



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 15, 2024 – 06:42 PM EDT

PDB ID : 2H9E
Title : Crystal Structure of FXa/selectide/NAPC2 ternary complex
Authors : Murakami, M.T.; Geiger, G.; Tulinsky, A.; Arni, R.K.
Deposited on : 2006-06-09
Resolution : 2.20 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 : 4.02b-467
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 1.20.1
EDS : 2.37.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

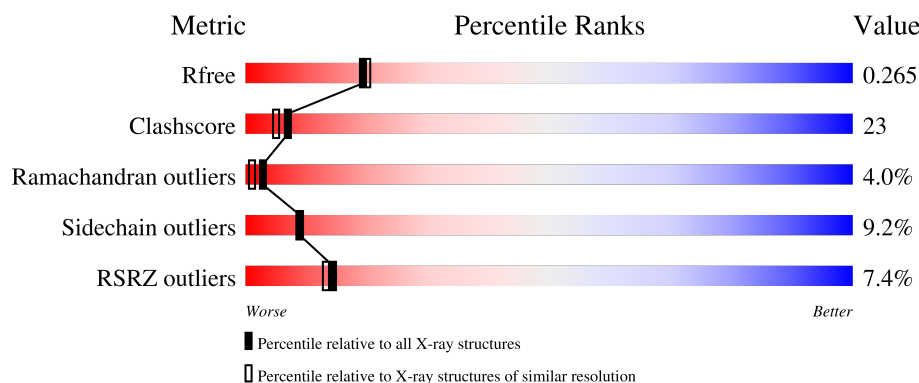
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	H	233	<div> <div>3%</div> <div>65%</div> <div>27%</div> <div>7%</div> </div>
2	L	149	<div> <div>20%</div> <div>10%</div> <div>68%</div> </div>
3	C	84	<div> <div>20%</div> <div>26%</div> <div>24%</div> <div>11%</div> <div>38%</div> </div>
4	S	5	<div> <div>40%</div> <div>60%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	DTY	S	1	X	-	-	-
6	ACT	H	703	-	-	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 2944 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 Coagulation factor X heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	233	Total	C	N	O	S	0	1	0
			1851	1165	322	350	14			

- Molecule 2 is a protein called Coagulation factor X light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	48	Total	C	N	O	S	0	1	0
			351	208	61	75	7			

- Molecule 3 is a protein called Anti-coagulant protein C2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	52	Total	C	N	O	S	0	0	0
			394	238	60	89	7			

- Molecule 4 is a protein called selectide inhibitor DTY-ILE-ARG-LEU-LPD peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	S	5	Total	C	N	O	0	0	0
			47	32	9	6			

- Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	H	1	Total	O	P	0	0
			5	4	1		
5	H	1	Total	O	P	0	0
			5	4	1		
5	H	1	Total	O	P	0	0
			5	4	1		
5	H	1	Total	O	P	0	0
			5	4	1		
5	H	1	Total	O	P	0	0
			5	4	1		

- Molecule 6 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



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

- Molecule 7 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	H	1	Total	Na	0	0
			1	1		

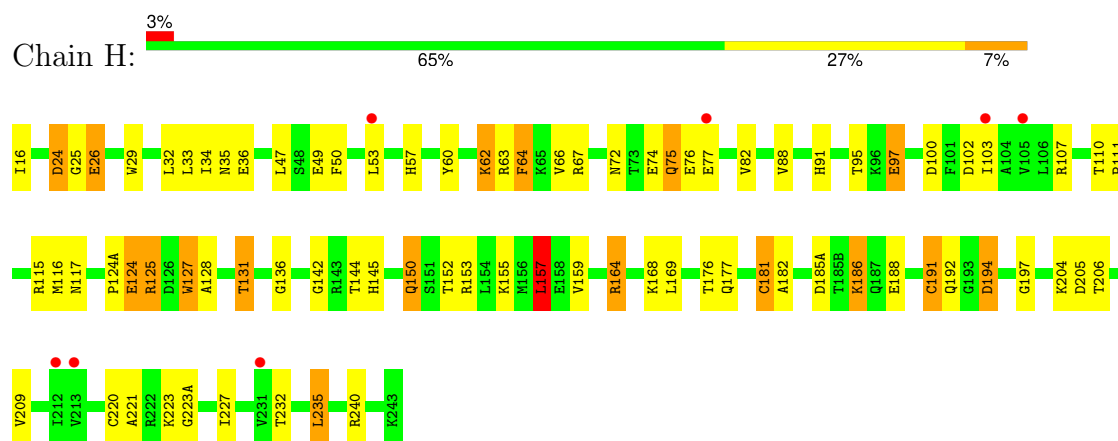
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	H	170	Total	O	0	0
			170	170		
8	L	56	Total	O	0	0
			56	56		
8	C	22	Total	O	0	0
			22	22		
8	S	10	Total	O	0	0
			10	10		

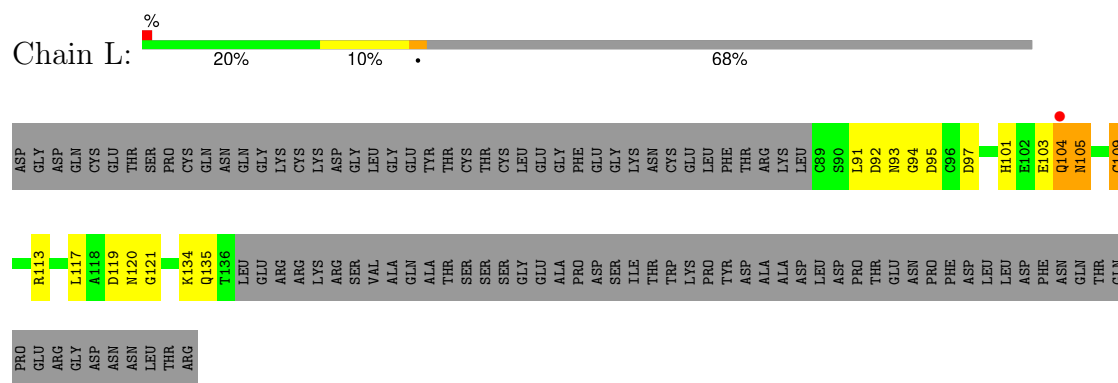
3 Residue-property plots [i](#)

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.

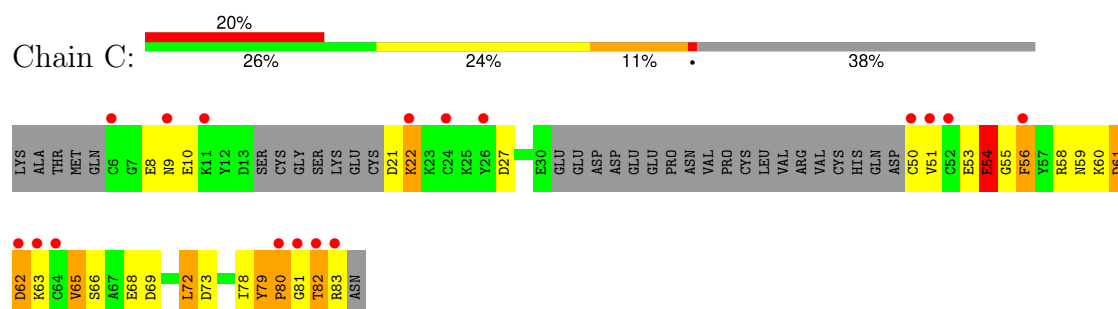
• Molecule 1: Coagulation factor X heavy chain



• Molecule 2: Coagulation factor X light chain



• Molecule 3: Anti-coagulant protein C2



- Molecule 4: selectide inhibitor DTY-ILE-ARG-LEU-LPD peptide

Chain S:  40% 60%

Y1	I2	R3	L4	P5
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4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	48.95Å 86.41Å 145.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	74.33 – 2.20 37.17 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.5 (74.33-2.20) 99.5 (37.17-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.67 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.220 , 0.268 0.219 , 0.265	Depositor DCC
R_{free} test set	1631 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	42.6	Xtriage
Anisotropy	0.143	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 78.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2944	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.57% 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: LPD, DTY, ACT, PO4, NA

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	H	1.15	5/1893 (0.3%)	1.03	7/2548 (0.3%)
2	L	1.31	1/362 (0.3%)	1.24	2/490 (0.4%)
3	C	0.65	0/398	0.86	0/534
4	S	0.97	0/26	2.60	2/33 (6.1%)
All	All	1.11	6/2679 (0.2%)	1.06	11/3605 (0.3%)

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
3	C	0	2
4	S	1	0
All	All	1	2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	127	TRP	CB-CG	-6.87	1.37	1.50
1	H	124	GLU	CG-CD	6.35	1.61	1.51
1	H	182	ALA	CA-CB	5.79	1.64	1.52
2	L	109	CYS	CB-SG	-5.75	1.72	1.81
1	H	26	GLU	CB-CG	-5.64	1.41	1.52
1	H	191	CYS	CB-SG	5.12	1.91	1.82

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	209	VAL	CG1-CB-CG2	10.96	128.44	110.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	S	3	ARG	NE-CZ-NH2	-10.23	115.19	120.30
4	S	3	ARG	NE-CZ-NH1	8.29	124.44	120.30
2	L	97	ASP	CB-CG-OD1	6.64	124.28	118.30
1	H	209	VAL	CB-CA-C	-6.52	99.00	111.40
2	L	91	LEU	C-N-CA	-6.32	105.91	121.70
1	H	169	LEU	CB-CG-CD1	-6.30	100.28	111.00
1	H	157	LEU	CA-CB-CG	6.05	129.21	115.30
1	H	194	ASP	CB-CG-OD2	5.93	123.64	118.30
1	H	181	CYS	CA-CB-SG	5.15	123.28	114.00
1	H	136	GLY	N-CA-C	-5.12	100.29	113.10

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	S	1	DTY	CA

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	81	GLY	Peptide
3	C	82	THR	Peptide

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	H	1851	0	1803	76	0
2	L	351	0	309	11	0
3	C	394	0	308	39	0
4	S	47	0	53	1	0
5	H	30	0	0	1	0
6	H	12	0	9	3	0
7	H	1	0	0	0	0
8	C	22	0	0	1	0
8	H	170	0	0	9	0
8	L	56	0	0	1	0
8	S	10	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	2944	0	2482	119	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 23.

All (119) 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)
3:C:9:ASN:O	3:C:53:GLU:HG3	1.09	1.23
3:C:9:ASN:CB	3:C:56:PHE:CD2	2.29	1.10
1:H:62:LYS:H	1:H:62:LYS:HD2	1.17	1.09
1:H:62:LYS:H	1:H:62:LYS:CD	1.63	1.09
3:C:9:ASN:HB3	3:C:56:PHE:CD2	1.52	1.07
3:C:9:ASN:O	3:C:53:GLU:CG	2.03	1.04
1:H:36:GLU:CG	1:H:63:ARG:HB2	1.98	0.93
3:C:9:ASN:HB3	3:C:56:PHE:HD2	1.34	0.92
1:H:62:LYS:HD3	1:H:63:ARG:H	1.35	0.90
1:H:62:LYS:CD	1:H:62:LYS:N	2.31	0.88
3:C:79:TYR:CB	3:C:80:PRO:HD3	2.05	0.87
1:H:36:GLU:HB2	1:H:62:LYS:HE3	1.56	0.86
1:H:97:GLU:HG3	8:H:832:HOH:O	1.75	0.86
1:H:36:GLU:HG3	1:H:63:ARG:HB2	1.56	0.86
3:C:9:ASN:C	3:C:53:GLU:HG3	1.95	0.85
3:C:53:GLU:O	3:C:55:GLY:N	2.11	0.83
1:H:35:ASN:HB2	1:H:62:LYS:HE2	1.63	0.81
1:H:232:THR:HA	1:H:235:LEU:HD22	1.62	0.81
1:H:164:ARG:NH2	1:H:176:THR:O	2.17	0.78
1:H:36:GLU:OE1	1:H:63:ARG:NE	2.18	0.76
1:H:127:TRP:O	1:H:131:THR:HG23	1.84	0.76
1:H:62:LYS:HD3	1:H:62:LYS:N	2.02	0.75
1:H:152:THR:HG23	1:H:153:ARG:HG3	1.69	0.74
1:H:50:PHE:CZ	1:H:111:PRO:HG3	2.23	0.73
1:H:62:LYS:HD3	1:H:63:ARG:N	2.03	0.73
1:H:36:GLU:OE1	1:H:63:ARG:HD3	1.90	0.72
3:C:79:TYR:OH	8:C:87:HOH:O	2.07	0.72
1:H:57:HIS:NE2	8:H:867:HOH:O	1.96	0.70
1:H:36:GLU:OE1	1:H:63:ARG:CD	2.42	0.68
3:C:79:TYR:HB3	3:C:80:PRO:HD3	1.74	0.68
3:C:79:TYR:HB2	3:C:80:PRO:HD3	1.79	0.65
8:H:867:HOH:O	4:S:1:DTY:N	2.01	0.64
1:H:75:GLN:O	1:H:77:GLU:HG3	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:92:ASP:C	2:L:94:GLY:H	2.01	0.64
1:H:36:GLU:HG2	1:H:63:ARG:HB2	1.78	0.63
1:H:67:ARG:NH1	1:H:82:VAL:CG2	2.62	0.62
1:H:67:ARG:HH11	1:H:82:VAL:HG22	1.64	0.62
1:H:206:THR:OG1	2:L:134:LYS:NZ	2.33	0.61
2:L:92:ASP:C	2:L:94:GLY:N	2.54	0.60
3:C:53:GLU:C	3:C:55:GLY:N	2.51	0.60
1:H:25:GLY:N	1:H:117:ASN:OD1	2.26	0.60
3:C:69:ASP:O	3:C:72:LEU:HB2	2.01	0.60
1:H:88:VAL:HB	3:C:78:ILE:HB	1.83	0.59
3:C:21:ASP:O	3:C:22:LYS:HB2	2.01	0.59
1:H:107:ARG:NH1	8:H:813:HOH:O	2.19	0.59
1:H:232:THR:HA	1:H:235:LEU:CD2	2.32	0.59
3:C:53:GLU:O	3:C:54:GLU:C	2.40	0.59
1:H:67:ARG:NH1	1:H:82:VAL:HG22	2.17	0.59
3:C:56:PHE:N	3:C:56:PHE:CD1	2.68	0.59
1:H:16:ILE:N	1:H:194:ASP:OD2	2.36	0.59
1:H:125:ARG:NH2	3:C:27:ASP:OD1	2.37	0.58
1:H:124(A):PRO:HB2	1:H:128:ALA:HB2	1.86	0.58
1:H:67:ARG:HG2	1:H:82:VAL:HG22	1.86	0.57
2:L:104:GLN:HG3	2:L:104:GLN:O	2.03	0.57
1:H:47:LEU:HD11	1:H:53:LEU:HB2	1.85	0.57
1:H:49[B]:GLU:HG3	1:H:111:PRO:HB3	1.84	0.57
1:H:232:THR:HG23	8:H:709:HOH:O	2.04	0.57
3:C:8:GLU:HG2	3:C:9:ASN:ND2	2.19	0.57
1:H:204:LYS:H	6:H:702:ACT:CH3	2.19	0.56
3:C:9:ASN:C	3:C:53:GLU:CG	2.65	0.56
1:H:223:LYS:N	5:H:606:PO4:O3	2.29	0.55
3:C:53:GLU:C	3:C:55:GLY:H	2.10	0.55
3:C:61:ASP:O	3:C:62:ASP:C	2.45	0.55
1:H:26:GLU:O	2:L:135:GLN:NE2	2.38	0.55
2:L:119:ASP:HB2	8:L:233:HOH:O	2.07	0.54
3:C:66:SER:OG	3:C:69:ASP:OD1	2.26	0.54
1:H:204:LYS:NZ	8:H:772:HOH:O	2.41	0.53
3:C:9:ASN:CB	3:C:56:PHE:HD2	1.96	0.53
3:C:61:ASP:O	3:C:63:LYS:N	2.41	0.53
1:H:144:THR:HG22	1:H:155:LYS:HE2	1.91	0.52
3:C:58:ARG:CB	3:C:62:ASP:OD1	2.57	0.52
1:H:191:CYS:SG	1:H:192:GLN:N	2.83	0.51
1:H:177:GLN:HE21	6:H:703:ACT:C	2.23	0.51
1:H:181:CYS:SG	1:H:227:ILE:CD1	2.99	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:72:ASN:C	1:H:72:ASN:OD1	2.50	0.50
1:H:220:CYS:O	1:H:221:ALA:HB3	2.11	0.50
3:C:69:ASP:O	3:C:72:LEU:HD23	2.12	0.50
1:H:142:GLY:HA2	1:H:150:GLN:NE2	2.28	0.49
1:H:124:GLU:OE1	2:L:101:HIS:CE1	2.66	0.49
2:L:103:GLU:O	2:L:104:GLN:C	2.51	0.49
3:C:79:TYR:CB	3:C:80:PRO:CD	2.85	0.49
1:H:36:GLU:CB	1:H:62:LYS:HE3	2.38	0.49
3:C:21:ASP:OD2	3:C:51:VAL:HG13	2.13	0.48
1:H:75:GLN:O	1:H:77:GLU:CG	2.62	0.47
1:H:72:ASN:OD1	1:H:74:GLU:N	2.33	0.47
1:H:36:GLU:CD	1:H:63:ARG:HD3	2.34	0.47
1:H:24:ASP:OD2	1:H:117:ASN:ND2	2.41	0.46
1:H:124:GLU:OE1	2:L:101:HIS:HE1	1.98	0.46
1:H:240:ARG:HB2	3:C:68:GLU:HG3	1.98	0.46
1:H:181:CYS:SG	1:H:227:ILE:HD13	2.56	0.45
1:H:72:ASN:HA	1:H:152:THR:O	2.17	0.45
1:H:76:GLU:C	1:H:77:GLU:HG3	2.35	0.45
3:C:55:GLY:HA3	3:C:56:PHE:CD1	2.51	0.45
3:C:69:ASP:HA	3:C:72:LEU:CD2	2.47	0.44
1:H:197:GLY:HA3	8:H:704:HOH:O	2.17	0.44
3:C:61:ASP:O	3:C:63:LYS:HG3	2.17	0.44
1:H:67:ARG:HH11	1:H:82:VAL:CG2	2.26	0.44
3:C:56:PHE:HB3	3:C:65:VAL:O	2.18	0.44
2:L:109:CYS:HB2	2:L:121:GLY:O	2.17	0.44
1:H:62:LYS:HD2	1:H:62:LYS:N	2.01	0.43
1:H:91:HIS:HB2	1:H:103:ILE:HG23	2.01	0.43
1:H:186:LYS:HG3	1:H:188:GLU:HG3	2.01	0.43
1:H:157:LEU:HD13	1:H:159:VAL:CG1	2.49	0.42
1:H:34:ILE:O	1:H:64:PHE:HA	2.18	0.42
3:C:59:ASN:HB2	3:C:73:ASP:OD2	2.20	0.42
3:C:69:ASP:HA	3:C:72:LEU:HD23	2.02	0.42
1:H:186:LYS:HE3	1:H:186:LYS:HB2	1.61	0.42
3:C:79:TYR:CD1	3:C:79:TYR:N	2.87	0.42
1:H:57:HIS:ND1	1:H:102:ASP:OD2	2.53	0.41
1:H:33:LEU:HD22	1:H:66:VAL:HG22	2.01	0.41
1:H:127:TRP:O	1:H:131:THR:CG2	2.64	0.41
3:C:10:GLU:OE1	3:C:50:CYS:HB3	2.20	0.41
1:H:60:TYR:O	3:C:83:ARG:NE	2.53	0.41
1:H:185(A):ASP:OD1	1:H:223(A):GLY:HA2	2.20	0.41
1:H:125:ARG:HA	1:H:235:LEU:HD23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:100:ASP:OD2	8:H:821:HOH:O	2.22	0.41
1:H:145:HIS:HB2	8:H:872:HOH:O	2.20	0.40
1:H:168:LYS:HZ1	6:H:703:ACT:C	2.35	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	H	232/233 (100%)	217 (94%)	14 (6%)	1 (0%)	34	37
2	L	47/149 (32%)	38 (81%)	4 (8%)	5 (11%)	0	0
3	C	46/84 (55%)	36 (78%)	3 (6%)	7 (15%)	0	0
4	S	3/5 (60%)	2 (67%)	1 (33%)	0	100	100
All	All	328/471 (70%)	293 (89%)	22 (7%)	13 (4%)	3	1

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	L	104	GLN
2	L	120	ASN
3	C	54	GLU
3	C	61	ASP
3	C	62	ASP
3	C	79	TYR
3	C	80	PRO
1	H	205	ASP
2	L	95	ASP
3	C	22	LYS
3	C	60	LYS
2	L	93	ASN

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Mol	Chain	Res	Type
2	L	105	ASN

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	H	199/198 (100%)	181 (91%)	18 (9%)	9	9
2	L	41/128 (32%)	38 (93%)	3 (7%)	14	15
3	C	41/77 (53%)	36 (88%)	5 (12%)	5	4
4	S	3/3 (100%)	3 (100%)	0	100	100
All	All	284/406 (70%)	258 (91%)	26 (9%)	9	9

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	24	ASP
1	H	29	TRP
1	H	32	LEU
1	H	62	LYS
1	H	64	PHE
1	H	75	GLN
1	H	95	THR
1	H	97	GLU
1	H	110	THR
1	H	115	ARG
1	H	116	MET
1	H	125	ARG
1	H	131	THR
1	H	150	GLN
1	H	157	LEU
1	H	164	ARG
1	H	186	LYS
1	H	235	LEU
2	L	105	ASN
2	L	113	ARG

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Mol	Chain	Res	Type
2	L	117	LEU
3	C	54	GLU
3	C	56	PHE
3	C	65	VAL
3	C	72	LEU
3	C	82	THR

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

Mol	Chain	Res	Type
1	H	30	GLN
1	H	133	GLN
1	H	150	GLN
1	H	177	GLN
3	C	9	ASN

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	$\# Z > 2$
4	LPD	S	5	4	8,8,8	0.59	0	10,10,10	0.98	1 (10%)

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	DTY	S	1	4	1/1/1/2	-	-
4	LPD	S	5	4	-	0/4/11/11	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
4	S	5	LPD	C-CA-N	-2.13	106.76	111.16

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	S	1	DTY	CA

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	S	1	DTY	1	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 1 is monoatomic - leaving 9 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	$\# Z > 2$
5	PO4	H	605	-	4,4,4	1.12	0	6,6,6	0.66	0
5	PO4	H	603	-	4,4,4	0.85	0	6,6,6	0.85	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	ACT	H	703	-	3,3,3	0.93	0	3,3,3	1.21	0
5	PO4	H	602	-	4,4,4	1.27	0	6,6,6	1.17	0
6	ACT	H	701	-	3,3,3	0.86	0	3,3,3	1.19	0
5	PO4	H	601	-	4,4,4	1.38	0	6,6,6	1.74	3 (50%)
5	PO4	H	604	-	4,4,4	0.83	0	6,6,6	1.03	0
5	PO4	H	606	-	4,4,4	1.08	0	6,6,6	0.71	0
6	ACT	H	702	-	3,3,3	1.00	0	3,3,3	1.44	0

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	H	601	PO4	O3-P-O2	2.42	115.44	107.91
5	H	601	PO4	O4-P-O1	2.32	119.17	110.95
5	H	601	PO4	O3-P-O1	-2.28	102.87	110.95

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	H	703	ACT	2	0
5	H	606	PO4	1	0
6	H	702	ACT	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	H	233/233 (100%)	0.10	7 (3%)	50	48	21, 38, 57, 63	15 (6%)
2	L	48/149 (32%)	0.07	1 (2%)	63	61	29, 42, 64, 66	4 (8%)
3	C	52/84 (61%)	1.68	17 (32%)	0	0	49, 64, 74, 78	21 (40%)
4	S	3/5 (60%)	-0.27	0	100	100	36, 36, 41, 43	0
All	All	336/471 (71%)	0.34	25 (7%)	14	13	21, 41, 67, 78	40 (11%)

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	51	VAL	8.7
3	C	81	GLY	8.4
3	C	52	CYS	6.1
3	C	11	LYS	4.2
3	C	6	CYS	3.9
3	C	64	CYS	3.8
3	C	83	ARG	3.6
1	H	77	GLU	3.2
3	C	80	PRO	3.1
3	C	22	LYS	3.0
3	C	50	CYS	3.0
3	C	9	ASN	2.9
1	H	231	VAL	2.9
3	C	24	CYS	2.7
3	C	82	THR	2.6
1	H	212	ILE	2.5
3	C	56	PHE	2.5
1	H	53	LEU	2.5
3	C	63	LYS	2.4
1	H	103	ILE	2.4
2	L	104	GLN	2.2

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Mol	Chain	Res	Type	RSRZ
3	C	62	ASP	2.2
3	C	26	TYR	2.1
1	H	105	VAL	2.1
1	H	213	VAL	2.1

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
4	DTY	S	1	12/13	0.91	0.12	27,32,34,34	0
4	LPD	S	5	8/8	0.94	0.15	44,44,45,45	0

6.3 Carbohydrates [i](#)

There are no monosaccharides 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
6	ACT	H	701	4/4	0.59	0.27	79,79,79,80	0
6	ACT	H	703	4/4	0.64	0.17	81,82,82,82	0
5	PO4	H	603	5/5	0.78	0.18	53,53,55,56	5
6	ACT	H	702	4/4	0.79	0.16	58,60,60,60	0
5	PO4	H	605	5/5	0.82	0.34	65,65,65,67	5
5	PO4	H	606	5/5	0.90	0.20	50,50,51,52	5
5	PO4	H	604	5/5	0.90	0.13	50,51,52,53	5
5	PO4	H	601	5/5	0.92	0.20	38,40,43,44	5
7	NA	H	501	1/1	0.93	0.17	52,52,52,52	0
5	PO4	H	602	5/5	0.94	0.15	42,42,45,46	5

6.5 Other polymers [i](#)

There are no such residues in this entry.