



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 10:09 AM UTC

PDB ID : 6HEK / pdb_00006hek
Title : Structure of human USP28 bound to Ubiquitin-PA
Authors : Gersch, M.; Komander, D.
Deposited on : 2018-08-20
Resolution : 3.03 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

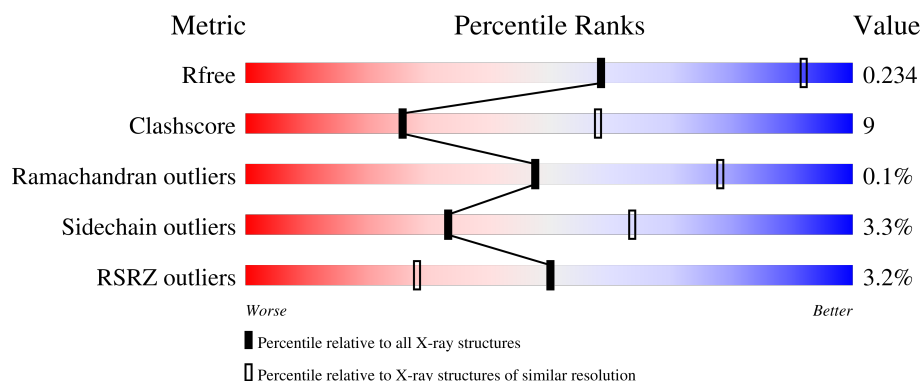
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.03 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	3685 (3.08-3.00)
Clashscore	190562	4007 (3.08-3.00)
Ramachandran outliers	187476	3834 (3.08-3.00)
Sidechain outliers	187428	3836 (3.08-3.00)
RSRZ outliers	180081	3684 (3.08-3.00)

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	556	 3% 66% 14% 19%
1	C	556	 3% 66% 16% 17%
2	B	78	 74% 21% 5%
2	D	78	 3% 68% 26% 5%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 8503 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 carboxyl-terminal hydrolase 28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	453	Total	C	N	O	S	0	0	0
			3649	2331	611	687	20			
1	C	459	Total	C	N	O	S	0	0	0
			3673	2337	623	694	19			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	148	GLY	-	expression tag	UNP Q96RU2
C	148	GLY	-	expression tag	UNP Q96RU2

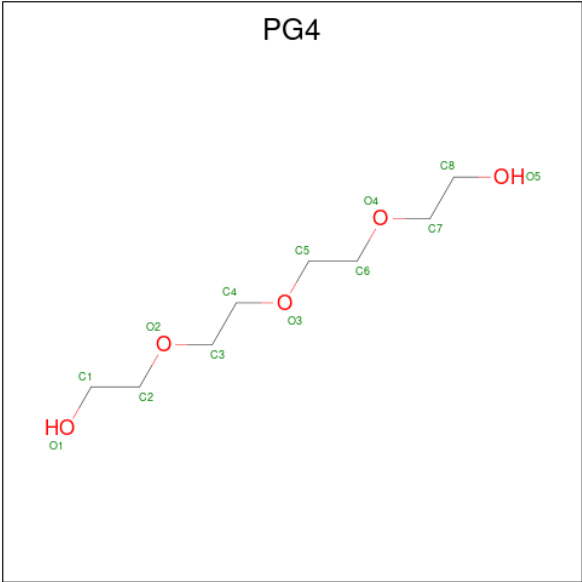
- Molecule 2 is a protein called Polyubiquitin-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	78	Total	C	N	O	S	0	0	0
			589	373	103	112	1			
2	D	75	Total	C	N	O		0	0	0
			574	360	100	114				

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	GLY	-	expression tag	UNP P0CG47
B	0	PRO	-	expression tag	UNP P0CG47
D	-1	GLY	-	expression tag	UNP P0CG47
D	0	PRO	-	expression tag	UNP P0CG47

- Molecule 3 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: C₈H₁₈O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			10	6	4		
3	A	1	Total	C	O	0	0
			7	5	2		

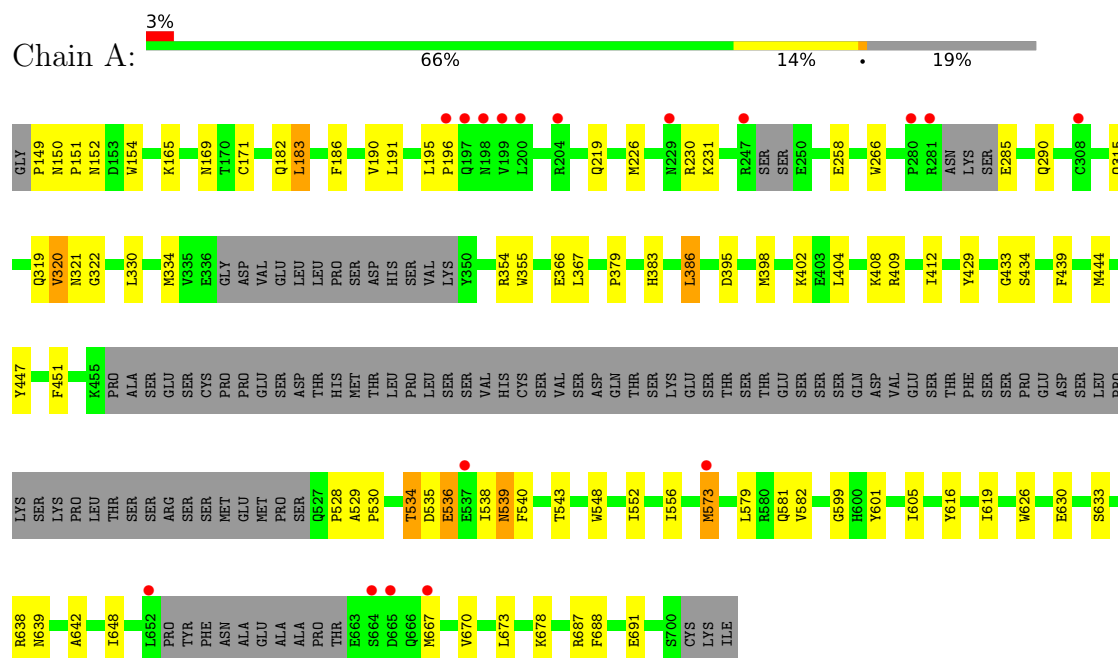
- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Cl	0	0
			1	1		

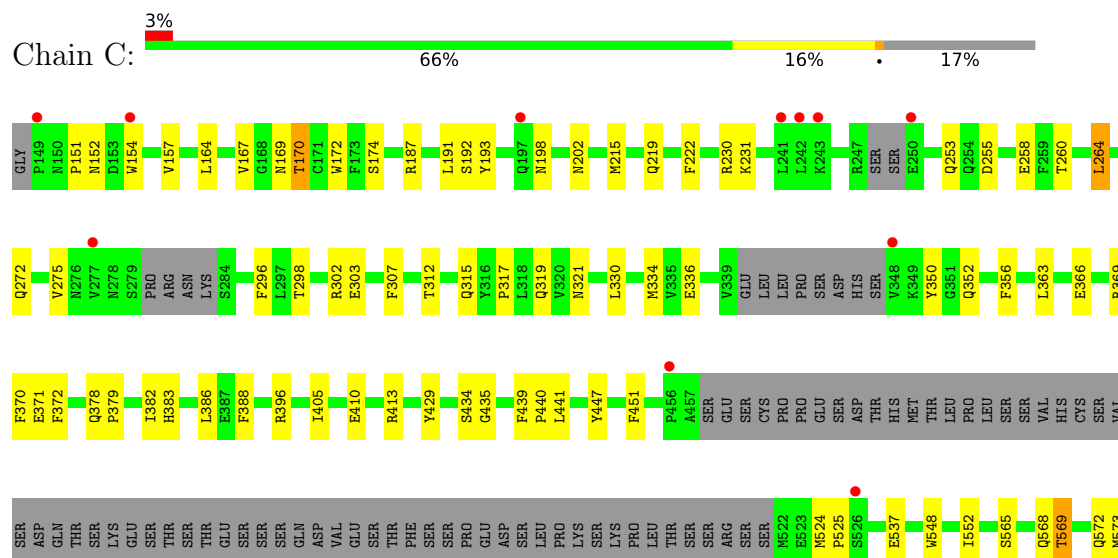
3 Residue-property plots [i](#)

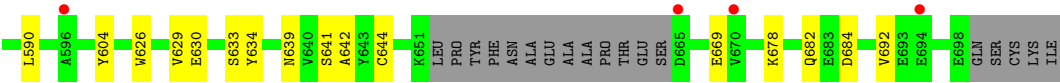
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Ubiquitin carboxyl-terminal hydrolase 28

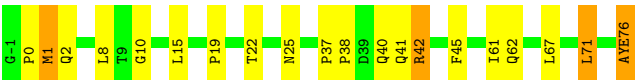


• Molecule 1: Ubiquitin carboxyl-terminal hydrolase 28





● Molecule 2: Polyubiquitin-B



● Molecule 2: Polyubiquitin-B



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	103.20Å 199.79Å 204.91Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	143.05 – 3.03 143.05 – 3.03	Depositor EDS
% Data completeness (in resolution range)	73.6 (143.05-3.03) 73.7 (143.05-3.03)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.47 (at 3.01Å)	Xtriage
Refinement program	PHENIX (1.13_2998), REFMAC	Depositor
R, R_{free}	0.218 , 0.237 0.214 , 0.234	Depositor DCC
R_{free} test set	1518 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	93.6	Xtriage
Anisotropy	0.057	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 67.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.029 for -h,-l,-k	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	8503	wwPDB-VP
Average B, all atoms (Å ²)	91.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.32% 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: PG4, CL, AYE

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	0.24	0/3737	0.43	1/5071 (0.0%)
1	C	0.15	0/3760	0.39	0/5106
2	B	0.38	0/592	0.80	0/801
2	D	0.19	0/576	0.64	0/780
All	All	0.22	0/8665	0.46	1/11758 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	149	PRO	CA-N-CD	-5.29	104.59	112.00

There are no chirality outliers.

There are no planarity outliers.

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	3649	0	3407	69	0
1	C	3673	0	3401	71	0
2	B	589	0	600	27	0
2	D	574	0	570	22	0
3	A	17	0	19	1	0
4	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	8503	0	7997	156	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 9.

All (156) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:151:PRO:HG3	1:C:692:VAL:HA	1.39	1.02
2:B:38:PRO:HA	2:B:41:GLN:NE2	1.75	1.01
1:A:539:ASN:O	1:A:543:THR:HG23	1.57	1.01
2:B:37:PRO:C	2:B:41:GLN:HE21	1.78	0.91
1:C:253:GLN:HB3	2:D:74:ARG:HB3	1.53	0.91
2:B:38:PRO:CA	2:B:41:GLN:NE2	2.43	0.81
1:A:444:MET:HE1	1:C:447:TYR:CD2	2.17	0.80
2:B:42:ARG:HG3	2:B:42:ARG:HH11	1.48	0.79
1:C:258:GLU:HG3	2:D:49:GLN:HE22	1.53	0.73
1:C:157:VAL:HG12	1:C:231:LYS:HE3	1.71	0.71
1:C:167:VAL:H	1:C:170:THR:CG2	2.04	0.70
2:B:38:PRO:N	2:B:41:GLN:HE21	1.90	0.70
1:C:170:THR:O	1:C:170:THR:OG1	2.05	0.69
1:A:230:ARG:HD3	3:A:801:PG4:H32	1.74	0.67
1:A:367:LEU:HD13	1:A:386:LEU:HD13	1.76	0.67
1:A:539:ASN:O	1:A:543:THR:CG2	2.40	0.66
1:C:187:ARG:NH2	1:C:669:GLU:OE2	2.27	0.66
1:A:528:PRO:HB3	1:C:429:TYR:CE1	2.32	0.65
2:B:22:THR:HG23	2:B:25:ASN:H	1.64	0.63
1:C:372:PHE:CD2	2:D:36:ILE:HG12	2.35	0.62
1:C:260:THR:HG22	1:C:264:LEU:HD23	1.81	0.62
1:C:296:PHE:HB3	1:C:356:PHE:HA	1.82	0.62
2:D:22:THR:HG23	2:D:25:ASN:H	1.64	0.61
2:B:38:PRO:CA	2:B:41:GLN:HE21	2.12	0.60
2:B:38:PRO:N	2:B:41:GLN:NE2	2.48	0.60
2:B:1:MET:CE	2:B:19:PRO:HG3	2.32	0.60
1:C:312:THR:O	2:D:46:ALA:HA	2.02	0.59
1:C:260:THR:HG22	1:C:315:GLN:HE22	1.68	0.59
1:C:336:GLU:HG2	1:C:350:TYR:OH	2.04	0.58
1:A:150:ASN:OD1	1:A:152:ASN:N	2.37	0.58
1:C:151:PRO:CG	1:C:692:VAL:HA	2.26	0.57
1:A:379:PRO:HD3	2:B:40:GLN:OE1	2.05	0.57
2:B:42:ARG:HH11	2:B:42:ARG:CG	2.14	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:285:GLU:OE2	1:A:290:GLN:NE2	2.38	0.57
1:A:540:PHE:HZ	1:C:537:GLU:HG3	1.68	0.57
1:C:568:GLN:O	1:C:572:GLN:HG3	2.04	0.57
2:B:1:MET:HE1	2:B:19:PRO:HG3	1.87	0.56
1:C:319:GLN:HG2	1:C:321:ASN:HB2	1.88	0.56
1:A:447:TYR:OH	1:C:435:GLY:HA3	2.06	0.55
1:A:687:ARG:O	1:A:691:GLU:HG3	2.06	0.55
2:B:42:ARG:NH1	2:B:71:LEU:O	2.34	0.55
1:C:198:ASN:O	1:C:202:ASN:N	2.38	0.55
1:C:371:GLU:HB2	1:C:382:ILE:HD11	1.88	0.55
2:D:8:LEU:HD11	2:D:71:LEU:HD13	1.89	0.55
1:A:169:ASN:HB3	2:B:76:AYE:H1	1.88	0.55
1:C:253:GLN:HG3	2:D:75:GLY:C	2.32	0.54
1:C:524:MET:CB	1:C:525:PRO:HD2	2.37	0.54
1:A:633:SER:HB3	1:A:642:ALA:HB2	1.89	0.54
1:C:379:PRO:HB3	2:D:71:LEU:HD23	1.89	0.54
1:A:319:GLN:NE2	2:B:8:LEU:O	2.40	0.54
1:A:150:ASN:OD1	1:A:151:PRO:HD2	2.08	0.53
2:B:2:GLN:O	2:B:2:GLN:HG3	2.07	0.53
1:A:315:GLN:NE2	1:A:366:GLU:OE2	2.41	0.53
1:A:638:ARG:O	1:A:639:ASN:ND2	2.40	0.53
1:A:379:PRO:HB3	2:B:71:LEU:HD23	1.90	0.53
1:A:670:VAL:HA	1:A:673:LEU:HG	1.90	0.53
2:D:4:PHE:HB2	2:D:66:THR:HG22	1.90	0.53
2:D:36:ILE:O	2:D:41:GLN:NE2	2.37	0.53
1:A:534:THR:OG1	1:A:536:GLU:HG3	2.08	0.53
1:C:230:ARG:NH2	1:C:684:ASP:OD1	2.35	0.52
1:A:540:PHE:CZ	1:C:537:GLU:HG3	2.44	0.52
1:A:605:ILE:HB	1:A:616:TYR:CE1	2.45	0.52
2:B:8:LEU:HD11	2:B:71:LEU:HD13	1.92	0.52
1:C:255:ASP:OD2	1:C:258:GLU:N	2.28	0.51
1:A:383:HIS:CE1	1:A:639:ASN:HA	2.46	0.51
1:C:590:LEU:HD22	1:C:644:CYS:HB2	1.91	0.51
1:C:678:LYS:O	1:C:682:GLN:HG3	2.11	0.51
1:C:370:PHE:CZ	2:D:70:VAL:HB	2.45	0.51
1:C:260:THR:HG22	1:C:264:LEU:CD2	2.41	0.50
1:C:388:PHE:H	1:C:634:TYR:HE1	1.60	0.50
1:C:330:LEU:O	1:C:334:MET:HG2	2.12	0.50
1:A:383:HIS:ND1	1:A:639:ASN:HA	2.27	0.50
1:A:182:GLN:HG3	1:A:605:ILE:HG21	1.94	0.50
2:B:45:PHE:HB2	2:B:67:LEU:HD22	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:369:ARG:CZ	1:C:641:SER:HB2	2.41	0.49
1:A:258:GLU:OE1	2:B:42:ARG:HD3	2.13	0.49
1:C:439:PHE:CG	1:C:440:PRO:HD2	2.47	0.49
1:C:253:GLN:CB	2:D:74:ARG:HB3	2.35	0.49
1:C:258:GLU:CD	2:D:72:ARG:HE	2.20	0.49
1:C:396:ARG:HA	1:C:405:ILE:HD11	1.95	0.49
1:A:191:LEU:HD13	1:A:673:LEU:HD21	1.95	0.48
1:A:320:VAL:HG13	1:A:321:ASN:H	1.77	0.48
2:B:42:ARG:CG	2:B:42:ARG:NH1	2.73	0.48
1:A:226:MET:HE1	1:A:673:LEU:HD21	1.96	0.48
1:C:372:PHE:CE2	2:D:36:ILE:HG12	2.49	0.48
1:A:434:SER:O	1:C:447:TYR:OH	2.32	0.48
1:A:154:TRP:HA	1:A:231:LYS:HD2	1.94	0.47
1:A:398:MET:HE1	1:A:582:VAL:HG21	1.95	0.47
2:B:37:PRO:O	2:B:41:GLN:HG3	2.13	0.47
1:C:191:LEU:HD21	1:C:222:PHE:HB3	1.97	0.47
1:C:383:HIS:HD2	1:C:639:ASN:H	1.62	0.47
1:A:226:MET:HE3	1:A:670:VAL:HG12	1.96	0.47
1:A:439:PHE:HB3	1:A:444:MET:HE3	1.97	0.47
1:A:667:MET:O	1:A:667:MET:HG3	2.15	0.47
1:A:599:GLY:O	2:B:76:AYE:N1	2.48	0.47
1:A:605:ILE:HB	1:A:616:TYR:HE1	1.78	0.47
1:A:355:TRP:CH2	1:A:402:LYS:HA	2.50	0.46
1:C:626:TRP:O	1:C:630:GLU:HG3	2.15	0.46
1:A:183:LEU:HB3	1:A:186:PHE:HB3	1.97	0.46
1:A:529:ALA:HB1	1:A:530:PRO:HD2	1.97	0.46
1:C:302:ARG:NH2	2:D:64:GLU:OE1	2.39	0.46
1:A:444:MET:CE	1:C:447:TYR:CD2	2.94	0.46
1:C:307:PHE:HZ	1:C:352:GLN:HG2	1.81	0.46
2:B:37:PRO:C	2:B:41:GLN:NE2	2.60	0.46
1:A:165:LYS:HA	1:A:619:ILE:HG22	1.99	0.45
1:A:626:TRP:O	1:A:630:GLU:HG3	2.16	0.45
1:C:383:HIS:CD2	1:C:639:ASN:H	2.35	0.45
2:D:63:LYS:O	2:D:64:GLU:HB2	2.16	0.45
1:A:433:GLY:CA	1:C:447:TYR:CE1	2.99	0.45
2:B:2:GLN:HA	2:B:15:LEU:O	2.15	0.45
1:A:395:ASP:OD1	1:A:582:VAL:N	2.48	0.45
1:A:404:LEU:HD21	1:A:408:LYS:HE3	1.98	0.45
1:C:565:SER:O	1:C:569:THR:HG23	2.15	0.45
2:B:1:MET:HE2	2:B:19:PRO:HG3	1.99	0.45
1:A:429:TYR:HB3	1:A:556:ILE:HD11	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:330:LEU:O	1:A:334:MET:HG2	2.17	0.44
1:C:192:SER:O	1:C:192:SER:OG	2.34	0.44
1:A:190:VAL:O	1:A:219:GLN:NE2	2.45	0.44
1:C:169:ASN:HA	2:D:76:AYE:C3	2.47	0.44
1:C:172:TRP:CD1	1:C:172:TRP:H	2.34	0.44
1:A:433:GLY:HA2	1:C:447:TYR:CE1	2.51	0.44
1:C:272:GLN:HA	1:C:275:VAL:HG22	1.99	0.44
1:A:230:ARG:CZ	1:A:688:PHE:HB2	2.48	0.44
1:A:319:GLN:HE22	2:B:10:GLY:N	2.16	0.44
1:C:548:TRP:O	1:C:552:ILE:HG12	2.17	0.44
1:A:183:LEU:HD12	1:A:183:LEU:HA	1.74	0.43
2:D:62:GLN:HG2	2:D:63:LYS:H	1.84	0.43
1:A:195:LEU:HD22	1:A:196:PRO:HD2	2.01	0.43
1:A:266:TRP:CD1	1:A:266:TRP:N	2.87	0.43
1:C:317:PRO:HA	1:C:366:GLU:O	2.18	0.43
1:C:370:PHE:CE1	2:D:8:LEU:HD21	2.53	0.43
1:A:536:GLU:HG3	1:A:536:GLU:H	1.54	0.42
1:C:260:THR:HG22	1:C:315:GLN:NE2	2.34	0.42
1:A:409:ARG:HA	1:A:412:ILE:HG22	2.00	0.42
1:A:408:LYS:O	1:A:573:MET:HE1	2.19	0.42
1:A:451:PHE:CD1	1:C:441:LEU:HD21	2.55	0.42
1:A:528:PRO:HB3	1:C:429:TYR:CZ	2.54	0.42
1:C:604:TYR:CD1	1:C:629:VAL:HG22	2.54	0.42
1:C:633:SER:HB3	1:C:642:ALA:HB2	2.01	0.42
2:D:22:THR:OG1	2:D:24:GLU:OE2	2.33	0.42
1:A:321:ASN:HB3	1:A:322:GLY:H	1.59	0.42
1:A:334:MET:HE3	1:A:354:ARG:HB3	2.01	0.42
1:A:171:CYS:SG	1:A:601:TYR:HB2	2.60	0.42
1:A:673:LEU:O	1:A:678:LYS:HE3	2.19	0.42
1:C:370:PHE:HE1	2:D:8:LEU:HD21	1.84	0.42
1:A:548:TRP:CE3	1:C:451:PHE:HE2	2.37	0.41
1:C:378:GLN:CD	1:C:379:PRO:HD2	2.44	0.41
1:C:410:GLU:HA	1:C:413:ARG:HG2	2.01	0.41
2:D:45:PHE:HB2	2:D:67:LEU:HD22	2.03	0.41
1:A:429:TYR:CD2	1:A:552:ILE:HG23	2.55	0.41
1:C:319:GLN:CG	1:C:321:ASN:HB2	2.51	0.41
1:C:154:TRP:O	1:C:231:LYS:HB2	2.20	0.41
1:C:164:LEU:HD12	1:C:174:SER:HA	2.02	0.40
1:C:193:TYR:HB3	1:C:219:GLN:NE2	2.36	0.40
1:A:150:ASN:OD1	1:A:151:PRO:CD	2.70	0.40
1:A:395:ASP:HB2	1:A:579:LEU:O	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	441/556 (79%)	427 (97%)	14 (3%)	0	100	100
1	C	447/556 (80%)	427 (96%)	20 (4%)	0	100	100
2	B	75/78 (96%)	73 (97%)	1 (1%)	1 (1%)	9	35
2	D	72/78 (92%)	71 (99%)	1 (1%)	0	100	100
All	All	1035/1268 (82%)	998 (96%)	36 (4%)	1 (0%)	48	78

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	0	PRO

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	382/513 (74%)	371 (97%)	11 (3%)	37	67
1	C	381/513 (74%)	370 (97%)	11 (3%)	37	67
2	B	63/69 (91%)	58 (92%)	5 (8%)	11	36
2	D	62/69 (90%)	60 (97%)	2 (3%)	34	64
All	All	888/1164 (76%)	859 (97%)	29 (3%)	33	64

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	183	LEU
1	A	320	VAL
1	A	386	LEU
1	A	534	THR
1	A	535	ASP
1	A	536	GLU
1	A	538	ILE
1	A	539	ASN
1	A	573	MET
1	A	581	GLN
1	A	648	ILE
2	B	1	MET
2	B	42	ARG
2	B	61	ILE
2	B	62	GLN
2	B	71	LEU
1	C	152	ASN
1	C	170	THR
1	C	215	MET
1	C	264	LEU
1	C	298	THR
1	C	303	GLU
1	C	363	LEU
1	C	386	LEU
1	C	434	SER
1	C	569	THR
1	C	573	MET
2	D	14	THR
2	D	63	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	229	ASN
1	A	261	HIS
1	A	276	ASN
1	A	310	ASN
1	A	315	GLN
1	A	319	GLN
1	A	572	GLN
2	B	41	GLN

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Mol	Chain	Res	Type
1	C	216	GLN
1	C	315	GLN
1	C	378	GLN
2	D	49	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 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	$\# Z > 2$
2	AYE	B	76	2,1	3,3,3	2.25	1 (33%)	2,2,2	3.08	1 (50%)
2	AYE	D	76	2,1	3,3,3	2.31	1 (33%)	2,2,2	3.20	1 (50%)

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	AYE	B	76	2,1	-	0/1/1/1	-
2	AYE	D	76	2,1	-	0/1/1/1	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	76	AYE	C3-C2	3.88	1.54	1.29
2	B	76	AYE	C3-C2	3.77	1.53	1.29

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	76	AYE	C1-C2-C3	-4.20	114.87	126.38
2	B	76	AYE	C1-C2-C3	-3.94	115.57	126.38

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
2	B	76	AYE	2	0
2	D	76	AYE	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 1 is 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	$\# Z > 2$
3	PG4	A	801	-	9,9,12	0.82	0	8,8,11	0.56	0
3	PG4	A	802	-	6,6,12	0.96	0	5,5,11	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
3	PG4	A	801	-	-	5/7/7/10	-
3	PG4	A	802	-	-	3/4/4/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	801	PG4	O2-C3-C4-O3
3	A	802	PG4	C6-C5-O3-C4
3	A	801	PG4	C5-C6-O4-C7
3	A	801	PG4	C6-C5-O3-C4
3	A	801	PG4	C8-C7-O4-C6
3	A	802	PG4	O2-C3-C4-O3
3	A	802	PG4	C4-C3-O2-C2
3	A	801	PG4	O3-C5-C6-O4

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	801	PG4	1	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

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	453/556 (81%)	-0.08	17 (3%) 44 24	40, 77, 129, 164	0
1	C	459/556 (82%)	0.07	15 (3%) 49 27	41, 95, 150, 169	0
2	B	77/78 (98%)	-0.02	0 100 100	64, 98, 114, 132	0
2	D	74/78 (94%)	0.44	2 (2%) 56 32	87, 154, 180, 187	0
All	All	1063/1268 (83%)	0.02	34 (3%) 50 28	40, 88, 154, 187	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	281	ARG	3.8
1	A	229	ASN	3.2
1	A	280	PRO	3.2
2	D	20	SER	3.1
1	C	242	LEU	2.9
1	C	670	VAL	2.9
2	D	66	THR	2.9
1	C	250	GLU	2.9
1	A	665	ASP	2.8
1	A	537	GLU	2.8
1	A	196	PRO	2.7
1	A	204	ARG	2.6
1	C	149	PRO	2.6
1	A	199	VAL	2.6
1	C	665	ASP	2.5
1	A	198	ASN	2.5
1	C	197	GLN	2.5
1	C	277	VAL	2.4
1	A	308	CYS	2.4
1	C	456	PRO	2.4
1	A	652	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	197	GLN	2.3
1	A	247	ARG	2.3
1	A	667	MET	2.3
1	A	200	LEU	2.3
1	C	154	TRP	2.2
1	C	241	LEU	2.2
1	C	243	LYS	2.2
1	C	694	GLU	2.1
1	C	348	VAL	2.1
1	A	664	SER	2.1
1	A	573	MET	2.1
1	C	596	ALA	2.1
1	C	526	SER	2.0

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. 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	AYE	D	76	4/4	0.84	0.16	118,118,121,125	0
2	AYE	B	76	4/4	0.97	0.09	72,78,81,86	0

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
3	PG4	A	802	7/13	0.70	0.36	69,76,88,103	0
4	CL	A	803	1/1	0.88	0.22	112,112,112,112	1
3	PG4	A	801	10/13	0.94	0.11	53,65,78,81	0

6.5 Other polymers [i](#)

There are no such residues in this entry.