



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 12:45 PM UTC

PDB ID : 6DC6 / pdb_00006dc6
Title : Crystal structure of human ubiquitin activating enzyme E1 (Uba1) in complex with ubiquitin
Authors : Lv, Z.; Yuan, L.; Williams, K.M.; Atkison, J.H.; Olsen, S.K.
Deposited on : 2018-05-04
Resolution : 3.14 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

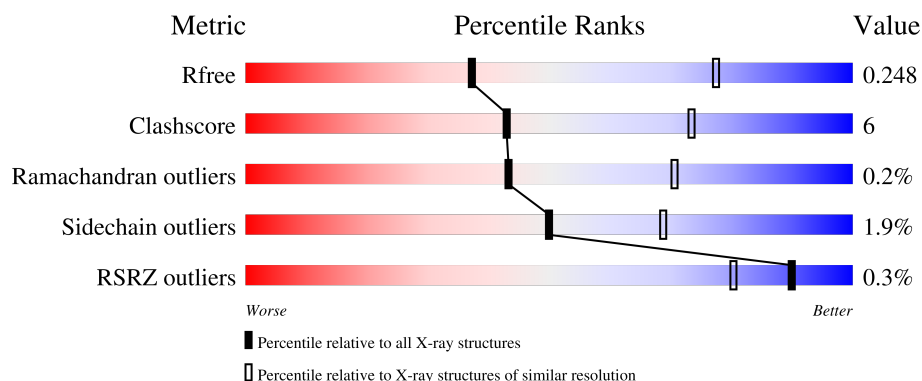
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

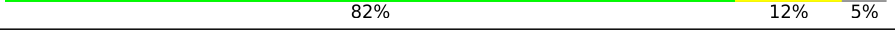
The reported resolution of this entry is 3.14 Å.

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	2351 (3.18-3.10)
Clashscore	190562	2452 (3.18-3.10)
Ramachandran outliers	187476	2324 (3.18-3.10)
Sidechain outliers	187428	2324 (3.18-3.10)
RSRZ outliers	180081	2351 (3.18-3.10)

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	1015	
1	C	1015	
2	B	80	
2	D	80	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 16888 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 Ubiquitin-like modifier-activating enzyme 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	992	Total	C	N	O	S	0	0	0
			7819	4965	1340	1475	39			
1	C	996	Total	C	N	O	S	0	0	0
			7843	4978	1345	1481	39			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	44	GLY	-	expression tag	UNP P22314
A	45	ALA	-	expression tag	UNP P22314
A	46	MET	-	expression tag	UNP P22314
A	47	GLY	-	expression tag	UNP P22314
A	48	SER	-	expression tag	UNP P22314
A	632	ALA	CYS	engineered mutation	UNP P22314
C	44	GLY	-	expression tag	UNP P22314
C	45	ALA	-	expression tag	UNP P22314
C	46	MET	-	expression tag	UNP P22314
C	47	GLY	-	expression tag	UNP P22314
C	48	SER	-	expression tag	UNP P22314
C	632	ALA	CYS	engineered mutation	UNP P22314

- Molecule 2 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	76	Total	C	N	O	S	0	0	0
			602	378	105	118	1			
2	D	76	Total	C	N	O	S	0	0	0
			602	378	105	118	1			

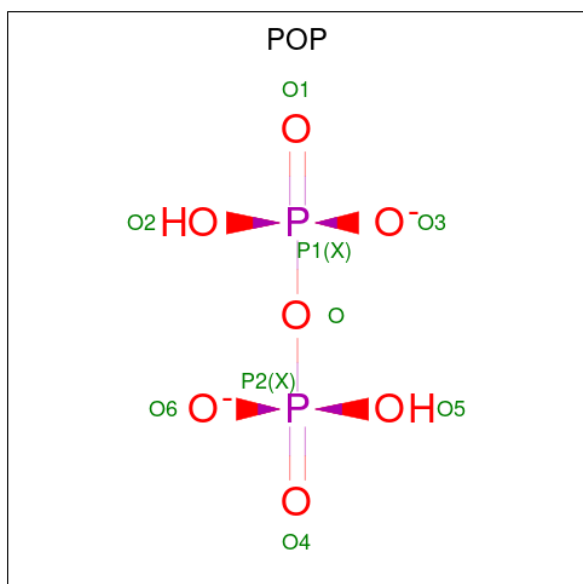
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	GLY	-	expression tag	UNP P62979
B	-2	ALA	-	expression tag	UNP P62979
B	-1	MET	-	expression tag	UNP P62979
B	0	ALA	-	expression tag	UNP P62979
D	-3	GLY	-	expression tag	UNP P62979
D	-2	ALA	-	expression tag	UNP P62979
D	-1	MET	-	expression tag	UNP P62979
D	0	ALA	-	expression tag	UNP P62979

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total Mg 2 2	0	0
3	C	2	Total Mg 2 2	0	0

- Molecule 4 is PYROPHOSPHATE 2- (CCD ID: POP) (formula: $\text{H}_2\text{O}_7\text{P}_2$).

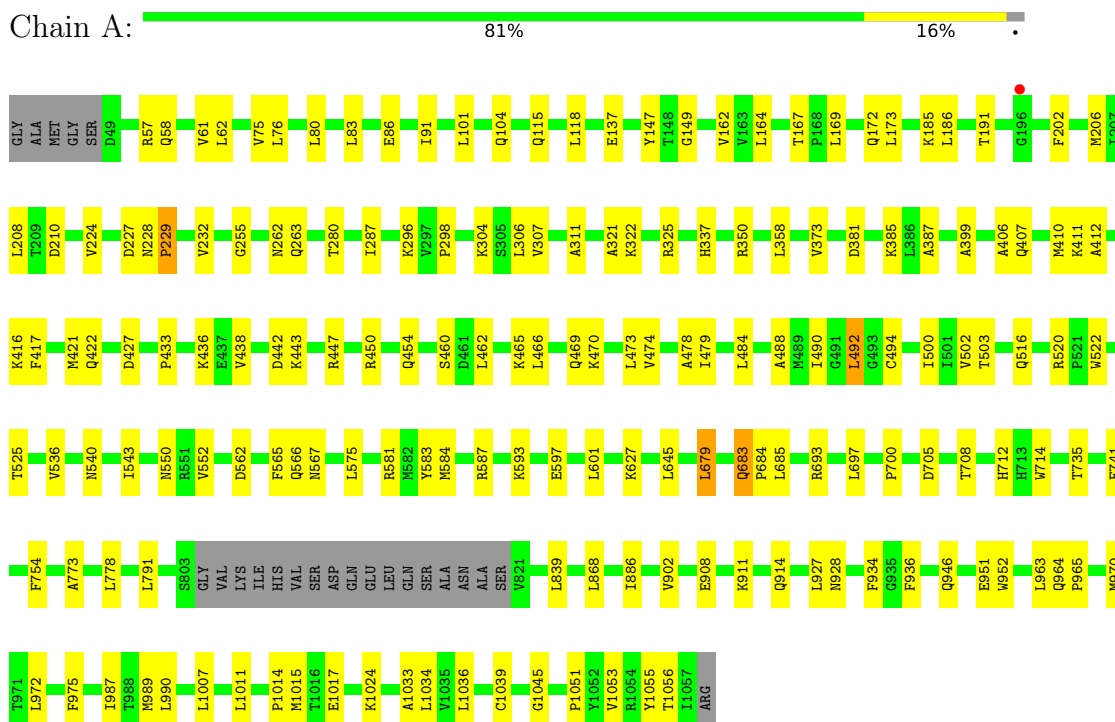


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O P 9 7 2	0	0
4	C	1	Total O P 9 7 2	0	0

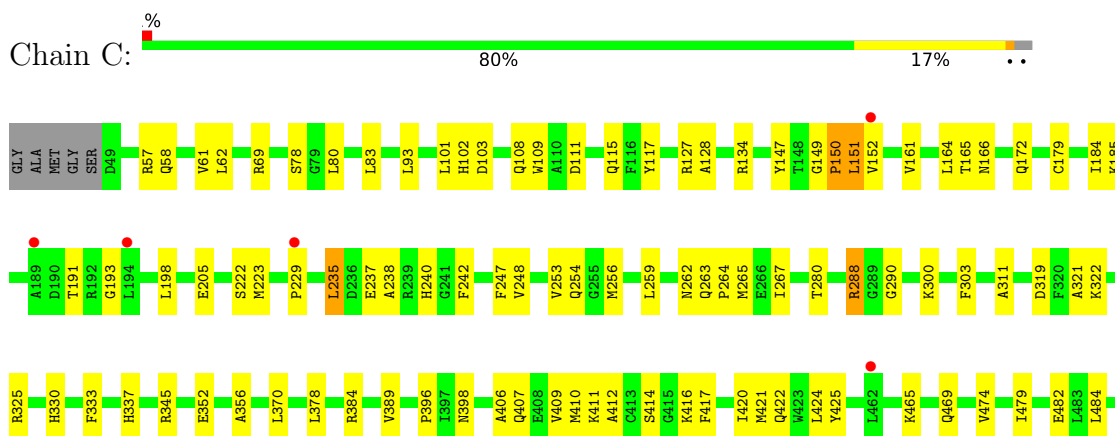
3 Residue-property plots

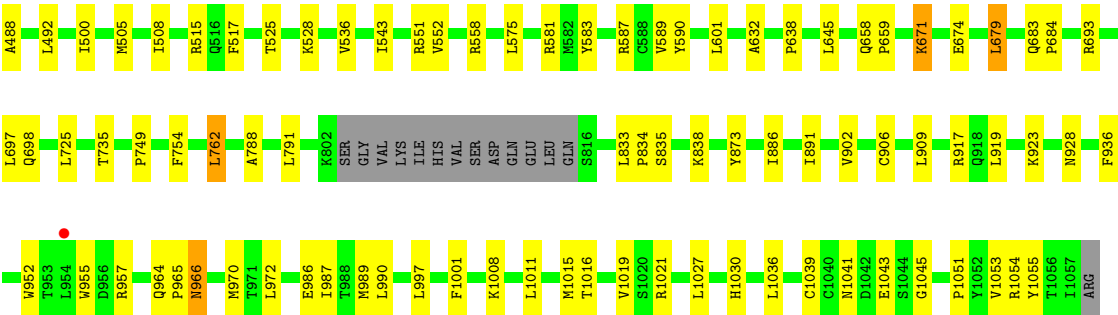
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Ubiquitin-like modifier-activating enzyme 1

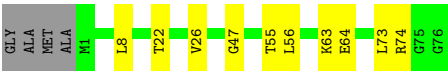
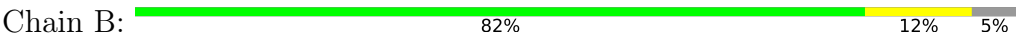


- Molecule 1: Ubiquitin-like modifier-activating enzyme 1

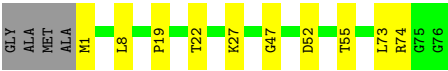
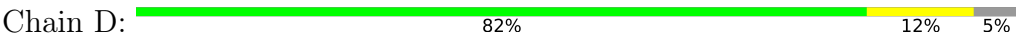




● Molecule 2: Ubiquitin



● Molecule 2: Ubiquitin



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	105.00Å 70.44Å 188.85Å 90.00° 95.19° 90.00°	Depositor
Resolution (Å)	41.70 – 3.14 41.70 – 3.14	Depositor EDS
% Data completeness (in resolution range)	94.5 (41.70-3.14) 92.4 (41.70-3.14)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 3.12Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.212 , 0.250 0.214 , 0.248	Depositor DCC
R_{free} test set	2000 reflections (4.35%)	wwPDB-VP
Wilson B-factor (Å ²)	65.0	Xtriage
Anisotropy	0.553	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 53.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	16888	wwPDB-VP
Average B, all atoms (Å ²)	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.28% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0/7994	0.31	0/10845
1	C	0.13	0/8018	0.32	0/10878
2	B	0.12	0/608	0.27	0/816
2	D	0.10	0/608	0.25	0/816
All	All	0.13	0/17228	0.31	0/23355

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	C	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	238	ALA	Peptide

5.2 Too-close contacts [i](#)

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	7819	0	7696	97	0
1	C	7843	0	7717	104	0
2	B	602	0	629	9	0
2	D	602	0	629	8	0
3	A	2	0	0	0	0
3	C	2	0	0	0	0
4	A	9	0	0	1	0
4	C	9	0	0	2	0
All	All	16888	0	16671	207	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 6.

All (207) 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:A:683:GLN:H	1:A:684:PRO:HD2	1.54	0.72
1:A:80:LEU:HD11	1:A:101:LEU:HD22	1.72	0.72
1:A:83:LEU:HD22	1:A:191:THR:HG23	1.72	0.72
1:A:57:ARG:NH1	4:A:1103:POP:O1	2.23	0.71
1:C:322:LYS:HB3	1:C:325:ARG:HG3	1.72	0.71
1:C:693:ARG:HG3	1:C:697:LEU:HD23	1.73	0.71
1:C:528:LYS:NZ	4:C:1103:POP:O5	2.24	0.70
1:C:57:ARG:NH1	4:C:1103:POP:O3	2.25	0.70
1:A:442:ASP:O	1:A:447:ARG:NH2	2.28	0.67
2:B:22:THR:HG22	2:B:55:THR:HG22	1.78	0.66
1:A:484:LEU:HB3	1:A:536:VAL:HG21	1.77	0.66
1:C:164:LEU:HD23	1:C:172:GLN:HG2	1.78	0.65
1:C:964:GLN:HG3	1:C:965:PRO:HD2	1.78	0.65
1:C:957:ARG:HD2	1:C:1054:ARG:HB2	1.78	0.65
1:C:319:ASP:OD2	1:C:923:LYS:NZ	2.30	0.64
1:A:989:MET:HB3	1:A:1039:CYS:HB2	1.78	0.64
1:C:161:VAL:HG11	1:C:409:VAL:HG13	1.80	0.64
1:A:1017:GLU:HG2	1:C:1001:PHE:HE2	1.62	0.63
1:C:78:SER:HA	1:C:102:HIS:HB3	1.81	0.63
1:A:350:ARG:NH1	1:A:438:VAL:O	2.32	0.63
1:A:987:ILE:HD11	1:A:990:LEU:HB2	1.81	0.62
1:C:396:PRO:HB3	1:C:906:CYS:HB2	1.82	0.60
1:A:304:LYS:H	1:A:422:GLN:HE22	1.48	0.60
2:B:22:THR:HA	2:B:55:THR:HA	1.84	0.59
1:C:762:LEU:HD11	1:C:788:ALA:HB2	1.84	0.58
1:C:986:GLU:HB3	1:C:1041:ASN:HB2	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:1:MET:HE3	2:D:19:PRO:HD3	1.84	0.58
1:A:462:LEU:HD22	1:A:914:GLN:HG2	1.84	0.58
1:C:80:LEU:HD12	1:C:128:ALA:HA	1.86	0.58
1:C:987:ILE:HD11	1:C:990:LEU:HB2	1.86	0.58
1:A:80:LEU:HD21	1:A:101:LEU:HB3	1.86	0.57
1:C:484:LEU:HB3	1:C:536:VAL:HG21	1.86	0.57
1:C:1036:LEU:HB2	1:C:1053:VAL:HB	1.86	0.57
1:C:590:TYR:OH	1:C:1054:ARG:NH1	2.38	0.57
1:A:927:LEU:HD22	1:A:934:PHE:HD1	1.70	0.56
1:C:500:ILE:HD12	1:C:543:ILE:HD11	1.87	0.56
1:A:990:LEU:HD21	1:A:1015:MET:HE1	1.86	0.56
1:C:166:ASN:O	1:C:166:ASN:ND2	2.39	0.56
1:A:581:ARG:NE	1:A:597:GLU:OE2	2.35	0.56
1:C:80:LEU:HD11	1:C:101:LEU:HD13	1.87	0.55
1:C:311:ALA:HB1	1:C:370:LEU:HD21	1.87	0.55
1:C:333:PHE:O	1:C:337:HIS:ND1	2.34	0.55
1:A:185:LYS:HG3	1:A:412:ALA:HB1	1.88	0.55
2:D:22:THR:HG22	2:D:55:THR:HG22	1.88	0.55
1:A:433:PRO:HB2	1:A:436:LYS:HB3	1.89	0.55
2:D:22:THR:HA	2:D:55:THR:HA	1.89	0.54
1:C:149:GLY:N	1:C:150:PRO:HD3	2.22	0.54
1:C:970:MET:HE2	1:C:1055:TYR:HE1	1.72	0.54
1:A:972:LEU:HD12	1:A:1011:LEU:HD23	1.89	0.54
1:C:679:LEU:HD21	1:C:683:GLN:HB2	1.90	0.54
1:A:164:LEU:HD23	1:A:172:GLN:HG2	1.89	0.54
1:A:1036:LEU:HB2	1:A:1053:VAL:HB	1.88	0.54
1:C:693:ARG:HG2	1:C:698:GLN:HG2	1.89	0.54
1:C:474:VAL:HG12	1:C:575:LEU:HD21	1.90	0.54
1:A:115:GLN:HG2	1:A:118:LEU:HG	1.89	0.53
1:A:311:ALA:O	1:A:373:VAL:HG21	2.08	0.53
1:A:562:ASP:O	1:A:566:GLN:HG2	2.09	0.53
1:A:500:ILE:HD12	1:A:543:ILE:HD11	1.91	0.53
1:A:488:ALA:HB2	1:A:536:VAL:HG13	1.88	0.53
1:A:928:ASN:ND2	2:B:8:LEU:O	2.41	0.53
1:C:262:ASN:OD1	1:C:263:GLN:N	2.40	0.53
1:C:966:ASN:N	1:C:966:ASN:OD1	2.42	0.53
1:C:536:VAL:HG12	1:C:543:ILE:HG21	1.91	0.52
1:A:443:LYS:HB3	1:A:460:SER:H	1.74	0.52
1:C:256:MET:HG3	1:C:259:LEU:HD12	1.91	0.52
1:C:671:LYS:HG3	1:C:674:GLU:HG2	1.92	0.52
1:C:103:ASP:OD2	1:C:127:ARG:NE	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:928:ASN:ND2	2:D:8:LEU:O	2.43	0.52
1:A:693:ARG:HA	1:A:697:LEU:HB2	1.92	0.52
1:C:833:LEU:HD12	1:C:834:PRO:HD2	1.92	0.51
1:A:1045:GLY:HA2	1:C:632:ALA:HB1	1.92	0.51
1:C:61:VAL:HG13	1:C:62:LEU:HG	1.92	0.51
1:A:581:ARG:NH1	2:B:74:ARG:O	2.43	0.51
1:C:406:ALA:O	1:C:410:MET:HG3	2.10	0.51
1:C:352:GLU:O	1:C:356:ALA:N	2.42	0.51
1:C:83:LEU:HD22	1:C:191:THR:HG22	1.92	0.50
1:A:358:LEU:HD12	1:A:387:ALA:HB2	1.93	0.50
1:C:835:SER:HB2	1:C:838:LYS:HD3	1.93	0.50
1:C:378:LEU:HD23	1:C:378:LEU:H	1.76	0.50
1:C:952:TRP:CD2	1:C:1051:PRO:HG3	2.47	0.50
1:C:990:LEU:HD21	1:C:1015:MET:HE1	1.92	0.50
1:C:117:TYR:HB3	1:C:134:ARG:HD2	1.95	0.49
1:A:406:ALA:O	1:A:410:MET:HG2	2.13	0.49
1:A:583:TYR:CZ	1:A:587:ARG:HD2	2.47	0.49
1:C:78:SER:O	1:C:165:THR:OG1	2.22	0.49
1:C:989:MET:HB3	1:C:1039:CYS:HB2	1.94	0.49
1:A:224:VAL:HG23	1:A:232:VAL:HG22	1.95	0.48
1:C:254:GLN:OE1	1:C:288:ARG:NE	2.46	0.48
1:A:474:VAL:HG12	1:A:575:LEU:HD21	1.94	0.48
1:C:330:HIS:ND1	1:C:425:TYR:OH	2.36	0.48
1:A:952:TRP:CG	1:A:1051:PRO:HG3	2.48	0.48
1:C:193:GLY:HA3	1:C:389:VAL:HG12	1.95	0.48
1:C:997:LEU:HD11	1:C:1019:VAL:HG12	1.96	0.48
2:B:63:LYS:HG2	2:B:64:GLU:HG2	1.96	0.48
1:C:479:ILE:HG23	1:C:902:VAL:HG22	1.96	0.47
1:A:494:CYS:HA	1:A:543:ILE:HA	1.96	0.47
1:A:714:TRP:HE1	1:A:868:LEU:HD13	1.79	0.47
1:C:411:LYS:HG2	1:C:417:PHE:HB2	1.96	0.47
1:A:466:LEU:O	1:A:492:LEU:HA	2.14	0.47
1:A:773:ALA:HB1	1:A:778:LEU:HB2	1.96	0.47
1:A:601:LEU:HB3	2:B:73:LEU:HD22	1.95	0.47
1:C:482:GLU:HB2	1:C:902:VAL:HG21	1.96	0.47
1:C:248:VAL:HG13	1:C:267:ILE:HG13	1.97	0.47
1:A:325:ARG:NH1	1:A:427:ASP:OD2	2.48	0.46
1:C:247:PHE:HB3	1:C:264:PRO:HB3	1.96	0.46
1:C:581:ARG:NH1	2:D:74:ARG:O	2.48	0.46
1:A:86:GLU:HG2	1:A:399:ALA:HA	1.97	0.46
1:A:964:GLN:HB3	1:A:965:PRO:HD2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:167:THR:O	1:A:172:GLN:NE2	2.49	0.46
1:A:708:THR:O	1:A:712:HIS:ND1	2.42	0.46
1:C:191:THR:HG21	1:C:398:ASN:OD1	2.15	0.46
1:C:205:GLU:HG3	1:C:300:LYS:HE3	1.98	0.46
1:C:465:LYS:O	1:C:469:GLN:HG2	2.16	0.46
1:A:186:LEU:HD21	1:A:306:LEU:HD12	1.98	0.46
1:A:173:LEU:HD22	1:A:307:VAL:HG22	1.96	0.46
1:C:253:VAL:HG22	1:C:290:GLY:HA3	1.98	0.46
1:C:558:ARG:HH11	1:C:1030:HIS:HB3	1.81	0.46
1:C:638:PRO:HD2	1:C:873:TYR:CE2	2.51	0.46
1:C:583:TYR:CZ	1:C:587:ARG:HD2	2.51	0.45
1:C:1016:THR:HG23	1:C:1027:LEU:HD12	1.99	0.45
1:A:552:VAL:HG11	1:A:584:MET:SD	2.56	0.45
1:C:248:VAL:HG22	1:C:267:ILE:HD11	1.97	0.45
1:A:454:GLN:HE22	1:A:490:ILE:HG23	1.82	0.45
1:C:508:ILE:HG12	1:C:528:LYS:HG2	1.99	0.45
1:A:255:GLY:HA3	1:A:287:ILE:HG13	1.99	0.45
1:C:69:ARG:HE	1:C:414:SER:HA	1.81	0.45
1:A:450:ARG:HH12	1:A:540:ASN:HA	1.81	0.45
1:C:972:LEU:HB3	1:C:1011:LEU:HA	1.97	0.45
1:C:420:ILE:HG21	1:C:424:LEU:HB2	1.97	0.45
1:A:76:LEU:HD23	1:A:162:VAL:HG13	2.00	0.44
1:A:115:GLN:HG2	1:A:118:LEU:CG	2.47	0.44
1:C:421:MET:HA	1:C:422:GLN:HA	1.60	0.44
1:A:210:ASP:HB3	1:A:416:LYS:O	2.18	0.44
1:C:754:PHE:HZ	1:C:791:LEU:HD13	1.82	0.44
1:C:58:GLN:HE21	1:C:62:LEU:HD12	1.82	0.44
1:C:645:LEU:HD13	1:C:886:ILE:HB	1.99	0.44
1:A:61:VAL:HG13	1:A:62:LEU:HG	1.98	0.44
1:C:505:MET:HG2	1:C:551:ARG:HB2	2.00	0.44
1:C:247:PHE:HA	1:C:265:MET:O	2.18	0.44
1:A:478:ALA:HA	1:A:516:GLN:HG2	2.00	0.44
1:A:754:PHE:HZ	1:A:791:LEU:HD13	1.83	0.44
1:C:321:ALA:HB2	2:D:47:GLY:HA3	1.99	0.44
1:C:303:PHE:CE2	1:C:421:MET:HG2	2.53	0.43
1:A:503:THR:OG1	1:A:550:ASN:O	2.34	0.43
2:D:27:LYS:NZ	2:D:52:ASP:OD1	2.42	0.43
1:A:75:VAL:HG11	1:A:91:ILE:HD13	2.01	0.43
1:A:421:MET:HA	1:A:422:GLN:HA	1.65	0.43
1:A:1034:LEU:HB3	1:A:1055:TYR:HB3	2.00	0.43
1:A:936:PHE:O	2:B:47:GLY:HA2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:102:HIS:CD2	1:C:149:GLY:HA2	2.53	0.43
1:C:601:LEU:HB3	2:D:73:LEU:HD22	2.00	0.43
1:A:946:GLN:HA	1:A:951:GLU:HA	2.00	0.43
1:C:407:GLN:HG3	1:C:411:LYS:HE3	2.01	0.43
1:A:104:GLN:HG2	1:A:149:GLY:HA2	2.01	0.43
1:A:470:LYS:HE2	1:A:567:ASN:HD22	1.83	0.43
1:A:1014:PRO:HG2	1:A:1017:GLU:HB2	2.00	0.43
1:A:262:ASN:OD1	1:A:263:GLN:N	2.51	0.43
1:A:473:LEU:HD23	1:A:502:VAL:HG22	2.00	0.43
1:A:627:LYS:H	1:A:627:LYS:HD2	1.83	0.43
1:A:927:LEU:HD22	1:A:934:PHE:CD1	2.51	0.43
2:B:26:VAL:HG21	2:B:56:LEU:HD21	2.00	0.43
1:C:488:ALA:HB2	1:C:536:VAL:HG13	2.01	0.42
1:C:1021:ARG:HA	1:C:1021:ARG:HD2	1.86	0.42
1:C:923:LYS:HE2	1:C:936:PHE:HB3	2.01	0.42
1:A:411:LYS:HG2	1:A:417:PHE:HB2	2.01	0.42
1:A:479:ILE:HG23	1:A:902:VAL:HG22	2.01	0.42
1:A:952:TRP:CD1	1:A:1051:PRO:HG3	2.53	0.42
1:C:240:HIS:HD2	1:C:242:PHE:HB2	1.83	0.42
1:C:179:CYS:HB2	1:C:184:ILE:HB	2.02	0.42
1:A:227:ASP:OD1	1:A:228:ASN:N	2.47	0.42
1:A:679:LEU:O	1:A:684:PRO:HD3	2.19	0.42
1:A:296:LYS:HE2	1:A:296:LYS:HB3	1.88	0.42
1:A:645:LEU:HD13	1:A:886:ILE:HB	2.01	0.42
1:A:137:GLU:OE1	1:A:520:ARG:NH1	2.46	0.42
1:A:970:MET:HE2	1:A:975:PHE:HA	2.02	0.42
1:A:407:GLN:HG3	1:A:411:LYS:HE3	2.02	0.41
1:A:228:ASN:HB3	1:A:229:PRO:HD3	2.03	0.41
1:A:735:THR:HG22	1:A:741:PHE:HD1	1.85	0.41
1:A:58:GLN:O	1:A:61:VAL:HG12	2.20	0.41
1:A:169:LEU:HB2	1:A:337:HIS:ND1	2.36	0.41
1:A:322:LYS:HB3	1:A:325:ARG:HD2	2.02	0.41
1:A:208:LEU:O	1:A:298:PRO:HA	2.20	0.41
1:C:725:LEU:HD23	1:C:749:PRO:HG3	2.03	0.41
1:C:583:TYR:O	1:C:587:ARG:HG3	2.21	0.41
1:C:683:GLN:N	1:C:684:PRO:HD2	2.36	0.41
1:C:151:LEU:H	1:C:151:LEU:HD22	1.86	0.41
1:A:700:PRO:HA	1:A:705:ASP:OD2	2.20	0.41
1:C:658:GLN:HB3	1:C:659:PRO:HD3	2.03	0.41
1:A:465:LYS:O	1:A:469:GLN:HG2	2.21	0.41
1:A:754:PHE:CZ	1:A:791:LEU:HD13	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:93:LEU:HD11	1:C:517:PHE:HB3	2.03	0.41
1:C:185:LYS:HG2	1:C:412:ALA:HB1	2.02	0.41
1:C:474:VAL:HG13	1:C:552:VAL:HG21	2.03	0.41
1:A:1033:ALA:HA	1:A:1056:THR:HA	2.03	0.41
1:C:589:VAL:HA	1:C:955:TRP:CZ3	2.56	0.41
1:A:565:PHE:O	1:A:593:LYS:HE2	2.21	0.40
1:C:420:ILE:HD13	1:C:424:LEU:HD13	2.03	0.40
1:A:908:GLU:OE2	1:A:911:LYS:NZ	2.48	0.40
1:C:198:LEU:HB3	1:C:424:LEU:HB3	2.03	0.40
1:C:109:TRP:C	1:C:111:ASP:H	2.29	0.40
1:A:381:ASP:O	1:A:385:LYS:HG2	2.21	0.40
1:C:108:GLN:HG2	1:C:109:TRP:H	1.85	0.40
1:C:222:SER:HB2	1:C:235:LEU:HA	2.03	0.40
1:C:410:MET:O	1:C:414:SER:OG	2.28	0.40
1:A:202:PHE:HB3	1:A:206:MET:HG3	2.04	0.40
1:A:321:ALA:HB2	2:B:47:GLY:HA3	2.04	0.40
1:C:492:LEU:HD11	1:C:909:LEU:HD21	2.04	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	988/1015 (97%)	926 (94%)	60 (6%)	2 (0%)	43	70
1	C	992/1015 (98%)	933 (94%)	56 (6%)	3 (0%)	36	64
2	B	74/80 (92%)	72 (97%)	2 (3%)	0	100	100
2	D	74/80 (92%)	71 (96%)	3 (4%)	0	100	100
All	All	2128/2190 (97%)	2002 (94%)	121 (6%)	5 (0%)	43	70

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	1045	GLY
1	C	150	PRO
1	A	683	GLN
1	C	229	PRO
1	A	229	PRO

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	851/868 (98%)	840 (99%)	11 (1%)	61	73
1	C	853/868 (98%)	829 (97%)	24 (3%)	38	62
2	B	68/69 (99%)	68 (100%)	0	100	100
2	D	68/69 (99%)	68 (100%)	0	100	100
All	All	1840/1874 (98%)	1805 (98%)	35 (2%)	50	69

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	147	TYR
1	A	280	THR
1	A	492	LEU
1	A	522	TRP
1	A	525	THR
1	A	679	LEU
1	A	685	LEU
1	A	839	LEU
1	A	963	LEU
1	A	1007	LEU
1	A	1024	LYS
1	C	115	GLN
1	C	147	TYR
1	C	151	LEU
1	C	152	VAL
1	C	223	MET
1	C	235	LEU

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Mol	Chain	Res	Type
1	C	237	GLU
1	C	280	THR
1	C	288	ARG
1	C	345	ARG
1	C	384	ARG
1	C	416	LYS
1	C	515	ARG
1	C	525	THR
1	C	671	LYS
1	C	679	LEU
1	C	735	THR
1	C	762	LEU
1	C	891	ILE
1	C	917	ARG
1	C	919	LEU
1	C	966	ASN
1	C	1008	LYS
1	C	1043	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	166	ASN
1	A	181	ASN
1	A	486	ASN
1	A	514	ASN
1	A	550	ASN
1	A	683	GLN
1	A	720	ASN
1	A	724	GLN
1	A	727	HIS
1	A	914	GLN
1	A	949	ASN
1	C	328	GLN
1	C	374	GLN
1	C	469	GLN
1	C	550	ASN
1	C	713	HIS
1	C	724	GLN
1	C	881	HIS
1	C	914	GLN
1	C	949	ASN

5.3.3 RNA ⓘ

There are no RNA molecules 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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 6 ligands modelled in this entry, 4 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	$\# Z > 2$
4	POP	A	1103	3	6,8,8	0.75	0	12,13,13	0.92	0
4	POP	C	1103	3	6,8,8	0.76	0	12,13,13	0.85	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
4	POP	A	1103	3	-	0/6/6/6	-
4	POP	C	1103	3	-	0/6/6/6	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1103	POP	1	0
4	C	1103	POP	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	992/1015 (97%)	-0.21	1 (0%) 92 86	37, 74, 119, 166	0
1	C	996/1015 (98%)	0.03	6 (0%) 85 70	50, 95, 156, 189	0
2	B	76/80 (95%)	-0.18	0 100 100	44, 87, 125, 135	0
2	D	76/80 (95%)	-0.13	0 100 100	56, 104, 143, 151	0
All	All	2140/2190 (97%)	-0.09	7 (0%) 90 80	37, 86, 144, 189	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	462	LEU	2.8
1	C	152	VAL	2.5
1	C	194	LEU	2.4
1	C	954	LEU	2.4
1	A	196	GLY	2.2
1	C	189	ALA	2.2
1	C	229	PRO	2.1

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($\text{\AA}^2$)	Q<0.9
3	MG	A	1102	1/1	0.95	0.14	23,23,23,23	0
3	MG	C	1102	1/1	0.95	0.11	30,30,30,30	0
3	MG	A	1101	1/1	0.96	0.09	36,36,36,36	0
4	POP	A	1103	9/9	0.96	0.07	3,57,79,86	0
4	POP	C	1103	9/9	0.97	0.06	26,45,90,99	0
3	MG	C	1101	1/1	0.98	0.09	33,33,33,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.