



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 24, 2016 – 06:19 PM EDT

PDB ID : 5IFS
Title : Quantitative interaction mapping reveals an extended ubiquitin regulatory domain in ASPL that disrupts functional p97 hexamers and induces cell death
Authors : Roske, Y.; Arumughan, A.; Heinemann, U.; Wanker, E.
Deposited on : 2016-02-26
Resolution : 2.46 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

<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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027939
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) : rb-20027939

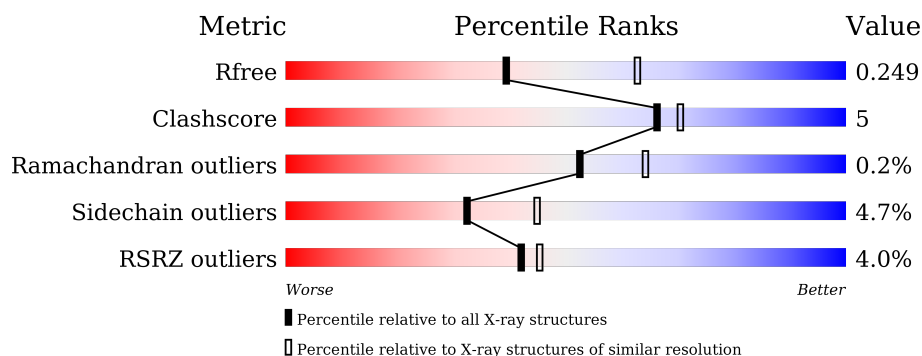
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.46 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	4776 (2.50-2.42)
Clashscore	102246	1030 (2.48-2.44)
Ramachandran outliers	100387	1024 (2.48-2.44)
Sidechain outliers	100360	1024 (2.48-2.44)
RSRZ outliers	91569	4787 (2.50-2.42)

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	237	<div> <div>3%</div> <div> <div></div> <div>62%</div> <div>13%</div> <div>•</div> <div>24%</div> </div> </div>
1	C	237	<div> <div>4%</div> <div> <div></div> <div>61%</div> <div>10%</div> <div>•</div> <div>27%</div> </div> </div>
2	B	481	<div> <div>3%</div> <div> <div></div> <div>77%</div> <div>15%</div> <div>8%</div> </div> </div>
2	D	481	<div> <div>4%</div> <div> <div></div> <div>81%</div> <div>10%</div> <div>8%</div> </div> </div>

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 10322 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.

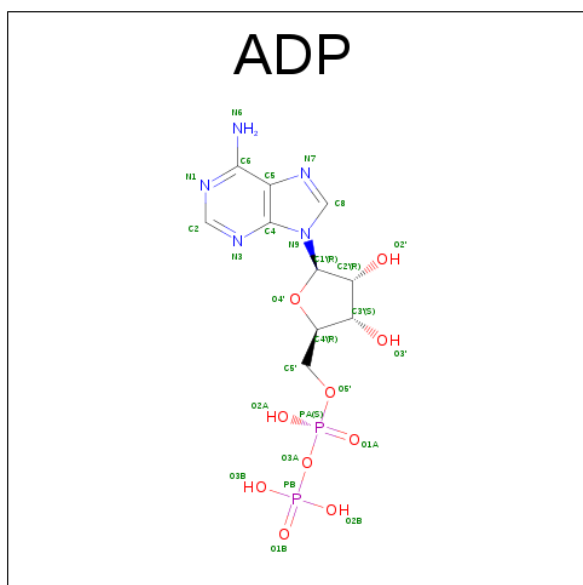
- Molecule 1 is a protein called Tether containing UBX domain for GLUT4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	181	Total	C	N	O	S	0	2	0
			1475	949	258	266	2			
1	C	174	Total	C	N	O	S	0	1	0
			1418	915	245	256	2			

- Molecule 2 is a protein called Transitional endoplasmic reticulum ATPase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	444	Total	C	N	O	S	0	1	0
			3479	2182	617	661	19			
2	D	443	Total	C	N	O	S	0	0	0
			3463	2172	615	658	18			

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).

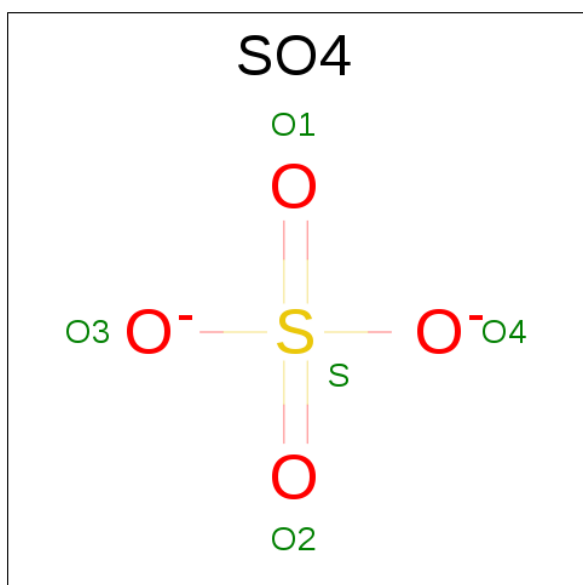


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	D	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Mg	0	0
			1	1		
4	D	1	Total	Mg	0	0
			1	1		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



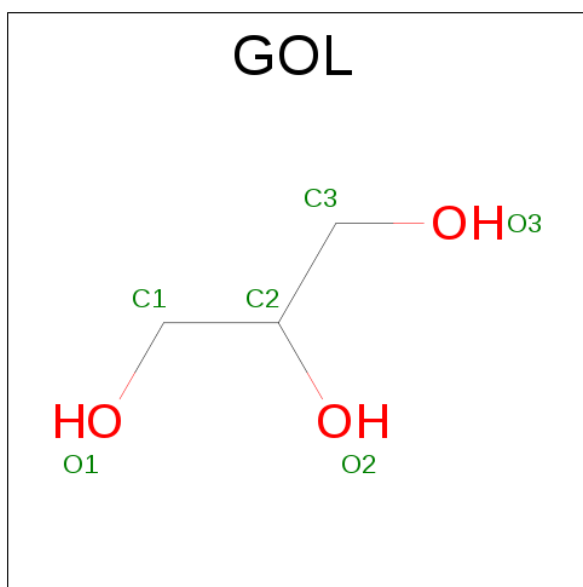
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			4	2	2		
6	B	1	Total	C	O	0	0
			4	2	2		
6	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	C	O	0	0
			6	3	3		

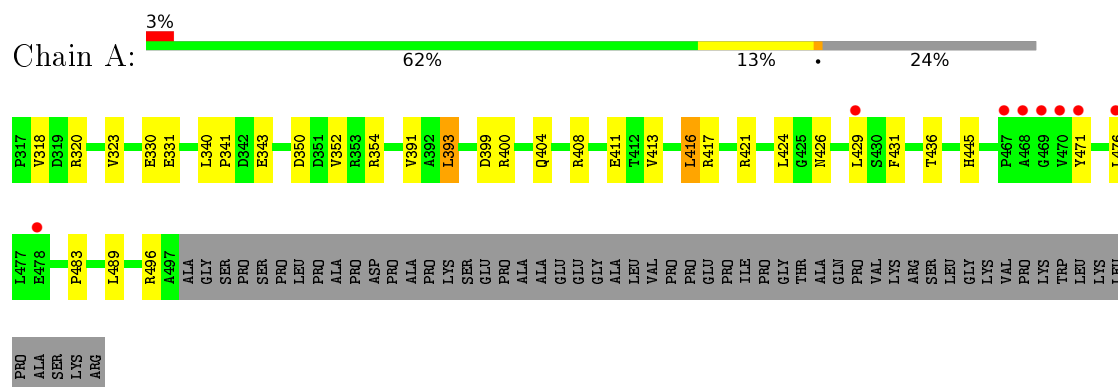
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	63	Total 63	O 63	0	0
8	B	165	Total 165	O 165	0	0
8	C	48	Total 48	O 48	0	0
8	D	132	Total 132	O 132	0	0

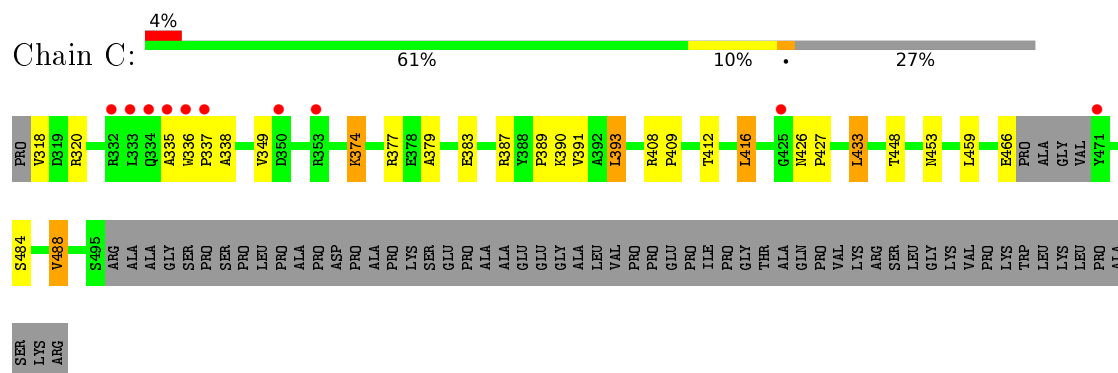
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

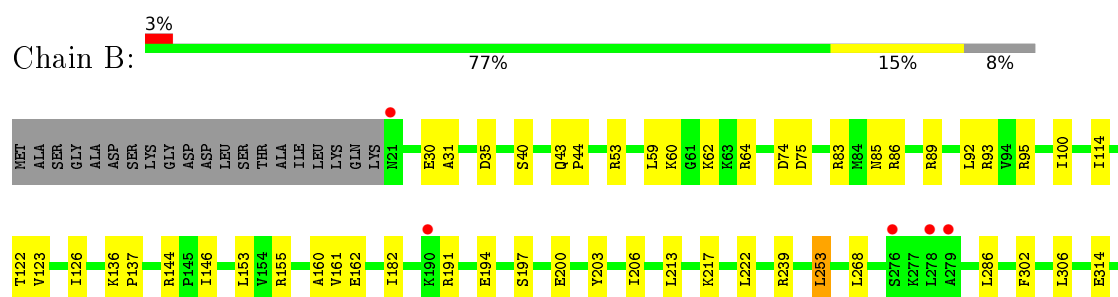
- Molecule 1: Tether containing UBX domain for GLUT4

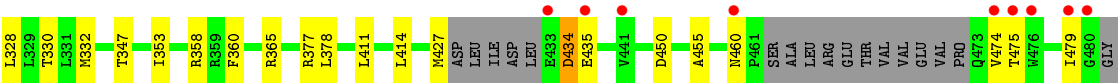


- Molecule 1: Tether containing UBX domain for GLUT4

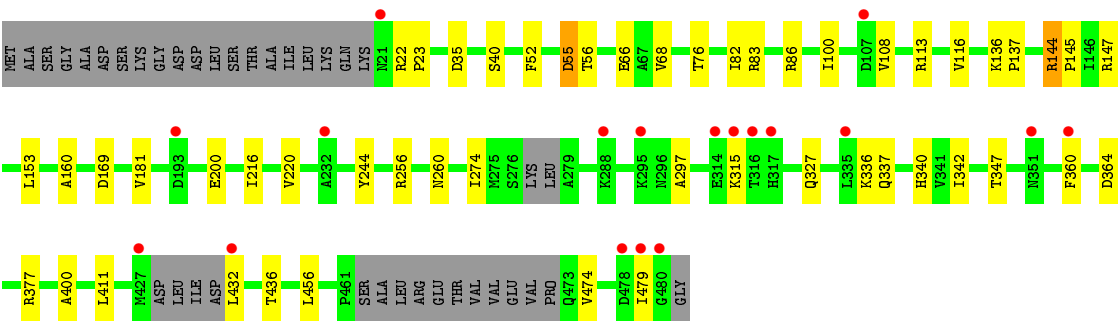
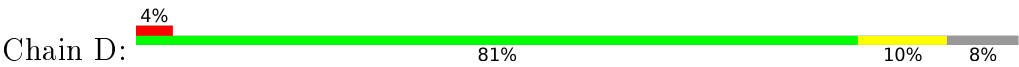


- Molecule 2: Transitional endoplasmic reticulum ATPase





● Molecule 2: Transitional endoplasmic reticulum ATPase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	69.84Å 132.91Å 96.12Å 90.00° 110.15° 90.00°	Depositor
Resolution (Å)	33.77 – 2.46 33.77 – 2.46	Depositor EDS
% Data completeness (in resolution range)	98.0 (33.77-2.46) 98.1 (33.77-2.46)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.68 (at 2.45Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.201 , 0.251 0.201 , 0.249	Depositor DCC
R_{free} test set	2930 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	40.7	Xtriage
Anisotropy	0.219	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 34.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.029 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10322	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.83% 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: GOL, MG, EDO, ADP, SO4

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	0.34	0/1519	0.56	0/2065
1	C	0.32	0/1456	0.52	0/1977
2	B	0.32	0/3536	0.56	0/4779
2	D	0.32	0/3516	0.55	1/4751 (0.0%)
All	All	0.32	0/10027	0.55	1/13572 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	144	ARG	NE-CZ-NH2	-5.07	117.76	120.30

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	1475	0	1478	19	0
1	C	1418	0	1417	13	0
2	B	3479	0	3514	40	0
2	D	3463	0	3491	24	0
3	B	27	0	12	4	0
3	D	27	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	1	0	0	0	0
4	D	1	0	0	0	0
5	B	5	0	0	0	0
6	B	8	0	12	0	0
6	D	4	0	6	0	0
7	B	6	0	8	1	0
8	A	63	0	0	0	0
8	B	165	0	0	6	0
8	C	48	0	0	0	0
8	D	132	0	0	3	0
All	All	10322	0	9950	98	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 5.

All (98) 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)
2:B:377:ARG:HG2	2:B:411:LEU:HD11	1.56	0.88
2:B:122:THR:HG21	2:B:162:GLU:H	1.37	0.86
2:B:122:THR:CG2	2:B:161:VAL:HA	2.12	0.79
1:A:496[B]:ARG:HA	1:A:496[B]:ARG:NH1	1.98	0.79
2:D:377:ARG:HG2	2:D:411:LEU:HD11	1.68	0.76
2:B:182:ILE:H	7:B:506:GOL:H32	1.51	0.75
3:B:501:ADP:C8	3:B:501:ADP:H5'	2.24	0.72
2:B:122:THR:HG21	2:B:162:GLU:N	2.11	0.66
2:B:377:ARG:NH2	8:B:601:HOH:O	2.29	0.64
2:B:122:THR:HG21	2:B:161:VAL:HA	1.79	0.63
2:B:306:LEU:HD23	2:B:353:ILE:HD13	1.80	0.63
2:B:40:SER:HB2	2:B:83:ARG:HB2	1.82	0.62
2:B:153:LEU:HD11	2:B:160:ALA:HB1	1.81	0.62
2:B:206:ILE:HG12	2:B:253:LEU:HD13	1.82	0.61
3:B:501:ADP:H8	3:B:501:ADP:C5'	2.14	0.60
2:B:123:VAL:HG12	2:B:126:ILE:HD11	1.82	0.60
1:A:496[B]:ARG:CZ	1:A:496[B]:ARG:HA	2.30	0.60
3:B:501:ADP:H5'	3:B:501:ADP:H8	1.67	0.59
2:D:377:ARG:NH1	2:D:400:ALA:O	2.36	0.59
2:D:56:THR:HG21	2:D:108:VAL:HG21	1.83	0.59
1:C:393:LEU:HD23	1:C:416:LEU:HG	1.83	0.59
3:B:501:ADP:C8	3:B:501:ADP:C5'	2.86	0.59
2:B:85:ASN:HB2	8:B:668:HOH:O	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:391:VAL:HG12	1:C:393:LEU:HD13	1.87	0.56
2:D:377:ARG:NH2	8:D:602:HOH:O	2.38	0.55
2:D:35:ASP:OD1	2:D:144:ARG:NH2	2.39	0.55
2:B:358:ARG:HD2	8:B:612:HOH:O	2.05	0.55
1:C:336:TRP:O	1:C:338:ALA:N	2.39	0.54
2:D:35:ASP:CG	2:D:144:ARG:HH22	2.13	0.53
2:B:35:ASP:OD1	2:B:144:ARG:NH2	2.43	0.52
1:A:320:ARG:HH22	1:A:411:GLU:CD	2.11	0.52
1:A:318:VAL:HG21	1:A:408:ARG:HG3	1.92	0.52
1:C:336:TRP:H	1:C:337:PRO:HD2	1.75	0.52
2:D:220:VAL:HG12	2:D:342:ILE:HD13	1.91	0.52
1:A:352:VAL:HG13	2:B:222:LEU:HD22	1.93	0.51
2:B:59:LEU:HD22	2:B:100:ILE:HD13	1.92	0.51
2:D:86:ARG:NH2	2:D:200:GLU:O	2.44	0.51
2:B:95:ARG:NH1	8:B:602:HOH:O	2.43	0.50
2:D:360:PHE:HA	2:D:364:ASP:HB3	1.94	0.50
2:B:162:GLU:OE1	2:B:191:ARG:NH2	2.45	0.50
2:B:434:ASP:OD1	2:B:434:ASP:N	2.44	0.50
1:A:391:VAL:HG12	1:A:393:LEU:HD13	1.94	0.49
1:C:416:LEU:HD13	1:C:433:LEU:HD23	1.95	0.49
2:B:86:ARG:HG3	2:B:89:ARG:NH2	2.28	0.48
2:B:328:LEU:O	2:B:332:MET:HG2	2.12	0.48
2:D:66:GLU:HG2	2:D:147:ARG:HE	1.78	0.48
2:B:93:ARG:HH21	2:B:194:GLU:HG2	1.79	0.48
1:A:318:VAL:CG2	1:A:408:ARG:HG3	2.44	0.47
1:A:417:ARG:NH2	1:A:431:PHE:O	2.47	0.47
1:A:330:GLU:HG2	1:A:483:PRO:HD2	1.96	0.47
2:B:197:SER:HB3	2:B:200:GLU:HG2	1.96	0.47
1:C:318:VAL:HG13	1:C:408:ARG:HH11	1.78	0.47
1:C:412:THR:HA	1:C:448:THR:HA	1.97	0.47
2:D:113:ARG:HG2	2:D:169:ASP:HB3	1.97	0.46
2:D:297:ALA:HB1	2:D:340:HIS:HB2	1.96	0.46
1:C:389:PRO:O	1:C:409:PRO:HD3	2.15	0.46
2:D:136:LYS:HB3	2:D:137:PRO:HD3	1.98	0.46
1:A:320:ARG:NH2	1:A:411:GLU:OE1	2.49	0.46
2:D:144:ARG:HG3	8:D:626:HOH:O	2.15	0.45
2:B:122:THR:HG22	2:B:161:VAL:HA	1.93	0.45
2:D:22:ARG:HA	2:D:23:PRO:HD3	1.78	0.45
2:D:216:ILE:O	2:D:220:VAL:HG22	2.16	0.45
2:D:52:PHE:O	2:D:55:ASP:HB2	2.16	0.45
2:D:260:ASN:HB3	8:D:681:HOH:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:426:ASN:HB2	1:A:429:LEU:HD23	1.98	0.45
2:D:244:TYR:HA	2:D:347:THR:O	2.16	0.44
1:A:399:ASP:O	1:A:400:ARG:HB2	2.17	0.44
2:B:136:LYS:HB3	2:B:137:PRO:HD3	1.99	0.44
2:B:35:ASP:CG	2:B:144:ARG:HH22	2.21	0.44
1:A:340:LEU:O	2:B:64:ARG:NH2	2.49	0.44
2:B:414:LEU:HD12	2:B:455:ALA:HB1	1.99	0.44
2:B:43:GLN:HB3	2:B:44:PRO:HD3	2.01	0.43
2:D:153:LEU:HD11	2:D:160:ALA:HB1	2.00	0.43
2:B:40:SER:HB3	2:B:74:ASP:HB2	2.00	0.43
2:D:82:ILE:HG21	2:D:100:ILE:HG12	2.00	0.43
1:A:393:LEU:HD23	1:A:416:LEU:HG	2.01	0.43
2:D:40:SER:HB2	2:D:83:ARG:HB2	2.01	0.42
1:C:484:SER:O	1:C:488:VAL:HG13	2.19	0.42
1:C:374:LYS:HG3	1:C:377:ARG:HH22	1.85	0.42
1:C:379:ALA:O	1:C:383:GLU:HB2	2.20	0.42
2:B:203:TYR:CE2	2:B:217:LYS:HE2	2.55	0.42
2:B:213:LEU:HD23	2:B:213:LEU:HA	1.95	0.42
2:D:68:VAL:HG12	2:D:145:PRO:HB2	2.01	0.42
1:A:413:VAL:O	1:A:417:ARG:HG3	2.20	0.41
1:C:336:TRP:N	1:C:337:PRO:HD2	2.33	0.41
1:C:426:ASN:HA	1:C:427:PRO:HD3	1.91	0.41
1:A:341:PRO:HB2	1:A:343:GLU:HG2	2.02	0.41
2:B:268:LEU:HD13	2:B:302:PHE:HD2	1.86	0.41
2:D:336:LYS:HD3	2:D:337:GLN:N	2.36	0.41
2:B:114:ILE:HG21	2:B:146:ILE:HD11	2.02	0.40
2:B:30:GLU:HG3	2:B:31:ALA:N	2.37	0.40
2:B:365:ARG:NH1	8:B:608:HOH:O	2.55	0.40
2:B:62:LYS:O	2:B:64:ARG:HG3	2.21	0.40
1:A:323:VAL:HG23	1:A:404:GLN:HB3	2.04	0.40
2:B:53:ARG:HG3	8:B:613:HOH:O	2.20	0.40
1:A:350:ASP:OD2	1:A:354:ARG:NH2	2.54	0.40
1:A:421:ARG:HA	1:A:424:LEU:HD12	2.02	0.40
2:B:347:THR:HB	2:B:353:ILE:HD11	2.03	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	181/237 (76%)	173 (96%)	7 (4%)	1 (1%)	30	35
1	C	171/237 (72%)	163 (95%)	7 (4%)	1 (1%)	30	35
2	B	439/481 (91%)	425 (97%)	14 (3%)	0	100	100
2	D	435/481 (90%)	419 (96%)	15 (3%)	1 (0%)	52	64
All	All	1226/1436 (85%)	1180 (96%)	43 (4%)	3 (0%)	52	64

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	335	ALA
2	D	315	LYS
1	A	471	TYR

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	159/202 (79%)	152 (96%)	7 (4%)	35	49
1	C	153/202 (76%)	141 (92%)	12 (8%)	16	20
2	B	380/410 (93%)	361 (95%)	19 (5%)	30	42
2	D	377/410 (92%)	365 (97%)	12 (3%)	46	63
All	All	1069/1224 (87%)	1019 (95%)	50 (5%)	32	45

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	331	GLU
1	A	393	LEU
1	A	416	LEU
1	A	436	THR
1	A	445	HIS
1	A	476	LEU
1	A	489	LEU
2	B	60	LYS
2	B	75	ASP
2	B	92	LEU
2	B	155	ARG
2	B	239	ARG
2	B	253	LEU
2	B	286	LEU
2	B	314	GLU
2	B	330	THR
2	B	360	PHE
2	B	378	LEU
2	B	427	MET
2	B	434	ASP
2	B	435	GLU
2	B	450	ASP
2	B	460	ASN
2	B	474	VAL
2	B	475	THR
2	B	479	ILE
1	C	320	ARG
1	C	349	VAL
1	C	374	LYS
1	C	387	ARG
1	C	390	LYS
1	C	393	LEU
1	C	416	LEU
1	C	433	LEU
1	C	453	ASN
1	C	459	LEU
1	C	466	GLU
1	C	488	VAL
2	D	55	ASP
2	D	76	THR
2	D	116	VAL
2	D	181	VAL
2	D	256	ARG

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Mol	Chain	Res	Type
2	D	274	ILE
2	D	327	GLN
2	D	432	LEU
2	D	436	THR
2	D	456	LEU
2	D	474	VAL
2	D	479	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 2 are monoatomic - leaving 7 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	ADP	B	501	4	24,29,29	1.00	1 (4%)	23,45,45	1.94	3 (13%)
5	SO4	B	503	-	4,4,4	0.34	0	6,6,6	0.16	0
6	EDO	B	504	-	3,3,3	0.43	0	2,2,2	0.59	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	EDO	B	505	-	3,3,3	0.40	0	2,2,2	0.60	0
7	GOL	B	506	-	5,5,5	0.29	0	5,5,5	0.36	0
3	ADP	D	501	4	24,29,29	1.07	1 (4%)	23,45,45	1.85	1 (4%)
6	EDO	D	503	-	3,3,3	0.46	0	2,2,2	0.34	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	ADP	B	501	4	-	0/12/32/32	0/3/3/3
5	SO4	B	503	-	-	0/0/0/0	0/0/0/0
6	EDO	B	504	-	-	0/1/1/1	0/0/0/0
6	EDO	B	505	-	-	0/1/1/1	0/0/0/0
7	GOL	B	506	-	-	0/4/4/4	0/0/0/0
3	ADP	D	501	4	-	0/12/32/32	0/3/3/3
6	EDO	D	503	-	-	0/1/1/1	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	501	ADP	C5-C4	2.94	1.47	1.40
3	D	501	ADP	C5-C4	3.27	1.47	1.40

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	501	ADP	N3-C2-N1	-7.41	123.05	128.87
3	B	501	ADP	N3-C2-N1	-7.26	123.17	128.87
3	B	501	ADP	C1'-N9-C4	-2.07	124.49	126.81
3	B	501	ADP	O4'-C1'-N9	2.41	112.66	108.11

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	501	ADP	4	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	506	GOL	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	181/237 (76%)	0.15	8 (4%) 38 41	26, 40, 70, 103	0
1	C	174/237 (73%)	0.25	10 (5%) 27 30	28, 45, 80, 111	0
2	B	444/481 (92%)	0.15	14 (3%) 51 54	23, 38, 72, 100	0
2	D	443/481 (92%)	0.15	18 (4%) 41 44	24, 40, 82, 111	0
All	All	1242/1436 (86%)	0.16	50 (4%) 42 45	23, 40, 79, 111	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	479	ILE	5.6
1	C	333	LEU	5.3
2	B	279	ALA	4.9
2	D	432	LEU	4.7
2	B	21	ASN	4.5
1	A	469	GLY	4.3
2	B	479	ILE	4.3
2	D	316	THR	4.0
1	C	425	GLY	3.8
2	B	276	SER	3.5
2	D	317	HIS	3.5
2	B	480	GLY	3.4
1	A	471	TYR	3.3
1	C	332	ARG	3.2
1	C	335	ALA	3.2
2	B	475	THR	3.2
2	D	288	LYS	3.1
2	B	476	TRP	3.0
1	A	468	ALA	3.0
2	D	315	LYS	3.0
2	D	193	ASP	2.9

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Mol	Chain	Res	Type	RSRZ
1	C	334	GLN	2.8
2	B	441	VAL	2.8
1	C	350	ASP	2.8
2	D	21	ASN	2.8
2	D	427	MET	2.8
2	D	478	ASP	2.8
1	A	470	VAL	2.7
2	B	278	LEU	2.5
1	A	467	PRO	2.5
2	D	360	PHE	2.5
2	B	433	GLU	2.5
1	C	353	ARG	2.5
2	B	435	GLU	2.5
2	D	107	ASP	2.4
1	C	337	PRO	2.4
2	B	460	ASN	2.3
2	B	474	VAL	2.3
1	C	336	TRP	2.3
1	C	471	TYR	2.3
2	D	295	LYS	2.3
2	D	314	GLU	2.2
2	D	480	GLY	2.1
1	A	478	GLU	2.1
2	D	335	LEU	2.1
2	D	351	ASN	2.1
1	A	429	LEU	2.0
2	D	232	ALA	2.0
2	B	190	LYS	2.0
1	A	476	LEU	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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
7	GOL	B	506	6/6	0.81	0.17	1.31	55,60,61,62	0
3	ADP	D	501	27/27	0.98	0.12	-0.34	28,30,31,32	0
3	ADP	B	501	27/27	0.98	0.14	-0.41	22,25,29,32	0
6	EDO	D	503	4/4	0.83	0.30	-	56,58,58,59	0
4	MG	B	502	1/1	0.83	0.23	-	57,57,57,57	0
6	EDO	B	505	4/4	0.94	0.20	-	47,47,50,50	0
5	SO4	B	503	5/5	0.96	0.12	-	53,54,55,57	0
4	MG	D	502	1/1	0.81	0.11	-	63,63,63,63	0
6	EDO	B	504	4/4	0.91	0.23	-	47,47,47,48	0

6.5 Other polymers

There are no such residues in this entry.