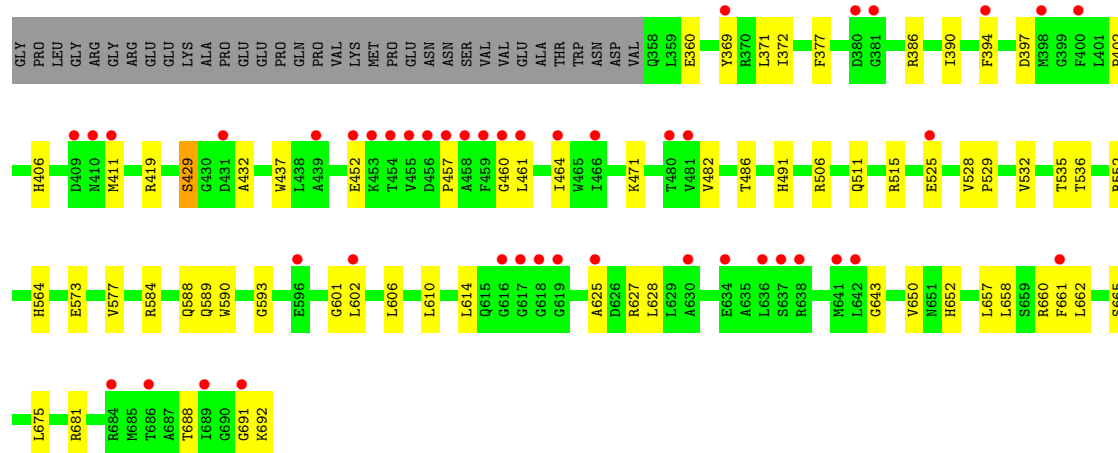
• Molecule 1: Flagellar biosynthesis protein FlhA

Chain A: 



• Molecule 1: Flagellar biosynthesis protein FlhA

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	52.92Å 93.08Å 187.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.28 – 2.40 41.28 – 2.40	Depositor EDS
% Data completeness (in resolution range)	98.8 (41.28-2.40) 98.7 (41.28-2.40)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.07 (at 2.39Å)	Xtriage
Refinement program	PHENIX 1.11.1 _2575	Depositor
R, R_{free}	0.241 , 0.277 0.241 , 0.277	Depositor DCC
R_{free} test set	1873 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	39.9	Xtriage
Anisotropy	0.608	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 31.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5357	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.11% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: MRD, CA

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.13	0/2620	0.34	0/3557
1	B	0.15	0/2638	0.36	0/3580
All	All	0.14	0/5258	0.35	0/7137

There are no bond length outliers.

There are no bond angle outliers.

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	2576	0	2643	43	0
1	B	2594	0	2664	41	0
2	A	8	0	14	0	0
2	B	8	0	14	0	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
4	A	82	0	0	9	0
4	B	86	0	0	5	0
All	All	5357	0	5335	80	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 8.

All (80) 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:B:573:GLU:OE2	4:B:901:HOH:O	1.86	0.93
1:A:382:GLU:OE1	4:A:901:HOH:O	1.93	0.85
1:B:525:GLU:OE2	4:B:902:HOH:O	1.95	0.85
1:A:676:GLU:OE2	4:A:902:HOH:O	1.95	0.83
1:A:367:VAL:HG13	1:A:371:LEU:HB2	1.71	0.71
1:A:591:PHE:O	1:A:681:ARG:NH1	2.19	0.69
1:B:602:LEU:HD21	1:B:610:LEU:HD12	1.74	0.68
1:A:665:SER:OG	4:A:904:HOH:O	2.12	0.68
1:A:621:GLU:HG2	1:A:624:LEU:H	1.58	0.68
1:A:601:GLY:HA3	1:A:685:MET:HE2	1.76	0.67
1:A:469:ALA:O	4:A:906:HOH:O	2.13	0.67
1:A:431:ASP:OD2	4:A:905:HOH:O	2.12	0.66
1:A:506:ARG:NH2	1:A:535:THR:OG1	2.28	0.66
1:A:605:ALA:HA	1:A:608:ARG:HE	1.60	0.66
1:A:359:LEU:N	4:A:915:HOH:O	2.32	0.62
1:A:391:ARG:HG2	1:A:402:PRO:HG2	1.83	0.60
1:B:506:ARG:NH2	1:B:535:THR:OG1	2.33	0.60
1:A:650:VAL:HG11	1:A:658:LEU:HD12	1.84	0.59
1:B:397:ASP:O	1:B:552:ARG:NH1	2.36	0.59
1:B:460:GLY:O	1:B:461:LEU:HD12	2.03	0.58
1:B:593:GLY:O	1:B:681:ARG:NH1	2.24	0.57
1:B:660:ARG:NH2	4:B:914:HOH:O	2.37	0.56
1:A:413:LEU:HD21	1:A:419:ARG:HG3	1.88	0.56
1:B:606:LEU:HD21	1:B:628:LEU:HD21	1.88	0.56
1:B:457:PRO:HB2	1:B:491:HIS:CG	2.41	0.55
1:A:608:ARG:O	1:A:612:GLN:HG2	2.08	0.53
1:B:625:ALA:HB1	1:B:661:PHE:HZ	1.74	0.53
1:A:370:ARG:HD2	1:A:415:PRO:HB3	1.92	0.52
1:B:460:GLY:O	1:B:461:LEU:CD1	2.57	0.51
1:B:369:TYR:HD2	1:B:411:MET:HE1	1.75	0.50
1:B:661:PHE:HD2	1:B:662:LEU:HD12	1.76	0.50
1:B:643:GLY:O	4:B:904:HOH:O	2.19	0.50
1:A:417:ARG:NH2	1:A:429:SER:HB2	2.29	0.48
1:A:457:PRO:O	4:A:908:HOH:O	2.20	0.47
1:A:565:ALA:HA	1:A:568:GLN:O	2.15	0.47
1:A:361:ASP:CG	1:B:406:HIS:HE2	2.22	0.47
1:B:614:LEU:HD11	1:B:657:LEU:HD22	1.96	0.47
1:B:371:LEU:HD21	1:B:432:ALA:HB3	1.95	0.47
1:B:452:GLU:O	1:B:464:ILE:HG23	2.15	0.47
1:B:584:ARG:NH1	1:B:588:GLN:HG3	2.30	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:394:PHE:HD2	1:A:402:PRO:HD3	1.79	0.46
1:A:436:ARG:NH1	1:A:452:GLU:OE2	2.49	0.46
1:A:380:ASP:OD1	1:A:381:GLY:N	2.49	0.46
1:A:359:LEU:HD23	1:B:372:ILE:HG23	1.98	0.45
1:A:397:ASP:O	1:A:552:ARG:NH1	2.48	0.45
1:B:650:VAL:HG11	1:B:658:LEU:HD12	1.98	0.45
1:A:590:TRP:CH2	1:A:670:VAL:HG21	2.52	0.45
1:A:624:LEU:HA	1:A:627:ARG:HB2	1.99	0.44
1:B:457:PRO:HB2	1:B:491:HIS:ND1	2.32	0.44
1:A:370:ARG:O	1:A:373:PRO:HD2	2.17	0.44
1:B:482:VAL:HG13	1:B:486:THR:HB	2.00	0.44
1:B:369:TYR:CD2	1:B:411:MET:HE1	2.52	0.44
1:A:404:VAL:HA	4:A:912:HOH:O	2.18	0.43
1:B:652:HIS:CG	1:B:675:LEU:HD12	2.53	0.43
1:B:419:ARG:HG2	1:B:429:SER:HB3	2.00	0.43
1:A:438:LEU:HD13	1:A:465:TRP:CE2	2.54	0.43
1:A:394:PHE:CE1	1:A:398:MET:HG3	2.54	0.43
1:B:564:HIS:CG	1:B:577:VAL:HG11	2.55	0.42
1:A:394:PHE:HE2	1:A:400:PHE:CE1	2.38	0.42
1:B:692:LYS:HE2	1:B:692:LYS:HB3	1.83	0.42
1:B:437:TRP:CE2	1:B:471:LYS:HD2	2.55	0.42
1:B:532:VAL:HG13	1:B:536:THR:OG1	2.20	0.42
1:A:507:GLN:HB3	1:B:377:PHE:CZ	2.55	0.41
1:B:627:ARG:HD3	4:B:913:HOH:O	2.19	0.41
1:A:655:ARG:HB3	1:A:656:PRO:HD3	2.01	0.41
1:B:606:LEU:HD13	1:B:691:GLY:HA2	2.02	0.41
1:B:386:ARG:O	1:B:390:ILE:HG12	2.21	0.41
1:B:528:VAL:HA	1:B:529:PRO:HA	1.79	0.41
1:B:589:GLN:HE21	1:B:590:TRP:NE1	2.17	0.41
1:A:514:ASP:O	1:A:517:SER:OG	2.37	0.41
1:A:528:VAL:HA	1:A:529:PRO:HA	1.78	0.41
1:B:511:GLN:HB3	1:B:515:ARG:NH2	2.36	0.41
1:B:601:GLY:O	1:B:688:THR:HA	2.20	0.41
1:A:370:ARG:HG3	1:A:415:PRO:C	2.46	0.41
1:A:406:HIS:CE1	1:B:406:HIS:CE1	3.09	0.41
1:A:564:HIS:NE2	4:A:907:HOH:O	2.19	0.41
1:A:371:LEU:HD21	1:A:432:ALA:HB3	2.02	0.40
1:A:441:ASN:CG	1:A:445:ALA:HB3	2.46	0.40
1:B:394:PHE:HD1	1:B:402:PRO:HD3	1.87	0.40
1:A:688:THR:HG22	1:A:689:ILE:H	1.86	0.40

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	331/369 (90%)	322 (97%)	9 (3%)	0	100	100
1	B	333/369 (90%)	321 (96%)	12 (4%)	0	100	100
All	All	664/738 (90%)	643 (97%)	21 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	277/308 (90%)	277 (100%)	0	100	100
1	B	279/308 (91%)	276 (99%)	3 (1%)	65	82
All	All	556/616 (90%)	553 (100%)	3 (0%)	81	91

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	360	GLU
1	B	429	SER
1	B	665	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	475	GLN
1	A	615	GLN
1	A	639	GLN
1	B	518	GLN
1	B	633	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 3 are monoatomic - leaving 2 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	MRD	A	801	-	7,7,7	0.30	0	9,10,10	0.34	0
2	MRD	B	801	-	7,7,7	0.29	0	9,10,10	0.29	0

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	MRD	A	801	-	-	1/5/5/5	-
2	MRD	B	801	-	-	0/5/5/5	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	801	MRD	C2-C3-C4-O4

There are no ring outliers.

No monomer is involved in short contacts.

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, 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	333/369 (90%)	0.67	28 (8%) 17 14	26, 48, 65, 79	0
1	B	335/369 (90%)	0.83	45 (13%) 7 5	24, 48, 69, 80	0
All	All	668/738 (90%)	0.75	73 (10%) 10 8	24, 48, 68, 80	0

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	618	GLY	4.9
1	B	459	PHE	4.6
1	A	691	GLY	4.5
1	B	616	GLY	4.3
1	B	617	GLY	4.2
1	B	452	GLU	4.2
1	B	369	TYR	4.1
1	B	619	GLY	4.0
1	B	691	GLY	4.0
1	B	409	ASP	3.7
1	A	369	TYR	3.7
1	B	641	MET	3.4
1	B	525	GLU	3.1
1	B	380	ASP	3.0
1	B	637	SER	3.0
1	A	690	GLY	3.0
1	B	461	LEU	3.0
1	B	481	VAL	2.9
1	B	464	ILE	2.9
1	B	642	LEU	2.8
1	A	613	ALA	2.8
1	B	411	MET	2.8
1	B	394	PHE	2.8
1	A	368	GLY	2.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	634	GLU	2.7
1	A	459	PHE	2.7
1	A	618	GLY	2.6
1	A	394	PHE	2.6
1	B	400	PHE	2.6
1	B	602	LEU	2.6
1	B	454	THR	2.6
1	A	621	GLU	2.6
1	A	398	MET	2.5
1	A	640	GLU	2.5
1	B	381	GLY	2.5
1	A	620	LEU	2.5
1	A	604	THR	2.5
1	A	682	HIS	2.4
1	A	446	ALA	2.4
1	A	525	GLU	2.4
1	A	367	VAL	2.4
1	B	630	ALA	2.4
1	B	457	PRO	2.4
1	B	456	ASP	2.4
1	A	608	ARG	2.4
1	B	596	GLU	2.4
1	B	460	GLY	2.3
1	B	455	VAL	2.3
1	B	439	ALA	2.3
1	B	458	ALA	2.3
1	B	638	ARG	2.3
1	A	609	LEU	2.3
1	B	431	ASP	2.3
1	A	617	GLY	2.3
1	B	689	ILE	2.3
1	B	480	THR	2.2
1	B	636	LEU	2.2
1	A	628	LEU	2.2
1	B	466	ILE	2.2
1	B	661	PHE	2.2
1	B	410	ASN	2.1
1	B	684	ARG	2.1
1	B	398	MET	2.1
1	A	615	GLN	2.1
1	A	458	ALA	2.1
1	B	453	LYS	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	400	PHE	2.1
1	A	481	VAL	2.1
1	A	482	VAL	2.0
1	B	625	ALA	2.0
1	A	413	LEU	2.0
1	A	619	GLY	2.0
1	B	686	THR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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	B-factors(Å ²)	Q<0.9
2	MRD	A	801	8/8	0.88	0.13	37,41,45,48	0
2	MRD	B	801	8/8	0.89	0.12	33,36,41,42	0
3	CA	B	802	1/1	0.90	0.09	63,63,63,63	0
3	CA	A	802	1/1	0.92	0.08	73,73,73,73	0
3	CA	A	803	1/1	0.95	0.05	55,55,55,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.