



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:27 AM UTC

PDB ID : 25C8 / pdb_000025c8
Title : CATALYTIC ANTIBODY 5C8, FAB-HAPTEN COMPLEX
Authors : Gruber, K.; Wilson, I.A.
Deposited on : 1998-03-18
Resolution : 2.00 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
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

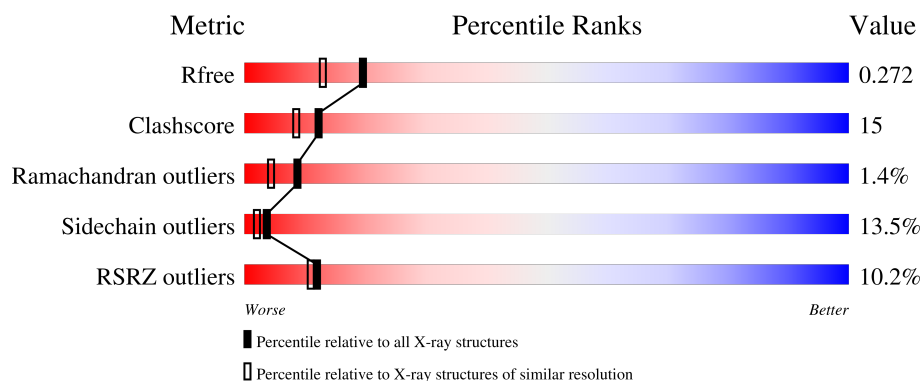
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	L	212	9% 65% 28% 8%
2	H	217	11% 61% 35% .

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3507 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 IGG 5C8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	212	Total	C	N	O	S	0	0	0
			1625	1008	274	335	8			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	32	ASN	TYR	conflict	UNP P01837
L	94	SER	PHE	conflict	UNP P01837
L	96	TYR	HIS	conflict	UNP P01837

- Molecule 2 is a protein called IGG 5C8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	217	Total	C	N	O	S	46	0	0
			1626	1028	262	330	6			

There are 24 discrepancies between the modelled and reference sequences:

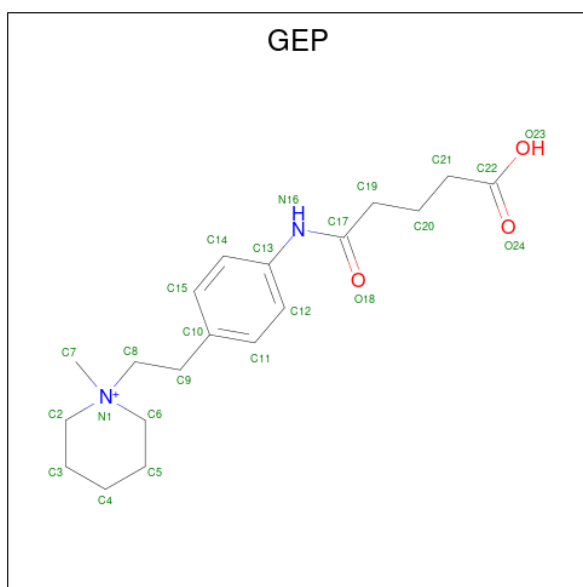
Chain	Residue	Modelled	Actual	Comment	Reference
H	3	GLN	LYS	conflict	UNP P01869
H	5	GLN	LEU	conflict	UNP P01869
H	6	GLN	GLU	conflict	UNP P01869
H	14	PRO	SER	conflict	UNP P01869
H	40	LYS	ARG	conflict	UNP P01869
H	49	ALA	GLY	conflict	UNP P01869
H	50	GLN	ARG	conflict	UNP P01869
H	56	ASN	GLU	conflict	UNP P01869
H	57	THR	ILE	conflict	UNP P01869
H	66	LYS	THR	conflict	UNP P01869
H	75	SER	THR	conflict	UNP P01869
H	81	HIS	GLN	conflict	UNP P01869
H	87	SER	THR	conflict	UNP P01869

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Chain	Residue	Modelled	Actual	Comment	Reference
H	93	ALA	VAL	conflict	UNP P01869
H	94	ALA	ARG	conflict	UNP P01869
H	95	ASP	ARG	conflict	UNP P01869
H	96	PRO	GLY	conflict	UNP P01869
H	97	PRO	TYR	conflict	UNP P01869
H	98	TYR	GLY	conflict	UNP P01869
H	99	TYR	SER	conflict	UNP P01869
H	100	GLY	SER	conflict	UNP P01869
H	100A	HIS	GLN	conflict	UNP P01869
H	100B	GLY	GLU	conflict	UNP P01869
H	101	ASP	PRO	conflict	UNP P01869

- Molecule 3 is N-METHYL-N-(PARA-GLUTARAMIDOPHENYL-ETHYL)-PIPERIDINIUM ION (CCD ID: GEP) (formula: $C_{19}H_{29}N_2O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	L	1	Total	C	N	O	0	0
			24	19	2	3		

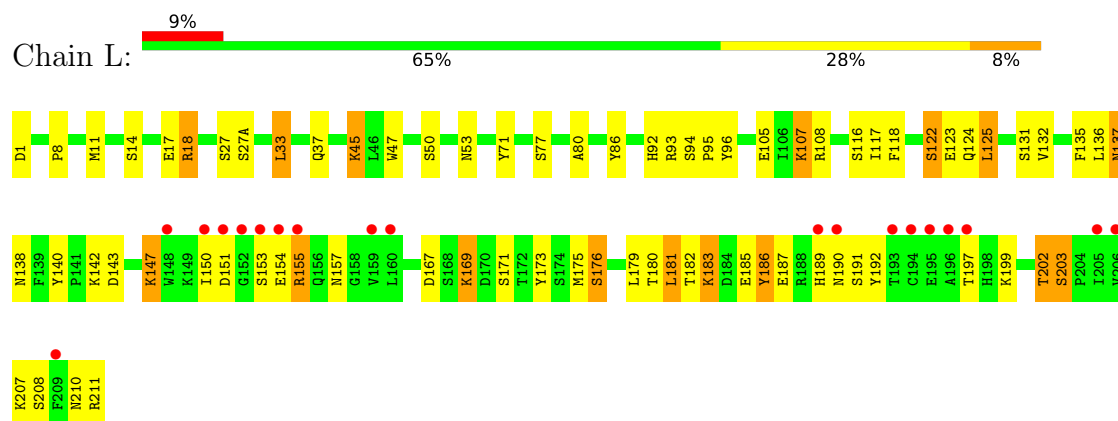
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	L	121	Total	O	0	0
			121	121		
4	H	111	Total	O	0	0
			111	111		

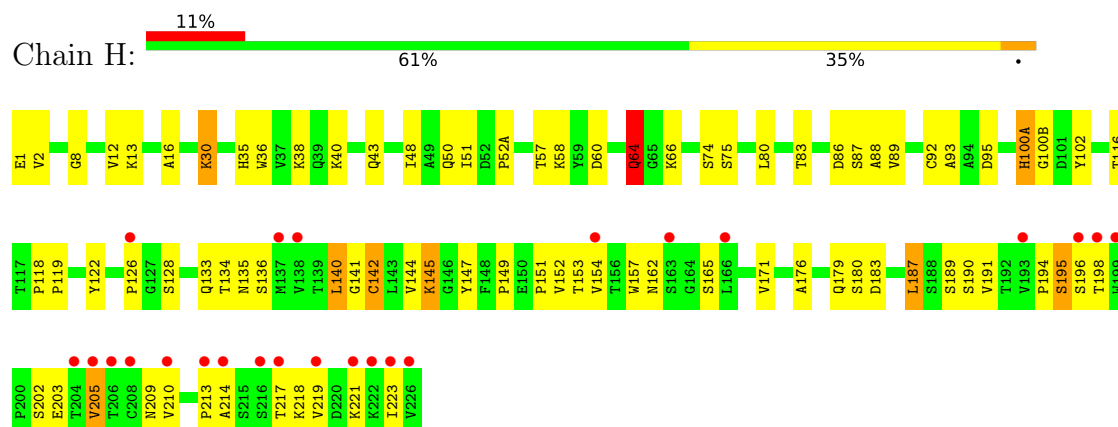
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: IGG 5C8



• Molecule 2: IGG 5C8



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	112.00Å 80.00Å 64.90Å 90.00° 118.00° 90.00°	Depositor
Resolution (Å)	25.00 – 2.00 25.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	96.7 (25.00-2.00) 93.8 (25.00-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.19 (at 1.90Å)	Xtriage
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.229 , 0.292 0.220 , 0.272	Depositor DCC
R_{free} test set	2902 reflections (7.58%)	wwPDB-VP
Wilson B-factor (Å ²)	30.5	Xtriage
Anisotropy	0.016	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 77.8	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	0.95	EDS
Total number of atoms	3507	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.89% 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: GEP

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	L	0.43	0/1664	0.91	3/2260 (0.1%)
2	H	0.47	0/1671	0.90	7/2291 (0.3%)
All	All	0.45	0/3335	0.91	10/4551 (0.2%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	137	ASN	N-CA-C	6.92	121.15	110.42
2	H	145	LYS	N-CA-C	6.69	120.08	109.50
2	H	60	ASP	N-CA-C	-6.50	101.45	109.65
2	H	95	ASP	N-CA-C	-6.33	101.34	110.08
2	H	92	CYS	N-CA-C	-5.91	100.06	109.76
1	L	186	TYR	N-CA-C	5.58	117.17	111.14
1	L	80	ALA	N-CA-C	5.43	117.90	111.33
2	H	8	GLY	N-CA-C	5.36	120.70	112.51
2	H	2	VAL	N-CA-C	-5.21	102.79	109.30
2	H	100(A)	HIS	N-CA-C	5.15	117.02	109.24

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	L	1625	0	1548	53	0
2	H	1626	0	1571	49	0
3	L	24	0	28	2	0
4	H	111	0	0	2	0
4	L	121	0	0	2	0
All	All	3507	0	3147	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 15.

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)
1:L:167:ASP:OD2	1:L:169:LYS:HG2	1.75	0.87
2:H:154:VAL:HG22	2:H:210:VAL:HG22	1.66	0.77
1:L:150:ILE:HD11	1:L:179:LEU:HD21	1.66	0.77
1:L:150:ILE:HD12	1:L:155:ARG:HG3	1.73	0.70
1:L:142:LYS:HG3	1:L:173:TYR:CD2	2.27	0.69
1:L:124:GLN:HE22	1:L:131:SER:CB	2.08	0.66
1:L:124:GLN:HE22	1:L:131:SER:HB2	1.59	0.66
1:L:18:ARG:HH11	1:L:18:ARG:HG3	1.60	0.65
1:L:182:THR:OG1	1:L:185:GLU:HG3	1.97	0.65
3:L:212:GEP:H12	3:L:212:GEP:O18	1.97	0.64
1:L:147:LYS:HD3	1:L:154:GLU:OE2	1.98	0.64
2:H:151:PRO:O	2:H:213:PRO:HD2	1.99	0.63
2:H:162:ASN:HD21	2:H:205:VAL:HA	1.64	0.62
2:H:198:THR:O	2:H:203:GLU:HB2	2.00	0.61
1:L:8:PRO:CG	1:L:11:MET:HE2	2.30	0.60
1:L:135:PHE:C	1:L:136:LEU:HD12	2.26	0.60
2:H:149:PRO:HD2	2:H:214:ALA:CB	2.31	0.60
1:L:45:LYS:HD3	1:L:47:TRP:HZ3	1.68	0.59
2:H:119:PRO:HB3	2:H:147:TYR:HB3	1.84	0.58
1:L:94:SER:HA	1:L:95:PRO:C	2.28	0.57
2:H:151:PRO:HD2	2:H:213:PRO:HG2	1.88	0.56
2:H:38:LYS:HB2	2:H:48:ILE:HD11	1.87	0.56
2:H:100(A):HIS:ND1	2:H:100(B):GLY:N	2.54	0.55
1:L:18:ARG:HG3	1:L:18:ARG:NH1	2.20	0.55
1:L:190:ASN:O	1:L:210:ASN:HA	2.07	0.54
2:H:126:PRO:HD3	2:H:140:LEU:HD23	1.89	0.54
2:H:35:HIS:HE1	2:H:50:GLN:HE21	1.54	0.54
1:L:182:THR:HG23	1:L:185:GLU:OE2	2.08	0.53
2:H:194:PRO:C	2:H:196:SER:H	2.17	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:157:ASN:HB3	4:L:333:HOH:O	2.07	0.52
2:H:89:VAL:HG23	4:H:271:HOH:O	2.09	0.52
2:H:87:SER:O	2:H:88:ALA:HB2	2.10	0.52
1:L:8:PRO:HG2	1:L:11:MET:HE2	1.92	0.51
2:H:171:VAL:HG23	2:H:191:VAL:HG23	1.94	0.50
2:H:153:THR:O	2:H:210:VAL:HA	2.11	0.50
2:H:93:ALA:HA	2:H:102:TYR:O	2.12	0.50
2:H:30:LYS:HA	2:H:52(A):PRO:HB2	1.92	0.50
1:L:167:ASP:OD2	1:L:169:LYS:CG	2.54	0.50
1:L:147:LYS:HD3	1:L:154:GLU:CD	2.37	0.49
1:L:150:ILE:CD1	1:L:181:LEU:HD21	2.42	0.49
2:H:180:SER:O	2:H:183:ASP:HB2	2.13	0.48
1:L:175:MET:HG2	1:L:176:SER:N	2.28	0.48
2:H:142:CYS:N	2:H:189:SER:O	2.46	0.48
2:H:51:ILE:HG13	2:H:57:THR:HG22	1.96	0.48
2:H:187:LEU:C	2:H:187:LEU:HD23	2.39	0.48
1:L:131:SER:OG	1:L:180:THR:HG22	2.15	0.47
1:L:186:TYR:HA	1:L:192:TYR:OH	2.15	0.47
2:H:157:TRP:HZ3	2:H:223:ILE:HG13	1.80	0.47
2:H:162:ASN:O	2:H:165:SER:HB2	2.15	0.47
2:H:12:VAL:HG12	2:H:16:ALA:HB3	1.97	0.47
2:H:40:LYS:O	2:H:43:GLN:HB2	2.15	0.47
1:L:202:THR:HG23	1:L:203:SER:H	1.80	0.46
1:L:123:GLU:HG2	2:H:122:TYR:CD1	2.50	0.46
1:L:14:SER:O	1:L:17:GLU:HB2	2.16	0.46
1:L:117:ILE:HG12	1:L:118:PHE:N	2.30	0.46
2:H:64:GLN:H	2:H:64:GLN:HG3	1.36	0.45
2:H:179:GLN:O	2:H:180:SER:HB3	2.17	0.45
1:L:180:THR:HG21	2:H:145:LYS:NZ	2.32	0.45
2:H:51:ILE:O	2:H:52(A):PRO:HD3	2.17	0.45
1:L:136:LEU:HD12	1:L:136:LEU:N	2.32	0.45
2:H:12:VAL:HG12	2:H:13:LYS:N	2.32	0.45
1:L:8:PRO:CD	1:L:11:MET:HE2	2.47	0.44
1:L:33:LEU:HD22	1:L:71:TYR:CG	2.52	0.44
1:L:96:TYR:CE2	2:H:50:GLN:NE2	2.86	0.44
1:L:210:ASN:O	1:L:211:ARG:HB2	2.17	0.44
2:H:141:GLY:HA2	2:H:190:SER:HA	1.98	0.44
1:L:123:GLU:HG2	2:H:122:TYR:CE1	2.53	0.44
1:L:92:HIS:CD2	1:L:93:ARG:HG2	2.53	0.44
1:L:167:ASP:O	1:L:171:SER:HA	2.17	0.44
2:H:162:ASN:CB	2:H:165:SER:HB2	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:37:GLN:HG3	1:L:86:TYR:CE2	2.53	0.43
1:L:151:ASP:OD2	1:L:189:HIS:HD2	2.00	0.43
1:L:142:LYS:HG3	1:L:173:TYR:CG	2.53	0.43
1:L:202:THR:HG23	1:L:203:SER:N	2.32	0.43
2:H:35:HIS:ND1	2:H:50:GLN:HB2	2.33	0.43
1:L:183:LYS:H	1:L:183:LYS:HG3	1.34	0.43
2:H:36:TRP:CE2	2:H:80:LEU:HB2	2.54	0.42
2:H:83:THR:O	2:H:86:ASP:HB2	2.18	0.42
2:H:12:VAL:CG1	2:H:16:ALA:HB3	2.49	0.42
2:H:50:GLN:OE1	2:H:58:LYS:HD2	2.20	0.42
1:L:122:SER:HA	1:L:125:LEU:HB2	2.01	0.42
1:L:137:ASN:HB2	4:L:303:HOH:O	2.19	0.42
1:L:180:THR:HG21	2:H:145:LYS:HZ3	1.84	0.42
3:L:212:GEP:O18	3:L:212:GEP:C12	2.64	0.42
1:L:96:TYR:HE2	2:H:50:GLN:NE2	2.16	0.42
1:L:33:LEU:HD22	1:L:71:TYR:CD2	2.54	0.42
1:L:147:LYS:HE3	1:L:154:GLU:OE1	2.19	0.42
2:H:118:PRO:HB3	2:H:217:THR:HG21	2.03	0.41
1:L:107:LYS:HA	1:L:140:TYR:OH	2.20	0.41
2:H:176:ALA:HA	2:H:187:LEU:HB2	2.01	0.41
1:L:187:GLU:H	1:L:187:GLU:HG2	1.60	0.41
1:L:50:SER:HB2	1:L:53:ASN:ND2	2.36	0.41
2:H:30:LYS:HB3	4:H:251:HOH:O	2.20	0.41
2:H:35:HIS:CE1	2:H:50:GLN:HG3	2.55	0.41
2:H:149:PRO:HD2	2:H:214:ALA:HB3	2.02	0.41
1:L:169:LYS:HG2	1:L:169:LYS:H	1.77	0.40
2:H:194:PRO:C	2:H:196:SER:N	2.79	0.40
1:L:190:ASN:HB2	1:L:211:ARG:H	1.86	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	L	210/212 (99%)	199 (95%)	10 (5%)	1 (0%)	24	21
2	H	215/217 (99%)	197 (92%)	13 (6%)	5 (2%)	5	2
All	All	425/429 (99%)	396 (93%)	23 (5%)	6 (1%)	9	4

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	128	SER
2	H	135	ASN
1	L	138	ASN
2	H	64	GLN
2	H	195	SER
2	H	134	THR

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	L	186/186 (100%)	157 (84%)	29 (16%)	2	1
2	H	184/184 (100%)	163 (89%)	21 (11%)	5	3
All	All	370/370 (100%)	320 (86%)	50 (14%)	4	2

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

Mol	Chain	Res	Type
1	L	1	ASP
1	L	18	ARG
1	L	27	SER
1	L	27(A)	SER
1	L	33	LEU
1	L	45	LYS
1	L	77	SER
1	L	105	GLU
1	L	107	LYS
1	L	108	ARG

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Mol	Chain	Res	Type
1	L	116	SER
1	L	122	SER
1	L	125	LEU
1	L	132	VAL
1	L	143	ASP
1	L	147	LYS
1	L	153	SER
1	L	155	ARG
1	L	169	LYS
1	L	176	SER
1	L	181	LEU
1	L	183	LYS
1	L	191	SER
1	L	197	THR
1	L	199	LYS
1	L	202	THR
1	L	203	SER
1	L	207	LYS
1	L	208	SER
2	H	1	GLU
2	H	30	LYS
2	H	64	GLN
2	H	66	LYS
2	H	74	SER
2	H	75	SER
2	H	116	THR
2	H	133	GLN
2	H	136	SER
2	H	140	LEU
2	H	142	CYS
2	H	144	VAL
2	H	152	VAL
2	H	187	LEU
2	H	195	SER
2	H	202	SER
2	H	205	VAL
2	H	209	ASN
2	H	218	LYS
2	H	219	VAL
2	H	221	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	32	ASN
1	L	38	GLN
1	L	53	ASN
1	L	124	GLN
1	L	161	ASN
2	H	5	GLN
2	H	39	GLN
2	H	50	GLN

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](#)

1 ligand is 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	$\# Z > 2$
3	GEP	L	212	-	25,25,25	1.05	1 (4%)	33,33,33	1.05	2 (6%)

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	GEP	L	212	-	-	3/16/26/26	0/2/2/2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L	212	GEP	C13-N16	3.22	1.48	1.41

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L	212	GEP	C19-C17-N16	3.19	120.15	114.59
3	L	212	GEP	C13-N16-C17	-2.67	122.79	127.52

There are no chirality outliers.

All (3) torsion outliers are listed below:

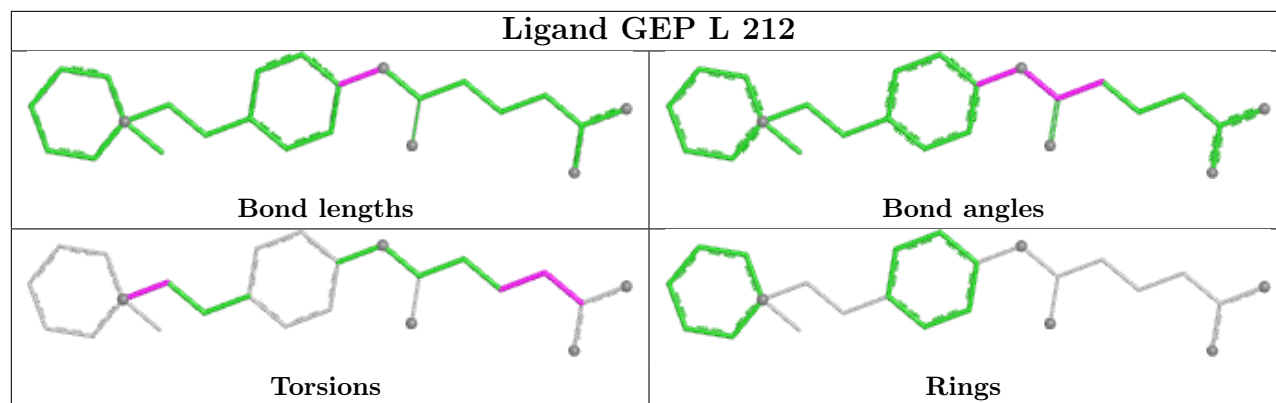
Mol	Chain	Res	Type	Atoms
3	L	212	GEP	C9-C8-N1-C7
3	L	212	GEP	C20-C21-C22-O23
3	L	212	GEP	C19-C20-C21-C22

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	L	212	GEP	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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	L	212/212 (100%)	0.46	19 (8%) 15 14	18, 38, 71, 99	0
2	H	210/217 (96%)	0.40	24 (11%) 10 9	14, 34, 75, 84	0
All	All	422/429 (98%)	0.43	43 (10%) 12 11	14, 36, 73, 99	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	223	ILE	4.7
1	L	150	ILE	4.1
1	L	193	THR	3.8
2	H	217	THR	3.8
2	H	206	THR	3.8
1	L	152	GLY	3.5
2	H	214	ALA	3.4
2	H	210	VAL	3.3
2	H	213	PRO	3.2
2	H	208	CYS	3.1
2	H	226	VAL	3.0
2	H	205	VAL	3.0
2	H	199	TRP	3.0
1	L	190	ASN	2.9
1	L	189	HIS	2.9
1	L	155	ARG	2.9
1	L	209	PHE	2.9
1	L	195	GLU	2.9
1	L	151	ASP	2.8
1	L	205	ILE	2.8
2	H	222	LYS	2.8
2	H	193	VAL	2.7
2	H	198	THR	2.7
1	L	206	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
2	H	221	LYS	2.7
2	H	216	SER	2.6
2	H	154	VAL	2.6
1	L	196	ALA	2.4
1	L	153	SER	2.4
2	H	163	SER	2.4
2	H	126	PRO	2.4
2	H	166	LEU	2.3
2	H	219	VAL	2.3
2	H	204	THR	2.3
1	L	160	LEU	2.3
1	L	197	THR	2.2
1	L	154	GLU	2.2
1	L	148	TRP	2.2
2	H	137	MET	2.2
1	L	159	VAL	2.1
2	H	138	VAL	2.1
1	L	194	CYS	2.0
2	H	196	SER	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

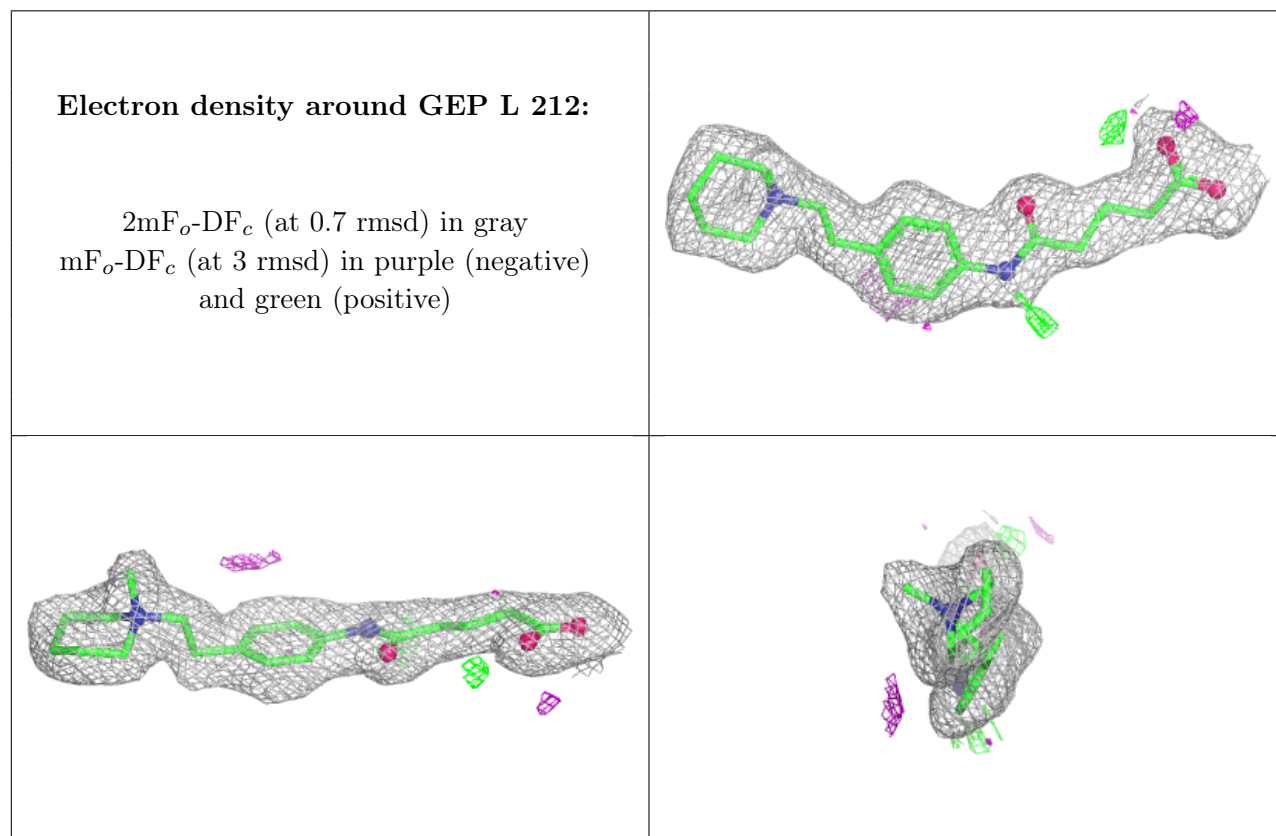
6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	GEP	L	212	24/24	0.93	0.07	18,23,38,42	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers

as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers [i](#)

There are no such residues in this entry.