



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:05 AM UTC

PDB ID : 7Q8H / pdb_00007q8h
Title : Peptide EVCKKKK in complex with human cathepsin V C25A mutant
Authors : Loboda, J.; Sosnowski, P.; Tusar, L.; Vidmar, R.; Vizovisek, M.; Horvat, J.;
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Deposited on : 2021-11-11
Resolution : 1.75 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

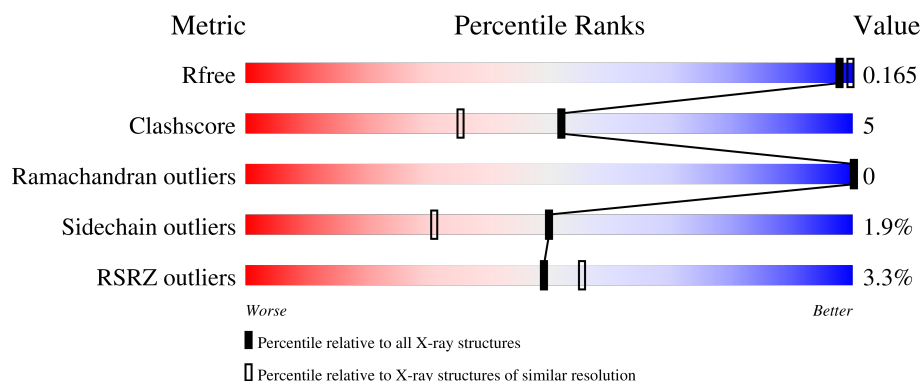
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	3183 (1.76-1.76)
Clashscore	190562	3299 (1.76-1.76)
Ramachandran outliers	187476	3274 (1.76-1.76)
Sidechain outliers	187428	3274 (1.76-1.76)
RSRZ outliers	180081	3183 (1.76-1.76)

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	AA	221	2% 85% 15%
1	BA	221	2% 89% 11%
2	PA	9	44% 67% 22% 11%
2	PB	9	11% 56% 11% 33%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 8321 atoms, of which 4282 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 Cathepsin L2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	AA	221	Total	C	H	N	O	S	1680	6	0
			3408	1091	1677	300	330	10			
1	BA	221	Total	C	H	N	O	S	1634	2	0
			3337	1073	1632	293	329	10			

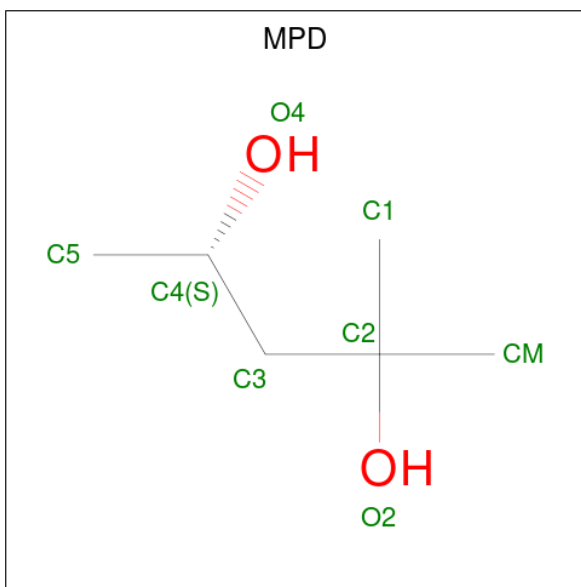
There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AA	25	ALA	CYS	engineered mutation	UNP O60911
AA	108	GLN	ASN	engineered mutation	UNP O60911
AA	179	GLN	ASN	engineered mutation	UNP O60911
BA	246	ALA	CYS	engineered mutation	UNP O60911
BA	329	GLN	ASN	engineered mutation	UNP O60911
BA	400	GLN	ASN	engineered mutation	UNP O60911

- Molecule 2 is a protein called EVCKKKK Peptide.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	PA	8	Total	C	H	N	O	S	74	0	1
			133	37	74	12	9	1			
2	PB	6	Total	C	H	N	O	S	59	0	1
			102	27	59	10	5	1			

- Molecule 3 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: C₆H₁₄O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	AA	1	Total C O 8 6 2	0	0
3	AA	1	Total C O 8 6 2	0	0
3	AA	1	Total C O 8 6 2	0	0
3	BA	1	Total C O 8 6 2	0	0
3	BA	1	Total C O 8 6 2	0	0

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

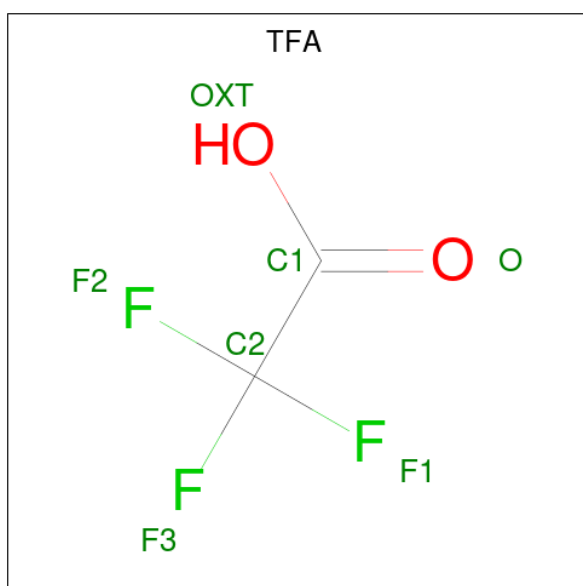
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	AA	1	Total Cl 1 1	0	0

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	AA	1	Total	C	O	0	0
			6	3	3		
5	BA	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is trifluoroacetic acid (CCD ID: TFA) (formula: $C_2HF_3O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	AA	1	Total	C	F	O	0	0
			7	2	3	2		
6	BA	1	Total	C	F	O	0	0
			7	2	3	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	BA	1	Total	C	F	O	0	0
			7	2	3	2		
6	BA	1	Total	C	F	O	0	0
			7	2	3	2		

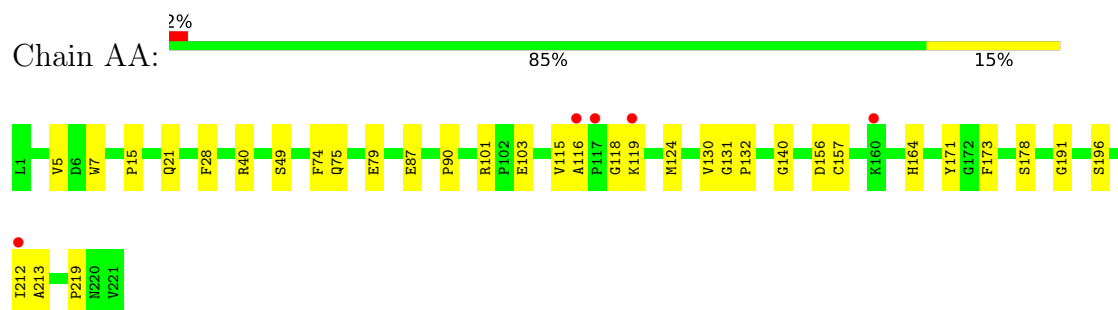
- Molecule 7 is water.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	AA	209	Total	H	O		418	0
			627	418	209			
7	BA	199	Total	H	O		398	0
			597	398	199			
7	PA	9	Total	H	O		18	0
			27	18	9			
7	PB	3	Total	H	O		6	0
			9	6	3			

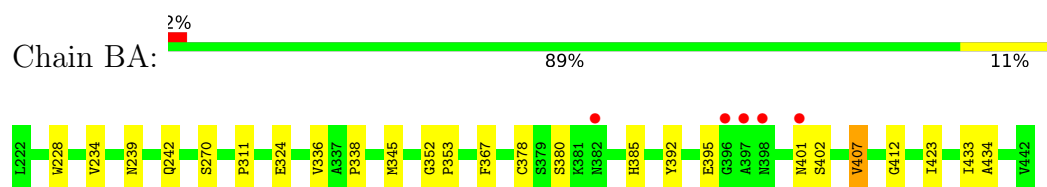
3 Residue-property plots [i](#)

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.

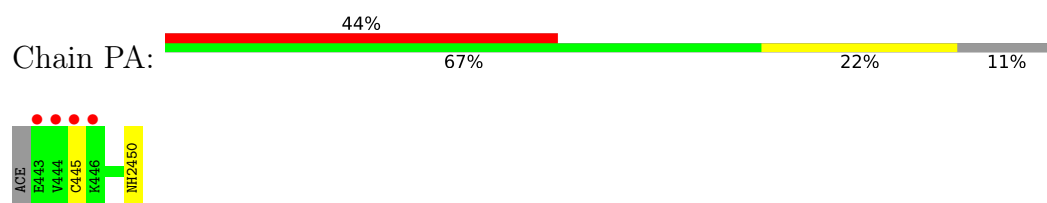
- Molecule 1: Cathepsin L2



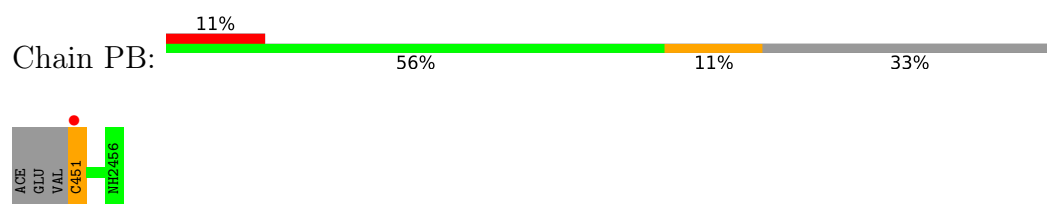
- Molecule 1: Cathepsin L2



- Molecule 2: EVCKKKK Peptide



- Molecule 2: EVCKKKK Peptide



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	93.75Å 93.75Å 124.29Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.87 – 1.75 46.87 – 1.75	Depositor EDS
% Data completeness (in resolution range)	100.0 (46.87-1.75) 99.9 (46.87-1.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.73 (at 1.75Å)	Xtriage
Refinement program	MAIN	Depositor
R, R_{free}	0.162 , 0.184 0.162 , 0.165	Depositor DCC
R_{free} test set	2804 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	20.5	Xtriage
Anisotropy	0.033	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 66.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	8321	wwPDB-VP
Average B, all atoms (Å ²)	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.97% 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: NH2, TFA, CL, MPD, GOL

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	AA	1.15	0/1784	1.25	8/2407 (0.3%)
1	BA	1.05	1/1747 (0.1%)	1.24	8/2361 (0.3%)
2	PA	0.62	0/57	1.01	0/71
2	PB	0.78	0/41	1.26	0/49
All	All	1.09	1/3629 (0.0%)	1.24	16/4888 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	BA	239	ASN	N-CA	5.22	1.52	1.46

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	118	GLY	CA-C-N	-6.69	114.14	122.84
1	AA	118	GLY	C-N-CA	-6.69	114.14	122.84
1	AA	49	SER	N-CA-C	6.26	118.38	108.67
1	AA	28	PHE	CA-CB-CG	-5.83	107.97	113.80
1	AA	191	GLY	CA-C-N	5.54	125.37	119.28
1	AA	191	GLY	C-N-CA	5.54	125.37	119.28
1	AA	90	PRO	N-CA-C	5.36	119.73	111.21
1	AA	130	VAL	N-CA-CB	-5.23	105.65	111.41
1	BA	234	VAL	N-CA-C	5.19	115.37	108.11
1	BA	367	PHE	CA-CB-CG	-5.11	108.69	113.80
1	BA	412	GLY	CA-C-N	5.11	125.18	119.87
1	BA	412	GLY	C-N-CA	5.11	125.18	119.87
1	BA	311	PRO	N-CA-C	5.09	119.48	111.38
1	BA	407	VAL	N-CA-C	5.09	115.17	107.75
1	BA	270	SER	N-CA-C	5.08	116.96	108.23
1	BA	385	HIS	ND1-CE1-NE2	5.04	113.44	108.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	1731	1677	1671	21	1
1	BA	1705	1632	1627	8	1
2	PA	59	74	71	1	0
2	PB	43	59	56	1	0
3	AA	24	0	42	3	0
3	BA	16	0	28	1	0
4	AA	1	0	0	0	0
5	AA	6	0	8	2	0
5	BA	6	0	8	0	0
6	AA	7	0	0	0	0
6	BA	21	0	0	1	0
7	AA	209	418	0	6	0
7	BA	199	398	0	2	0
7	PA	9	18	0	0	0
7	PB	3	6	0	0	0
All	All	4039	4282	3511	36	1

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 (36) 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)
5:AA:305:GOL:H32	7:AA:419:HOH:O	1.75	0.85
1:AA:87:GLU:HG3	7:AA:564:HOH:O	1.78	0.83
1:BA:433:ILE:HD12	1:BA:434:ALA:N	2.10	0.66
1:AA:101:ARG:HD2	1:AA:103:GLU:OE2	1.99	0.62
3:AA:304:MPD:O2	3:AA:304:MPD:H52	2.00	0.60
1:AA:164:HIS:HD1	2:PA:450:NH2:N	2.01	0.59
1:AA:140:GLY:HA3	7:AA:404:HOH:O	2.06	0.56
1:AA:212:ILE:HD12	1:AA:213:ALA:N	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:87:GLU:CG	7:AA:564:HOH:O	2.48	0.52
3:AA:304:MPD:H53	3:AA:304:MPD:H12	1.93	0.51
1:AA:21[B]:GLN:NE2	1:AA:21[B]:GLN:H	2.08	0.50
3:AA:304:MPD:H51	7:AA:528:HOH:O	2.11	0.50
6:BA:506:TFA:O	7:BA:601:HOH:O	2.19	0.50
1:BA:336:VAL:O	1:BA:338:PRO:HD3	2.12	0.49
3:BA:501:MPD:O4	3:BA:501:MPD:H13	2.12	0.48
1:AA:7:TRP:CE2	1:AA:131:GLY:HA2	2.50	0.47
1:AA:75[B]:GLN:O	1:AA:79:GLU:HG3	2.14	0.47
1:AA:115:VAL:O	1:AA:116:ALA:C	2.54	0.47
1:AA:40[B]:ARG:NH2	1:AA:40[B]:ARG:HG3	2.30	0.46
1:AA:40[B]:ARG:HG3	1:AA:40[B]:ARG:HH21	1.80	0.46
1:AA:5:VAL:HA	5:AA:305:GOL:H31	1.97	0.46
1:AA:116:ALA:CB	1:AA:119:LYS:HD2	2.47	0.45
1:AA:7:TRP:CG	1:AA:132:PRO:HD3	2.52	0.45
7:BA:730:HOH:O	2:PB:451:CYS:HB2	2.16	0.45
1:AA:75[A]:GLN:O	1:AA:79:GLU:HG3	2.17	0.44
1:BA:228:TRP:CE2	1:BA:352:GLY:HA2	2.51	0.44
1:BA:401:ASN:O	1:BA:402:SER:HB2	2.17	0.44
1:BA:228:TRP:CG	1:BA:353:PRO:HD3	2.53	0.44
1:BA:345:MET:HE3	1:BA:392:TYR:CE1	2.52	0.43
1:AA:124:MET:HE3	1:AA:171:TYR:CE1	2.54	0.42
1:AA:74:PHE:CZ	1:AA:219:PRO:HD3	2.55	0.41
1:AA:15:PRO:HD3	7:AA:410:HOH:O	2.19	0.41
1:AA:173:PHE:CD2	1:AA:178:SER:HA	2.56	0.41
1:AA:21[B]:GLN:H	1:AA:21[B]:GLN:HE21	1.68	0.40
1:BA:242:GLN:N	1:BA:242:GLN:CD	2.79	0.40
1:BA:407:VAL:HG21	1:BA:423:ILE:HD12	2.03	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:156:ASP:OD1	1:BA:380:SER:H[4_445]	1.59	0.01

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	AA	225/221 (102%)	216 (96%)	9 (4%)	0	100	100
1	BA	221/221 (100%)	214 (97%)	7 (3%)	0	100	100
2	PA	6/9 (67%)	6 (100%)	0	0	100	100
2	PB	4/9 (44%)	4 (100%)	0	0	100	100
All	All	456/460 (99%)	440 (96%)	16 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	AA	184/178 (103%)	182 (99%)	2 (1%)	65	52
1	BA	180/178 (101%)	177 (98%)	3 (2%)	53	36
2	PA	7/7 (100%)	6 (86%)	1 (14%)	3	0
2	PB	5/7 (71%)	4 (80%)	1 (20%)	1	0
All	All	376/370 (102%)	369 (98%)	7 (2%)	50	31

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AA	157	CYS
1	AA	196	SER

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Mol	Chain	Res	Type
1	BA	324	GLU
1	BA	378	CYS
1	BA	395	GLU
2	PA	445	CYS
2	PB	451	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	AA	179	GLN
1	AA	197	ASN
1	AA	220	ASN
1	BA	325	ASN
1	BA	398	ASN
1	BA	441	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 1 is monoatomic - leaving 11 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	MPD	AA	302	-	7,7,7	0.28	0	9,10,10	0.29	0
3	MPD	BA	502	-	7,7,7	0.35	0	9,10,10	0.43	0
5	GOL	BA	503	-	5,5,5	0.41	0	5,5,5	0.14	0
6	TFA	BA	506	-	6,6,6	2.37	1 (16%)	9,9,9	0.93	0
6	TFA	BA	504	-	6,6,6	0.94	1 (16%)	9,9,9	0.83	1 (11%)
3	MPD	AA	304	-	7,7,7	0.23	0	9,10,10	0.41	0
3	MPD	AA	301	-	7,7,7	0.23	0	9,10,10	0.40	0
5	GOL	AA	305	-	5,5,5	0.20	0	5,5,5	0.40	0
3	MPD	BA	501	-	7,7,7	0.42	0	9,10,10	0.38	0
6	TFA	AA	306	-	6,6,6	1.01	1 (16%)	9,9,9	1.23	1 (11%)
6	TFA	BA	505	-	6,6,6	0.94	1 (16%)	9,9,9	0.86	1 (11%)

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	MPD	AA	302	-	-	1/5/5/5	-
3	MPD	BA	502	-	-	0/5/5/5	-
5	GOL	BA	503	-	-	0/4/4/4	-
6	TFA	BA	506	-	-	1/6/6/6	-
6	TFA	BA	504	-	-	0/6/6/6	-
3	MPD	AA	304	-	-	3/5/5/5	-
3	MPD	AA	301	-	-	4/5/5/5	-
5	GOL	AA	305	-	-	0/4/4/4	-
3	MPD	BA	501	-	-	0/5/5/5	-
6	TFA	AA	306	-	-	2/6/6/6	-
6	TFA	BA	505	-	-	2/6/6/6	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	BA	506	TFA	OXT-C1	-5.64	1.10	1.30
6	AA	306	TFA	OXT-C1	-2.33	1.22	1.30
6	BA	505	TFA	OXT-C1	-2.28	1.22	1.30
6	BA	504	TFA	OXT-C1	-2.28	1.22	1.30

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	AA	306	TFA	OXT-C1-C2	2.37	121.83	112.58
6	BA	505	TFA	OXT-C1-C2	2.05	120.59	112.58
6	BA	504	TFA	OXT-C1-C2	2.03	120.50	112.58

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	AA	304	MPD	C2-C3-C4-O4
3	AA	304	MPD	C2-C3-C4-C5
6	BA	505	TFA	O-C1-C2-F1
6	AA	306	TFA	OXT-C1-C2-F3
3	AA	301	MPD	O2-C2-C3-C4
3	AA	302	MPD	O2-C2-C3-C4
6	AA	306	TFA	O-C1-C2-F3
6	BA	506	TFA	O-C1-C2-F1
3	AA	301	MPD	C2-C3-C4-O4
6	BA	505	TFA	OXT-C1-C2-F1
3	AA	301	MPD	C1-C2-C3-C4
3	AA	301	MPD	CM-C2-C3-C4
3	AA	304	MPD	C1-C2-C3-C4

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	BA	506	TFA	1	0
3	AA	304	MPD	3	0
5	AA	305	GOL	2	0
3	BA	501	MPD	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 [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	AA	221/221 (100%)	-0.44	5 (2%) 61 67	5, 10, 17, 40	7 (3%)
1	BA	221/221 (100%)	-0.13	5 (2%) 61 67	6, 12, 23, 53	3 (1%)
2	PA	7/9 (77%)	3.61	4 (57%) 0 0	9, 16, 79, 93	0
2	PB	5/9 (55%)	1.34	1 (20%) 3 3	11, 12, 19, 42	0
All	All	454/460 (98%)	-0.21	15 (3%) 49 55	5, 11, 21, 93	10 (2%)

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	PA	444	VAL	9.6
2	PA	445	CYS	6.5
2	PA	443	GLU	6.2
2	PB	451	CYS	5.6
1	BA	397	ALA	3.8
1	BA	396	GLY	3.5
1	BA	382	ASN	3.3
1	AA	160	LYS	2.9
1	BA	401	ASN	2.8
1	AA	117	PRO	2.8
2	PA	446	LYS	2.7
1	BA	398	ASN	2.2
1	AA	116	ALA	2.1
1	AA	119	LYS	2.1
1	AA	212	ILE	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(Å ²)	Q<0.9
5	GOL	AA	305	6/6	0.61	0.29	46,70,81,86	0
3	MPD	AA	301	8/8	0.78	0.22	57,62,70,71	0
6	TFA	BA	505	7/7	0.78	0.23	69,93,109,121	0
3	MPD	AA	302	8/8	0.87	0.16	37,50,58,62	0
6	TFA	BA	504	7/7	0.87	0.26	105,109,114,115	0
3	MPD	AA	304	8/8	0.87	0.21	61,66,73,77	0
5	GOL	BA	503	6/6	0.89	0.17	38,43,50,54	0
6	TFA	AA	306	7/7	0.89	0.11	27,36,41,54	0
6	TFA	BA	506	7/7	0.89	0.17	22,48,69,70	0
3	MPD	BA	501	8/8	0.90	0.13	28,32,38,38	0
3	MPD	BA	502	8/8	0.90	0.11	24,30,35,36	0
4	CL	AA	303	1/1	0.99	0.04	24,24,24,24	0

6.5 Other polymers [i](#)

There are no such residues in this entry.